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(54) Title: HUMAN TYPE II DIABETES GENE-Kv CHANNEL-INTERACTING PROTEIN (KChIP1) LOCATED ON CHROMOSOME 5

(57) Abstract: Association of Type II diabetes and a locus on chromosome 5 is disclosed. In particular, the gene KChIP1 within this locus is shown by linkage analysis to be a susceptibility gene for Type II diabetes. Pathway targeting for drug delivery and diagnosis applications in identifying those who have Type II diabetes or are at risk of developing Type II diabetes, in particular those that are non-obese are described.

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HUMAN TYPE II DIABETES GENE – K<sub>v</sub> CHANNEL-INTERACTING  
PROTEIN (KChIP1) LOCATED ON CHROMOSOME 5

RELATED APPLICATIONS

This application claims priority to U.S. Provisional Application NO.  
5 60/477,111 filed June 9, 2003, and to U.S. Provisional Application NO. 60/449,945,  
filed on February 25, 2003, and also to U.S. Provisional Application NO. 60/423,545,  
filed on November 1, 2002, the entire contents of all applications are incorporated  
herein by reference.

10 BACKGROUND OF THE INVENTION

Diabetes mellitus, a metabolic disease in which carbohydrate utilization is  
reduced and lipid and protein utilization is enhanced, is caused by an absolute or  
relative deficiency of insulin. In the more severe cases, diabetes is characterized by  
chronic hyperglycemia, glycosuria, water and electrolyte loss, ketoacidosis and coma.

15 Long term complications include development of neuropathy, retinopathy,  
nephropathy, generalized degenerative changes in large and small blood vessels and  
increased susceptibility to infection. The most common form of diabetes is Type II,  
non-insulin-dependent diabetes that is characterized by hyperglycemia due to  
impaired insulin secretion and insulin resistance in target tissues. Both genetic and  
20 environmental factors contribute to the disease. For example, obesity plays a major  
role in the development of the disease. Type II diabetes is often a mild form of  
diabetes mellitus of gradual onset.

The health implications of Type II diabetes are enormous. In 1995, there were  
135 million adults with diabetes worldwide. It is estimated that close to 300 million  
25 will have diabetes in the year 2025. (King H., *et al.*, *Diabetes Care*, 21(9): 1414-1431  
(1998)). The prevalence of Type II diabetes in the adult population in Iceland is 2.5%  
(Vilbergsson, S., *et al.*, *Diabet. Med.*, 14(6): 491-498 (1997)), which comprises  
approximately 5,000 people over the age of 34 who have the disease. The high  
prevalence of the disease and increasing population affected shows an unmet medical  
30 need to define the genetic factors involved in Type II diabetes to more precisely  
define the associated risk factors. Also needed are therapeutic agents for prevention  
of Type II diabetes.



## SUMMARY OF THE INVENTION

As described herein, a locus on chromosome 5q35 has been demonstrated which plays a major role in Type II diabetes. The locus, referred to as the Type II diabetes locus, comprises a nucleic acid that encodes, KChIP1.

5 The present invention relates to genes located within the Type II diabetes - related locus, particularly nucleic acids comprising the KChIP1 gene, and the amino acids encoded by these nucleic acids. The invention further relates to pathway targeting for drug delivery and diagnosis in identifying those who have Type II diabetes and those at risk of developing Type II diabetes. Also described are  
10 haplotypes and SNPs that can be used to identify individuals with Type II diabetes or at risk of developing Type II diabetes, particularly in those that are non-obese. As a consequence, intervention can be prescribed to these individuals before symptoms of the disease present, *e.g.*, dietary changes, exercise and/or medication. Identification of genes in the Type II diabetes locus can pave the way for a better understanding of  
15 the disease process, which in turn can lead to improved diagnostics and therapeutics.

The present invention pertains to methods of diagnosing a susceptibility to Type II diabetes in an individual, comprising detecting a polymorphism in a KChIP1 nucleic acid, wherein the presence of the polymorphism in the nucleic acid is indicative of a susceptibility to Type II diabetes. The invention additionally pertains  
20 to methods of diagnosing Type II diabetes in an individual, comprising detecting a polymorphism in a KChIP1 nucleic acid, wherein the presence of the polymorphism in the nucleic acid is indicative of Type II diabetes. In one embodiment, in diagnosing Type II diabetes or susceptibility to Type II diabetes by detecting the presence of a polymorphism in a KChIP1 nucleic acid, the presence of the  
25 polymorphism in the KChIP1 nucleic acid can be indicated, for example, by the presence of one or more of the polymorphisms indicated in Table 10.

In other embodiments, the invention relates to methods of diagnosing a susceptibility to Type II diabetes in an individual, comprising detecting an alteration in the expression or composition of a polypeptide encoded by a KChIP1 nucleic acid  
30 in a test sample, in comparison with the expression or composition of a polypeptide encoded by a KChIP1 nucleic acid in a control sample, wherein the presence of an

alteration in expression or composition of the polypeptide in the test sample is indicative of a susceptibility to Type II diabetes. The invention additionally relates to a method of diagnosing Type II diabetes in an individual, comprising detecting an alteration in the expression or composition of a polypeptide encoded by a KChIP1 nucleic acid in a test sample, in comparison with the expression or composition of a polypeptide encoded by KChIP1 nucleic acid in a control sample, wherein the presence of an alteration in expression or composition of the polypeptide in the test sample is indicative of Type II diabetes.

The invention also relates to an isolated nucleic acid molecule comprising a KChIP1 nucleic acid (*e.g.*, SEQ ID NO: 1 or the complement of SEQ ID NO: 1). In certain embodiments, the KChIP1 nucleic acid comprises one or more nucleotide sequence(s) selected from the group of nucleic acid sequences as shown in Table 10 (*e.g.*, SEQ ID NOs: 114-258) and the complements of the group of nucleic acid sequences as shown in Table 10. For example, in certain embodiments, the nucleotide sequence contains one or more polymorphism(s), such as those shown in Table 10. In another embodiment, the invention relates to an isolated nucleic acid molecule which hybridizes under high stringency conditions to a nucleotide sequence selected from the group of SEQ ID NO: 1 and the complement of SEQ ID NO: 1. In certain embodiments, the isolated nucleic acid molecule hybridizes under high stringency conditions to a nucleotide sequence comprising one or more nucleotide sequence(s) selected from the group of nucleic acid sequences as shown in Table 10 (*e.g.*, SEQ ID NOs: 114-258) and the complements of the group of nucleic acid sequences as shown in Table 10. For example, in certain embodiments, the nucleotide sequence contains one or more polymorphism(s), such as those shown in Table 10.

Also contemplated by the invention is a method of assaying for the presence of a first nucleic acid molecule in a sample, comprising contacting said sample with a second nucleic acid molecule, where the second nucleic acid molecule comprises at least one (or more) nucleic acid sequence(s) selected from the group of SEQ ID NOs: 1 and 114-258, inclusive, wherein the nucleic acid sequence hybridizes to the first nucleic acid under high stringency conditions. In certain embodiments, the second

nucleic acid molecule contains one or more polymorphism(s), such as those shown in Table 10.

The invention also relates to a vector comprising an isolated nucleic acid molecule of the invention (*e.g.*, SEQ ID NOs: 1 and 114-258; optionally including one or more of the polymorphisms shown in Table 10) operably linked to a regulatory sequence, as well as to a recombinant host cell comprising the vector. The invention also provides a method for producing a polypeptide encoded by an isolated nucleic acid molecule having a polymorphism, comprising culturing the recombinant host cell under conditions suitable for expression of the nucleic acid molecule.

Also contemplated by the invention is a method of assaying for the presence of a polypeptide encoded by an isolated nucleic acid molecule of the invention in a sample, the method comprising contacting the sample with an antibody that specifically binds to the encoded polypeptide.

The invention further pertains to a method of identifying an agent that alters expression of a KChIP1 nucleic acid, comprising: contacting a solution containing a nucleic acid comprising the promoter region of the KChIP1 gene operably linked to a reporter gene, with an agent to be tested; assessing the level of expression of the reporter gene in the presence of the agent; and comparing the level of expression of the reporter gene in the presence of the agent with a level of expression of the reporter gene in the absence of the agent; wherein if the level of expression of the reporter gene in the presence of the agent differs, by an amount that is statistically significant, from the level of expression in the absence of the agent, then the agent is an agent that alters expression of the KChIP1 gene or nucleic acid. An agent identified by this method is also contemplated.

The invention additionally comprises a method of identifying an agent that alters expression of a KChIP1 nucleic acid, comprising contacting a solution containing a nucleic acid of the invention or a derivative or fragment thereof, with an agent to be tested; comparing expression of the nucleic acid, derivative or fragment in the presence of the agent with expression of the nucleic acid, derivative or fragment in the absence of the agent; wherein if expression of the nucleic acid, derivative or fragment in the presence of the agent differs, by an amount that is statistically

significant, from the expression in the absence of the agent, then the agent is an agent that alters expression of the KChIP1 nucleic acid. In certain embodiments, the expression of the nucleic acid, derivative or fragment in the presence of the agent comprises expression of one or more splicing variants(s) that differ in kind or in quantity from the expression of one or more splicing variant(s) the absence of the agent. Agents identified by this method are also contemplated.

Representative agents that alter expression of a KChIP1 nucleic acid contemplated by the invention include, for example, antisense nucleic acids to a KChIP1 gene or nucleic acid; a KChIP1 gene or nucleic acid; a KChIP1 polypeptide; a KChIP1 gene or nucleic acid receptor, or other receptor; a KChIP1 binding agent; a peptidomimetic; a fusion protein; a prodrug thereof; an antibody; and a ribozyme. A method of altering expression of a KChIP1 nucleic acid, comprising contacting a cell containing a nucleic acid with such an agent is also contemplated.

The invention further pertains to a method of identifying a polypeptide which interacts with a KChIP1 polypeptide (*e.g.*, a KChIP1 polypeptide encoded by a nucleic acid of the invention, such as a nucleic acid comprising one or more polymorphism(s) indicated in Table 10), comprising employing a yeast two-hybrid system using a first vector which comprises a nucleic acid encoding a DNA binding domain and a KChIP1 polypeptide, splicing variant, or a fragment or derivative thereof, and a second vector which comprises a nucleic acid encoding a transcription activation domain and a nucleic acid encoding a test polypeptide. If transcriptional activation occurs in the yeast two-hybrid system, the test polypeptide is a polypeptide, which interacts with a KChIP1 polypeptide.

In certain methods of the invention, a Type II diabetes therapeutic agent is used. The Type II diabetes therapeutic agent can be an agent that alters (*e.g.*, enhances or inhibits) KChIP1 polypeptide activity and/or KChIP1 nucleic acid expression, as described herein (*e.g.*, a nucleic acid agonist or antagonist).

Type II diabetes therapeutic agents can alter polypeptide activity or nucleic acid expression of a KChIP1 nucleic acid by a variety of means, such as, for example, by providing additional polypeptide or upregulating the transcription or translation of the nucleic acid encoding the KChIP1 polypeptide; by altering posttranslational

processing of the KChIP1 polypeptide; by altering transcription of splicing variants; or by interfering with polypeptide activity (*e.g.*, by binding to the KChIP1 polypeptide, or by binding to another polypeptide that interacts with KChIP1, such as a KChIP1 binding agent as described herein), by altering (*e.g.*, downregulating) the expression, transcription or translation of a nucleic acid encoding KChIP1; or by  
5 altering interaction among KChIP1 and a KChIP1 binding agent.

In a further embodiment, the invention relates to Type II diabetes therapeutic agent, such as an agent selected from the group consisting of: a KChIP1 nucleic acid or fragment or derivative thereof; a polypeptide encoded by a KChIP1 nucleic acid  
10 (*e.g.*, encoded by a KChIP1 nucleic acid having one or more polymorphism(s) such as those set forth in Table 10); a KChIP1 receptor; a KChIP1 binding agent; a peptidomimetic; a fusion protein; a prodrug; an antibody; an agent that alters KChIP1 gene or nucleic acid expression; an agent that alters activity of a polypeptide encoded by a KChIP1 gene or nucleic acid; an agent that alters posttranscriptional processing  
15 of a polypeptide encoded by a KChIP1 gene or nucleic acid; an agent that alters interaction of a KChIP1 polypeptide with a KChIP1 binding agent or receptor; an agent that alters transcription of splicing variants encoded by a KChIP1 gene or nucleic acid; and ribozymes. The invention also relates to pharmaceutical compositions comprising at least one Type II diabetes therapeutic agent as described  
20 herein.

The invention also pertains to a method of treating a disease or condition associated with a KChIP1 polypeptide (*e.g.*, Type II diabetes) in an individual, comprising administering a Type II diabetes therapeutic agent to the individual, in a therapeutically effective amount. In certain embodiments, the Type II diabetes  
25 therapeutic agent is a KChIP1 agonist; in other embodiments, the Type II diabetes therapeutic agent is a KChIP1 antagonist. The invention additionally pertains to use of a Type II diabetes therapeutic agent as described herein, for the manufacture of a medicament for use in the treatment of Type II diabetes, such as by the methods described herein.

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A transgenic animal comprising a nucleic acid selected from the group consisting of: an exogenous KChIP1 gene or nucleic acid and a nucleic acid encoding a KChIP1 polypeptide, is further contemplated by the invention.

In yet another embodiment, the invention relates to a method for assaying a sample for the presence of a KChIP1 nucleic acid, comprising contacting the sample with a nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said KChIP1 nucleic acid under conditions appropriate for hybridization, and assessing whether hybridization has occurred between a KChIP1 nucleic acid and said nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said KChIP1 nucleic acid; wherein if hybridization has occurred, a KChIP1 nucleic acid is present in sample. In certain embodiments, the contiguous nucleotide sequence is completely complementary to a part of the sequence of said KChIP1 nucleic acid. If desired, amplification of at least part of said KChIP1 nucleic acid can be performed.

In certain other embodiments, the contiguous nucleotide sequence is 100 or fewer nucleotides in length and is either at least 80% identical to a contiguous sequence of nucleotides of one or more of SEQ ID NOs: 1 and 114-258; at least 80% identical to the complement of a contiguous sequence of nucleotides of one or more of SEQ ID NOs: 1 and 114-258; or capable of selectively hybridizing to said KChIP1 nucleic acid.

In other embodiments, the invention relates to a reagent for assaying a sample for the presence of a KChIP1 gene or nucleic acid, the reagent comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleic acid sequence of said KChIP1 gene or nucleic acid; or comprising a contiguous nucleotide sequence which is completely complementary to a part of the nucleic acid sequence of said KChIP1 gene or nucleic acid. Also contemplated by the invention is a reagent kit, *e.g.*, for assaying a sample for the presence of a KChIP1 nucleic acid, comprising (*e.g.*, in separate containers) one or more labeled nucleic acids comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleic acid sequence of the KChIP1 nucleic acid, and

reagents for detection of said label. In certain embodiments, the labeled nucleic acid comprises a contiguous nucleotide sequence that is completely complementary to a part of the nucleotide sequence of said KChIP1 gene or nucleic acid. In other embodiments, the labeled nucleic acid can comprise a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said KChIP1 gene or nucleic acid, and which is capable of acting as a primer for said KChIP1 nucleic acid when maintained under conditions for primer extension.

The invention also provides for the use of a nucleic acid which is 100 or fewer nucleotides in length and which is either: a) at least 80% identical to a contiguous sequence of nucleotides of one or more of SEQ ID NOs: 1 and 114-258; b) at least 80% identical to the complement of a contiguous sequence of nucleotides of one or more of SEQ ID NOs: 1 and 114-258; or c) capable of selectively hybridizing to said KChIP1 nucleic acid, for assaying a sample for the presence of a KChIP1 nucleic acid.

In yet another embodiment, the use of a first nucleic acid which is 100 or fewer nucleotides in length and which is either: a) at least 80% identical to a contiguous sequence of nucleotides of one or more of SEQ ID NOs: 1 and 114-258; b) at least 80% identical to the complement of a contiguous sequence of nucleotides of one or more of SEQ ID NOs: 1 and 114-258; or c) capable of selectively hybridizing to said KChIP1 nucleic acid; for assaying a sample for the presence of a KChIP1 gene or nucleic acid that has at least one nucleotide difference from the first nucleic acid (e.g., a SNP as set forth in Table 10), such as for diagnosing a susceptibility to a disease or condition associated with a KChIP1.

The invention also relates to a method of diagnosing Type II diabetes or a susceptibility to Type II diabetes in an individual, comprising determining the presence or absence in the individual of certain "haplotypes" (combinations of genetic markers). In one aspect of the invention of diagnosing a susceptibility of the disease, methods are described comprising screening for one of the at-risk haplotypes in the KChIP1 gene that is more frequently present in an individual susceptible to Type II diabetes, compared to the frequency of its presence in the general population, wherein the presence of an at-risk haplotype is indicative of a susceptibility to Type II

diabetes. An "at-risk haplotype" is intended to embrace one or a combination of haplotypes described herein over the KChIP1 gene that show high correlation to Type II diabetes. In one embodiment, the at-risk haplotype is characterized by the presence of at least one single nucleotide polymorphisms as described in Table 13. In one

5   embodiment, a haplotype associated with Type II diabetes or a susceptibility to Type II diabetes comprises one or more haplotypes identified in Table 2 (haplotypes identified as A1, A2, A3, A4, A5, A6, B1, B2, B3, B4 and B5) or Table 5 (haplotypes identified as D1, D2, D3, D4 and D5). In certain embodiments, a haplotype associated with Type II diabetes or a susceptibility to Type II diabetes comprises

10   markers DG5S879, DG5S881, D5S2075, DG5S883 and DG5S38 at the 5q35 locus; or DG5S1058 and DG5S37 at the 5q35 locus; or DG5S1058, DG5S37 and DG5S101 at the 5q35 locus; or DG5S881, DG5S1058, D5S2075, DG5S883 and DG5S38 at the 5q35 locus; or DG5S879, DG5S1058 and DG5S37; or DG5S881, D5S2075, DG5S883 and DG5S38 at the 5q35 locus; DG5S953, DG5S955, DG5S13

15   and DG5S959 at the 5q35 locus; or DG5S888 and DG5S953 at the 5q35 locus; or DG5S953, DG5S955 and DG5S124 at the 5q35 locus; or DG5S888, DG5S44 and DG5S953 at the 5q35 locus; or DG5S953, DG5S955, DG5S13, DG5S123, and DG5S959 at the 5q35 locus. The presence of the haplotype is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes. Also described herein is a

20   haplotype associated with Type II diabetes or a susceptibility to Type II diabetes comprising markers DG5S13, KCP\_1152, and D5S625 at the 5q35 locus; the presence of the haplotype is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes. In one particular embodiment, the presence of the -4, 1, 0 haplotype at DG5S13, KCP\_1152, and D5S625 is diagnostic of Type II diabetes or of a

25   susceptibility to Type II diabetes. In another embodiment, a haplotype associated with Type II diabetes or a susceptibility to Type II diabetes in an individual, comprises markers DG5S124, KCP\_1152, KCP\_2649, KPC\_4976 and KPC-16152 at the 5q35 locus. In one particular embodiment, the presence of the 0, 1, 1, 3 and 0 haplotype at DG5S124, KCP\_1152, KCP\_2649, KPC\_4976 and KPC-16152 is

30   diagnostic of Type II diabetes or of a susceptibility to Type II diabetes. In another embodiment, a haplotype associated with Type II diabetes or a susceptibility to Type



II diabetes in an individual, comprises markers KCP\_173982, KCP\_15400, and KCP\_18069. In one particular embodiment, the presence of the 0, 1, 1 haplotype at KCP\_173982, KCP\_15400, and KCP\_18069 is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes.

5 In additional embodiments, a haplotype associated with Type II diabetes or a susceptibility to Type II diabetes comprises markers DG5S124, KCP\_1152, KCP\_2649, KCP\_4976, and KCP\_16152 at the 5q35 locus, as well as one of the following 3 markers: KCP\_197678, KCP\_197775, and KCP\_202795 at the 5q35 locus; the presence of the haplotype is diagnostic of Type II diabetes or of a  
10 susceptibility to Type II diabetes. In particular embodiments, the presence of the 0, 3, 1, 1, 3, 0 haplotype at DG5S124, KCP\_197679, KCP\_1152, KCP\_2649, KCP\_4976, and KCP\_16152; the presence of the 0, 3, 1, 1, 3, 0 haplotype at DG5S124, KCP\_197775, KCP\_1152, KCP\_2649, KCP\_4976, and KCP\_16152; or the presence of the 0, 1, 1, 1, 3, 0 haplotype at DG5S124, KCP\_202795, KCP\_1152, KCP\_2649,  
15 KCP\_4976, and KCP\_16152; is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes.

The presence or absence of the haplotype can be determined by various methods, including, for example, using enzymatic amplification of nucleic acid from the individual, electrophoretic analysis, restriction fragment length polymorphism  
20 analysis and/or sequence analysis.

Also described herein is a method of diagnosing Type II diabetes in an individual, comprising determining the presence or absence in the individual of a haplotype comprising one or more markers and/or single nucleotide polymorphisms as shown in Table 10, Table 2, Table 5 and/or Table 13 in the locus on chromosome  
25 5q35, wherein the presence of the haplotype is diagnostic of Type II diabetes. Also contemplated is a method of diagnosing a susceptibility to Type II diabetes in an individual, comprising determining the presence or absence in the individual of a haplotype comprising one or more markers and/or single nucleotide polymorphisms as shown in Table 10 and/or Table 13 in the locus on chromosome 5q35, wherein the  
30 presence of the haplotype is diagnostic of a susceptibility to Type II diabetes.

A method for the diagnosis and identification of a susceptibility to Type II diabetes in an individual is also described, comprising: screening for an at-risk haplotype in the KChIP1 nucleic acid that is more frequently present in an individual susceptible to Type II diabetes compared to an individual who is not susceptible to Type II diabetes, wherein the at-risk haplotype increases the risk significantly. In certain embodiments, the significant increase is at least about 20% or the significant increase is identified as an odds ratio of at least about 1.2.

A major application of the current invention involves prediction of those at higher risk of developing a Type II diabetes. Diagnostic tests that define genetic factors contributing to Type II diabetes might be used together with or independent of the known clinical risk factors to define an individual's risk relative to the general population. Better means for identifying those individuals at risk for Type II diabetes should lead to better prophylactic and treatment regimens, including more aggressive management of the current clinical risk factors.

Another application of the current invention is the specific identification of a rate-limiting pathway involved in Type II diabetes. A disease gene with genetic variation that is significantly more common in diabetic patients as compared to controls represents a specifically validated causative step in the pathogenesis of Type II diabetes. That is, the uncertainty about whether a gene is causative or simply reactive to the disease process is eliminated. The protein encoded by the disease gene defines a rate-limiting molecular pathway involved in the biological process of Type II diabetes predisposition. The proteins encoded by such Type II genes or its interacting proteins in its molecular pathway may represent drug targets that may be selectively modulated by small molecule, protein, antibody, or nucleic acid therapies. Such specific information is greatly needed since the population affected with Type II diabetes is growing.

A third application of the current invention is its use to predict an individual's response to a particular drug, even drugs that do not act on KChIP1 or its pathway. It is a well-known phenomenon that in general, patients do not respond equally to the same drug. Much of the differences in drug response to a given drug is thought to be based on genetic and protein differences among individuals in certain genes and their

corresponding pathways. Our invention defines the association of KChIP1 with Type II diabetes. Some current or future therapeutic agents may be able to affect this gene directly or indirectly and therefore, be effective in those patients whose Type II diabetes risk is in part determined by the KChIP1 genetic variation. On the other hand, those same drugs may be less effective or ineffective in those patients who do not have at risk variation in the KChIP1 gene. Therefore, KChIP1 variation or haplotypes may be used as a pharmacogenomic diagnostic to predict drug response and guide choice of therapeutic agent in a given individual.

#### 10 BRIEF DESCRIPTION OF THE DRAWINGS

The foregoing and other objects, features and advantages of the invention will be apparent from the following more particular description of preferred embodiments of the invention, as illustrated in the accompanying drawings.

FIG. 1.1 through 1.148 show the KChIP1 genomic DNA (SEQ ID NO: 1).

15 This sequence is taken from NCBI Build 33. The numbering in FIG. 1, as well as the "start" and "end" numbers in all Tables refer to the location in Chromosome 5 in NCBI Build 33. The numbering in FIG. 1 refers to the last base in the line immediately preceding the number; the numbers are in decreasing order because of the "reverse orientation" of the gene.

20 FIG. 2 shows the amino acid sequence of KChIP1 as published by An *et al.* *Nature*, 403(6768): 553-6 (2000) (SEQ ID NO: 2).

FIG. 3 shows the nucleic acid sequence (SEQ ID NO: 3) encoding the amino acid sequence of KChIP1 as published by An *et al.*, *Nature*, 403(6768): 553-6 (2000) (SEQ ID NO: 2).

25 FIG. 4 is a series of graphs showing the results of a genome-wide scan using 906 microsatellite markers. Results are shown for three phenotypes: all Type II diabetics (solid lines), obese Type II diabetics (dotted lines) and non-obese Type II diabetics (dashed lines). The multipoint allele-sharing LOD-score is on the vertical axis, and the centimorgan distance from the P-terminus of the chromosome is on the horizontal axis.

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FIG. 5 graphically depicts the multipoint allele-sharing LOD-score of the locus on chromosome 5 after 38 microsatellite markers have been added to the framework set in a 40-cM interval, from 160 cM to 200 cM. Results are shown for the same three phenotypes as in FIG. 4; all Type II diabetics (solid line), non-obese Type II diabetics (dashed line) and obese Type II diabetics (dotted line). the results of a genome-wide scan using 906 microsatellite markers.

FIG. 6 graphically depicts the single-marker and haplotype association within the 1-LOD-drop for 590 non-obese diabetics vs 477 unrelated population controls. The location of the markers and haplotypes is on the horizontal axis and the corresponding two-sided P-value on the vertical axis. All haplotypes with a P-value less than 0.01 are shown. The horizontal bars indicate the span of the corresponding haplotypes and the marker density is shown at the bottom of the figure. All locations refer to NCBI Build 33 and the 1-LOD-drop spans from 167.64 to 171.28 Mb.

FIG. 7 schematically shows the location of genes and markers in region B. The microsatellites used in the locus-wide association study are shown as filled circles at the top. The filled boxes indicate the locations of exons, or clusters of exons, for KCHIP1. The shaded boxes indicated the location and size of the neighboring genes, LCP2, KCNMB1, GABRP and RANBP17, and the grey horizontal lines indicate the span of the five most significant microsatellite haplotypes in the region.

## DETAILED DESCRIPTION OF THE INVENTION

Extensive genealogical information for a population with population-based lists of patients with Type II diabetes has been combined with powerful gene sharing methods to map a locus on chromosome 5q35. Diabetics and their relatives were genotyped with a genome-wide marker set including 906 microsatellite markers, with an average marker density of 4cM. Due to the role obesity plays in the development of diabetes, the material was fractionated according to body mass index (BMI). Presented herein are results of a genome wide search of genes that cause Type II diabetes in Iceland.

*Loci Associated with Diabetes*

Evidence for genes causing the early onset monogenic form of diabetes have been previously identified. Mutations in six genes have been discovered that cause MODY, or maturity onset diabetes of the young. MODY1 – MODY6 are due to mutations in HNF4a, glucokinase, HNF1a, IPF1, HNF1b and NEUROD1 (MODY1: Yamagata K, *et al.*, *Nature* 384:458-460 (1996); MODY2: Froguel P, F *et al.*, *Nature* 356: 162-164(1992); MODY3: Yamagata, K., *et al.*, *Nature* 384: 455-458 (1996); MODY4: Yoshioka M., *et al.*, *Diabetes* May;46(5):887-94 (1997) MODY5: Horikawa, Y., *et al.*, *Nat. Genet.* 17: 384-385 (1997) MODY6: Kristinsson S.Y., *et al.*, *Diabetologia* Nov;44(11):2098-103 (2001)).

One gene has been identified as a disease gene that contributes to the late-onset form of diabetes, the calpain 10 gene (CAPN10). CAPN10, was identified through a genome-wide screen of Mexican American sibpairs with diabetes (Horikawa, Y., *et al.*, *Nat. Genet.* 26(2) 163-175(2000)). The risk allele has been shown to be associated with impaired regulation of glucose-induced secretion and decreased rate of insulin-stimulated glucose disposal (Lynn, S., *et al.*, *Diabetes*, 51(1): 247-250 (2002); Sreenan, S.K., *et al.*, *Diabetes* 50(9) 2013-2020 (2001) and Baier, L. J., *et al.*, *J. Clin. Invest.* 106(7) R69-73 (2000)).

Many genome-wide screens in a variety of populations have been performed that have resulted in major loci for Diabetes. Loci are reported on chromosome 2q37 (Hanis, C.L., *et al.*, *Nat. Genet.*, 13(2):161-166 (1996)), chromosome 15q21 (Cox, *et al.*, *Nat. Genet.* 21(2):213-215 (1999)), chromosome 10q26 (Duggirala, R., *et al.*, *Am. J. Hum. Genet.*, 68(5):1149-1164 (2001)), chromosome 3p (Ehm, M.G., *et al.*, *Am. J. Hum. Genet.*, 66(6):1871-1881 (2000)) in Mexican Americans, and chromosomes 1q21-23 and 11q23-q25 (Hanson R. L. *et al.*, *Am J. Hum Genet.*, 63(4):1130-1138 (1998)) in PIMA Indians. In the Caucasian population, linkages have been observed to chromosome 12q24 in Finns (Mahtani, *et al.*, *Nat. Genet.*, 14(1):90-4 (1994)), chromosome 1q21-q23 in Americans in Utah (Elbein, S.C., *et al.*, *Diabetes*, 48(5):1175-1182 (1999)), chromosome 3q27-pter in French families (Vionnet, N., *et al.*, *Am. J. Hum. Genet.* 67(6):1470-80 (2000) and chromosome 18p11 in Scandinavians (Parker, A., *et al.*, *Diabetes*, 50(3) 675-680 (2001)). A recent study

reported a major locus in indigenous Australians on chromosome 2q24.3 (Busfield, F., *et al.*, *Am. J. Hum. Genet.*, 70(2): 349-357 (2002)). Many other studies have resulted in suggestive loci or have replicated these loci.

Association studies have been reported for Type II diabetes. Most of these studies show modest association to the disease in a group of people but do not account for the disease. Altshuler *et al.*, reviewed the association work that has been done and concluded that association to only one of 16 genes revealed held up to scrutiny. Altshuler *et al.*, confirmed that the Pro12Ala polymorphism in PPAR $\gamma$  is associated with Type II diabetes. Until now, there have been no linkage studies in Type II diabetes linking the disease to chromosome 5q35

### *KChIP1*

The invention described herein has linked Type II diabetes to a gene encoding Kv channel-interacting protein 1 (KChIP1; also known as KCNIP1). In the brain and heart, rapidly inactivating (A-type) voltage-gated potassium (Kv) currents operate at subthreshold membrane potentials to control the excitability of neurons and cardiac myocytes. Although pore-forming  $\alpha$ -subunits of the Kv4, or Shal-related, channel family form A-Type currents in heterologous cells, these differ significantly from native A-Type currents. To identify proteins that interacted with the Kv4 subunit, An *et al.*, ("Modulation of A-Type potassium channels by a family of calcium sensors" *Nature* 403:553-6 (2000)) used the yeast two-hybrid system with the intracellular amino terminus of the rat Kv4.3 subunit to screen rat midbrain cDNA libraries. Two Kv channel-interacting proteins were identified and called KChIPs (KChIP-1 and KChIP2). Library screening and database mining identified mouse and human orthologs of these genes. The KChIP1 cDNA encodes a 216-amino acid protein. The KChIPs have 4 EF-hand-like domains and bind calcium ions. Both KChIPs have distinct N termini but share approximately 70% amino acid identity throughout a carboxy-terminal 185-amino acid core domain that contains the 4 EF-hand-like motifs. Although the KChIPs have around 40% amino acid similarity to neuronal calcium sensor-1 and are members of the recoverin /NCS subfamily of calcium-binding proteins, other members of this subfamily, such as hippocalcin, did not

interact with Kv4 channels in the yeast 2-hybrid assay. An *et al.*, (*supra*) additionally found that expression of KChIPs and Kv4 together reconstitutes several features of native A-Type currents by modulating the density, inactivation kinetics, and rate of recovery from inactivation of Kv4 channels in heterologous cells. Both KChIPs  
5 colocalize and coimmunoprecipitate with brain Kv4 alpha-subunits, and are thus integral components of native Kv4 channel complexes. As the activity and density of neuronal A-Type currents tightly control responses to excitatory synaptic inputs, these KChIPs may regulate A-Type currents, and hence neuronal excitability, in response to changes in intracellular calcium.

10 The glycosphingolipid sulfatide is present in secretory granules and at the surface of pancreatic  $\beta$ -cells (Buschard K, Fredman P. "Sulphatide as an antigen in diabetes mellitus". *Diabetes Nutr Metab* 4:221-228 (1996)), and antisulfatide antibodies (ASA; IgG1) are found in serum from the majority of patients with newly diagnosed Type I diabetes. Buschard *et al.*, ("Sulfatide controls insulin secretion by  
15 modulation of ATP-sensitive K(+)-channel activity and Ca(2+)-dependent exocytosis in rat pancreatic beta-cells" *Diabetes* 51:2514-21 (2002)) demonstrated that sulfatide produced a glucose- and concentration-dependent inhibition of insulin release from isolated rat pancreatic islets. This inhibition of insulin secretion was due to activation of ATP-sensitive K<sup>+</sup>-(K<sub>ATP</sub>) channels in single rat  $\beta$ -cells. No effect of sulfatide was  
20 observed on whole-cell Ca<sup>2+</sup>-channel activity or glucose-induced elevation of cytoplasmic Ca<sup>2+</sup> concentration. A key observation was that sulfatide stimulated Ca<sup>2+</sup>-dependent exocytosis determined by capacitance measurements and depolarized-induced insulin secretion from islets exposed to diazoxide and high external KCl. The monoclonal sulfatide antibody Sulph I as well as ASA-positive serum reduced  
25 glucose-induced insulin secretion by inhibition of Ca<sup>2+</sup>-dependent exocytosis. This suggests that sulfatide is important for the control of glucose-induced insulin secretion and that both an increase and a decrease in the sulfatide content have an impact on the secretory capacity of the individual  $\beta$ -cells.

## ASSESSMENT FOR AT-RISK HAPLOTYPES

A "haplotype," as described herein, refers to a combination of genetic markers ("alleles"), such as those set forth in Table 2 and Table 5. In a certain embodiment, the haplotype can comprise one or more alleles, two or more alleles, three or more alleles, four or more alleles, or five or more alleles. The genetic markers are particular "alleles" at "polymorphic sites" associated with KChPI1. A nucleotide position at which more than one sequence is possible in a population (either a natural population or a synthetic population, *e.g.*, a library of synthetic molecules) is referred to herein as a "polymorphic site". Where a polymorphic site is a single nucleotide in length, the site is referred to as a single nucleotide polymorphism ("SNP"). For example, if at a particular chromosomal location, one member of a population has an adenine and another member of the population has a thymine at the same position, then this position is a polymorphic site, and, more specifically, the polymorphic site is a SNP. Polymorphic sites can allow for differences in sequences based on substitutions, insertions or deletions. Each version of the sequence with respect to the polymorphic site is referred to herein as an "allele" of the polymorphic site. Thus, in the previous example, the SNP allows for both an adenine allele and a thymine allele.

Typically, a reference sequence is referred to for a particular sequence. Alleles that differ from the reference are referred to as "variant" alleles. For example, the reference KChPI1 sequence is described herein by SEQ ID NO: 1. The term, "variant KChPI1", as used herein, refers to a sequence that differs from SEQ ID NO: 1 but is otherwise substantially similar. The genetic markers that make up the haplotypes described herein are KChPI1 variants. Additional variants can include changes that affect a polypeptide, *e.g.*, the KChPI1 polypeptide. These sequence differences, when compared to a reference nucleotide sequence, can include the insertion or deletion of a single nucleotide, or of more than one nucleotide, resulting in a frame shift; the change of at least one nucleotide, resulting in a change in the encoded amino acid; the change of at least one nucleotide, resulting in the generation of a premature stop codon; the deletion of several nucleotides, resulting in a deletion of one or more amino acids encoded by the nucleotides; the insertion of one or several nucleotides, such as by unequal recombination or gene conversion, resulting in an



interruption of the coding sequence of a reading frame; duplication of all or a part of a sequence; transposition; or a rearrangement of a nucleotide sequence, as described in detail above. Such sequence changes alter the polypeptide encoded by a KChPII nucleic acid. For example, if the change in the nucleic acid sequence causes a frame shift, the frame shift can result in a change in the encoded amino acids, and/or can result in the generation of a premature stop codon, causing generation of a truncated polypeptide. Alternatively, a polymorphism associated with Type II diabetes or a susceptibility to Type II diabetes can be a synonymous change in one or more nucleotides (*i.e.*, a change that does not result in a change in the amino acid sequence). Such a polymorphism can, for example, alter splice sites, affect the stability or transport of mRNA, or otherwise affect the transcription or translation of the polypeptide. The polypeptide encoded by the reference nucleotide sequence is the "reference" polypeptide with a particular reference amino acid sequence, and polypeptides encoded by variant alleles are referred to as "variant" polypeptides with variant amino acid sequences.

Haplotypes are a combination of genetic markers, *e.g.*, particular alleles at polymorphic sites. The haplotypes described herein, *e.g.*, having markers such as those shown in Table 6, Table 7, Table 9, Table 11, Table 12 and Table 13 are found more frequently in individuals with Type II diabetes than in individuals without Type II diabetes. Therefore, these haplotypes have predictive value for detecting Type II diabetes or a susceptibility to Type II diabetes in an individual. The haplotypes described herein are a combination of various genetic markers, *e.g.*, SNPs and microsatellites. Therefore, detecting haplotypes can be accomplished by methods known in the art for detecting sequences at polymorphic sites, such as the methods described above.

In certain methods described herein, an individual who is at risk for Type II diabetes is an individual in whom an at-risk haplotype is identified. In one embodiment, the at-risk haplotype is one that confers a significant risk of Type II diabetes. In one embodiment, significance associated with a haplotype is measured by an odds ratio. In a further embodiment, the significance is measured by a percentage. In one embodiment, a significant risk is measured as an odds ratio of at

least about 1.2, including but not limited to: 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8 and 1.9. In a further embodiment, an odds ratio of at least 1.2 is significant. In a further embodiment, an odds ratio of at least about 1.5 is significant. In a further embodiment, a significant increase in risk is at least about 1.7 is significant. In a further embodiment, a significant increase in risk is at least about 20%, including but not limited to about 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% and 98%. In a further embodiment, a significant increase in risk is at least about 50%. It is understood however, that identifying whether a risk is medically significant may also depend on a variety of factors, including the specific disease, the haplotype, and often, environmental factors.

An at-risk haplotype in, or comprising portions of, the KChPI1 gene, is one where the haplotype is more frequently present in an individual at risk for Type II diabetes (affected), compared to the frequency of its presence in a healthy individual (control), and wherein the presence of the haplotype is indicative of Type II diabetes or susceptibility to Type II diabetes.

Standard techniques for genotyping for the presence of SNPs and/or microsatellite markers can be used, such as fluorescent-based techniques (Chen, *et al.*, *Genome Res.* 9, 492 (1999)), PCR, LCR, Nested PCR and other techniques for nucleic acid amplification. In one embodiment, the method comprises assessing in an individual the presence or frequency of SNPs and/or microsatellites in, comprising portions of, the KChIP1 gene, wherein an excess or higher frequency of the SNPs and/or microsatellites compared to a healthy control individual is indicative that the individual has Type II diabetes, or is susceptible to Type II diabetes. See, for example, Table 6, Table 7, Table 9, Table 11, Table 12 and 13 (below) for SNPs and markers that can form haplotypes that can be used as screening tools. These markers and SNPs can be identified in at-risk haplotypes. For example, an at-risk haplotype can include microsatellite markers and/or SNPs such as those set forth in Table 2 and Table 5. The presence of the haplotype is indicative a susceptibility to Type II diabetes, and therefore is indicative of an individual who falls within a target population for the treatment methods described herein.

## NUCLEIC ACID THERAPEUTIC AGENTS

In another embodiment, a nucleic acid of the invention; a nucleic acid complementary to a nucleic acid of the invention; or a portion of such a nucleic acid (e.g., an oligonucleotide as described below); or a nucleic acid encoding a KChIP1 polypeptide, can be used in "antisense" therapy, in which a nucleic acid (e.g., an oligonucleotide) which specifically hybridizes to the mRNA and/or genomic DNA of a nucleic acid is administered or generated *in situ*. The antisense nucleic acid that specifically hybridizes to the mRNA and/or DNA inhibits expression of the polypeptide encoded by that mRNA and/or DNA, e.g., by inhibiting translation and/or transcription. Binding of the antisense nucleic acid can be by conventional base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interaction in the major groove of the double helix.

An antisense construct can be delivered, for example, as an expression plasmid as described above. When the plasmid is transcribed in the cell, it produces RNA that is complementary to a portion of the mRNA and/or DNA that encodes a KChIP1 polypeptide. Alternatively, the antisense construct can be an oligonucleotide probe that is generated *ex vivo* and introduced into cells; it then inhibits expression by hybridizing with the mRNA and/or genomic DNA of the polypeptide. In one embodiment, the oligonucleotide probes are modified oligonucleotides that are resistant to endogenous nucleases, e.g., exonucleases and/or endonucleases, thereby rendering them stable *in vivo*. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphothioate and methylphosphonate analogs of DNA (see also U.S. Patent Nos. 5,176,996, 5,264,564 and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy are also described, for example, by Van der Krol *et al.* (*BioTechniques* 6:958-976 (1988)); and Stein *et al.* (*Cancer Res.* 48:2659-2668 (1988)). With respect to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site are preferred.

To perform antisense therapy, oligonucleotides (mRNA, cDNA or DNA) are designed that are complementary to mRNA encoding the polypeptide. The antisense oligonucleotides bind to mRNA transcripts and prevent translation. Absolute

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complementarity, although preferred, is not required. A sequence "complementary" to a portion of an RNA, as referred to herein, indicates that a sequence has sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid, as described in detail above. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures.

The oligonucleotides used in antisense therapy can be DNA, RNA, or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotides can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotides can include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, *Proc. Natl. Acad. Sci. USA* 86:6553-6556 (1989); Lemaitre *et al.*, *Proc. Natl. Acad. Sci. USA* 84:648-652 (1987); PCT International Publication NO: WO 88/09810) or the blood-brain barrier (see, *e.g.*, PCT International Publication NO: WO 89/10134), or hybridization-triggered cleavage agents (see, *e.g.*, Krol *et al.*, *BioTechniques* 6:958-976 (1988)) or intercalating agents. (See, *e.g.*, Zon, *Pharm.Res.* 5: 539-549 (1988)). To this end, the oligonucleotide may be conjugated to another molecule (*e.g.*, a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent).

The antisense molecules are delivered to cells that express a KChIP1 polypeptide *in vivo*. A number of methods can be used for delivering antisense DNA or RNA to cells; *e.g.*, antisense molecules can be injected directly into the tissue site, or modified antisense molecules, designed to target the desired cells (*e.g.*, antisense linked to peptides or antibodies that specifically bind receptors or antigens expressed on the target cell surface) can be administered systematically. Alternatively, in a another embodiment, a recombinant DNA construct is utilized in which the antisense

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oligonucleotide is placed under the control of a strong promoter (*e.g.*, pol III or pol II). The use of such a construct to transfect target cells in the patient results in the transcription of sufficient amounts of single stranded RNAs that will form complementary base pairs with the endogenous transcripts and thereby prevent translation of the mRNA. For example, a vector can be introduced *in vivo* such that it is taken up by a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art and described above.

For example, a plasmid, cosmid, YAC or viral vector can be used to prepare the recombinant DNA construct that can be introduced directly into the tissue site. Alternatively, viral vectors can be used which selectively infect the desired tissue, in which case administration may be accomplished by another route (*e.g.*, systemically). In another embodiment of the invention, small double-stranded interfering RNA (RNA interference (RNAi)) can be used. RNAi is a post-transcription process, in which double-stranded RNA is introduced, and sequence-specific gene silencing results, though catalytic degradation of the targeted mRNA. See, *e.g.*, Elbashir, S.M. *et al.*, *Nature* 411:494-498 (2001); Lee, N.S., *Nature Biotech.* 19:500-505 (2002); Lee, S-K. *et al.*, *Nature Medicine* 8(7):681-686 (2002); the entire teachings of these references are incorporated herein by reference.

Endogenous expression of a gene product can also be reduced by inactivating or "knocking out" the gene or its promoter using targeted homologous recombination (*e.g.*, see Smithies *et al.*, *Nature* 317:230-234 (1985); Thomas & Capecchi, *Cell* 51:503-512 (1987); Thompson *et al.*, *Cell* 5:313-321 (1989)). For example, an altered, non-functional gene (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous gene (either the coding regions or regulatory regions of the gene) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express the gene *in vivo*. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the gene. The recombinant DNA constructs can be directly administered or targeted to the required site *in vivo* using appropriate vectors, as described above.

Alternatively, expression of non-altered genes can be increased using a similar method: targeted homologous recombination can be used to insert a DNA construct comprising a non-altered functional gene, or the complement thereof, or a portion thereof, in place of an gene in the cell, as described above. In another embodiment, 5 targeted homologous recombination can be used to insert a DNA construct comprising a nucleic acid that encodes a polypeptide variant that differs from that present in the cell.

Alternatively, endogenous expression of a gene product can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region (*i.e.*, 10 the promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells in the body. (See generally, Helene, C., *Anticancer Drug Des.*, 6(6):569-84 (1991); Helene, C. *et al.*, *Ann. N.Y. Acad. Sci.* 660:27-36 (1992); and Maher, L. J., *Bioassays* 14(12):807-15 (1992)). Likewise, the antisense constructs described herein, by antagonizing the normal biological activity 15 of the gene product, can be used in the manipulation of tissue, *e.g.*, tissue differentiation, both *in vivo* and *for ex vivo* tissue cultures. Furthermore, the antisense techniques (*e.g.*, microinjection of antisense molecules, or transfection with plasmids whose transcripts are anti-sense with regard to a nucleic acid RNA or nucleic acid sequence) can be used to investigate the role of one or more members of 20 the KChIP1 pathway in the development of disease-related conditions. Such techniques can be utilized in cell culture, but can also be used in the creation of transgenic animals.

The therapeutic agents as described herein can be delivered in a composition, as described above, or alone. They can be administered systemically, or can be 25 targeted to a particular tissue. The therapeutic agents can be produced by a variety of means, including chemical synthesis; recombinant production; *in vivo* production (*e.g.*, a transgenic animal, such as U.S. Patent NO: 4,873,316 to Meade *et al.*), for example, and can be isolated using standard means such as those described herein. In addition, a combination of any of the above methods of treatment (*e.g.*, administration 30 of non-altered polypeptide in conjunction with antisense therapy targeting altered

mRNA; administration of a first splicing variant in conjunction with antisense therapy targeting a second splicing variant) can also be used.

The invention additionally pertains to use of such therapeutic agents, as described herein, for the manufacture of a medicament for the treatment of Type II diabetes e.g., using the methods described herein.

### MONITORING PROGRESS OF TREATMENT

The current invention also pertains to methods of monitoring the effectiveness of treatment on the regulation of expression (*e.g.*, relative or absolute expression) of one or more KChIP1 isoforms at the RNA or protein level or its enzymatic activity. KChIP1 message or protein or enzymatic activity can be measured in a sample of peripheral blood or cells derived therefrom. An assessment of the levels of expression or activity can be made before and during treatment with KChIP1 therapeutic agents. For example, in one embodiment of the invention, an individual who is a member of the target population can be assessed for response to treatment with a KChIP1 inhibitor, by examining calcium levels or Kv channel-interacting proteins activity or absolute and/or relative levels of KChIP1 protein or mRNA isoforms in peripheral blood in general or specific cell subfractions or combination of cell subfractions. In addition, variation such as haplotypes or mutations within or near (within 100 to 200kb) of the KChIP1 gene may be used to identify individuals who are at higher risk for Type II diabetes to increase the power and efficiency of clinical trials for pharmaceutical agents to prevent or treat Type II diabetes. The haplotypes and other variations may be used to exclude or fractionate patients in a clinical trial who are likely to have non- KChIP1 involvement in their Type II diabetes risk in order to enrich patients who have other genes or pathways involved and boost the power and sensitivity of the clinical trial. Such variation may be used as a pharmacogenomic test to guide selection of pharmaceutical agents for individuals.

Described herein is the first known linkage study of Type II diabetes showing a connection to chromosome 5q35. Based on the linkage studies conducted, a direct relationship between Type II diabetes and the locus on chromosome 5q35, in particular the KChIP1 gene, has been discovered.

## NUCLEIC ACIDS OF THE INVENTION

*KChIP1 Nucleic Acids, Portions and Variants*

5       Accordingly, the invention pertains to isolated nucleic acid molecules comprising human KChIP1 nucleic acid. The term, "KChIP1 nucleic acid," as used herein, refers to an isolated nucleic acid molecule encoding a KChIP1 polypeptide (e.g., a KChIP1 gene, such as shown in SEQ ID NO:1). The KChIP1 nucleic acid molecules of the present invention can be RNA, for example, mRNA, or DNA, such as cDNA and genomic DNA. DNA molecules can be double-stranded or single-  
10       stranded; single stranded RNA or DNA can be either the coding, or sense, strand or the non-coding, or antisense strand. The nucleic acid molecule can include all or a portion of the coding sequence of the gene and can further comprise additional non-coding sequences such as introns and non-coding 3' and 5' sequences (including  
15       regulatory sequences, for example).

For example, the KChIP1 nucleic acid can be the genomic sequence shown in FIG. 1, or a portion or fragment of the isolated nucleic acid molecule (e.g., cDNA or the gene) that encodes KChIP1 polypeptide. In certain embodiments, the isolated nucleic acid molecule comprises a nucleic acid molecule selected from the group  
20       consisting of SEQ ID NOs: 1 and 114-258 (e.g., in Table 10) or the complement of such a nucleic acid molecule.

Additionally, nucleic acid molecules of the invention can be fused to a marker sequence, for example, a sequence that encodes a polypeptide to assist in isolation or purification of the polypeptide. Such sequences include, but are not limited to, those  
25       that encode a glutathione-S-transferase (GST) fusion protein and those that encode a hemagglutinin A (HA) polypeptide marker from influenza.

An "isolated" nucleic acid molecule, as used herein, is one that is separated from nucleic acids that normally flank the gene or nucleotide sequence (as in genomic sequences) and/or has been completely or partially purified from other transcribed  
30       sequences (e.g., as in an RNA library). For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in



which it naturally occurs, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other  
5 circumstances, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid molecule comprises at least about 50, 80 or 90% (on a molar basis) of all macromolecular species present. With regard to genomic DNA, the term "isolated" also can refer to nucleic acid molecules that are separated from the  
10 chromosome with which the genomic DNA is naturally associated. For example, the isolated nucleic acid molecule can contain less than about 5 kb but not limited to 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotides which flank the nucleic acid molecule in the genomic DNA of the cell from which the nucleic acid molecule is derived.

The nucleic acid molecule can be fused to other coding or regulatory  
15 sequences and still be considered isolated. Thus, recombinant DNA contained in a vector is included in the definition of "isolated" as used herein. Also, isolated nucleic acid molecules include recombinant DNA molecules in heterologous host cells, as well as partially or substantially purified DNA molecules in solution. "Isolated" nucleic acid molecules also encompass *in vivo* and *in vitro* RNA transcripts of the  
20 DNA molecules of the present invention. An isolated nucleic acid molecule can include a nucleic acid molecule or nucleic acid sequence that is synthesized chemically or by recombinant means. Therefore, recombinant DNA contained in a vector is included in the definition of "isolated" as used herein. Also, isolated nucleic acid molecules include recombinant DNA molecules in heterologous organisms, as  
25 well as partially or substantially purified DNA molecules in solution. *In vivo* and *in vitro* RNA transcripts of the DNA molecules of the present invention are also encompassed by "isolated" nucleic acid sequences. Such isolated nucleic acid molecules are useful in the manufacture of the encoded polypeptide, as probes for isolating homologous sequences (e.g., from other mammalian species), for gene  
30 mapping (e.g., by *in situ* hybridization with chromosomes), or for detecting

expression of the gene in tissue (*e.g.*, human tissue), such as by Northern blot analysis.

The present invention also pertains to nucleic acid molecules which are not necessarily found in nature but which encode a KChIP1 polypeptide, or another  
5 splicing variant of a KChIP1 polypeptide or polymorphic variant thereof. Thus, for example, the invention pertains to DNA molecules comprising a sequence that is different from the naturally occurring nucleotide sequence but which, due to the degeneracy of the genetic code, encode a KChIP1 polypeptide of the present invention. The invention also encompasses nucleic acid molecules encoding portions  
10 (fragments), or encoding variant polypeptides such as analogues or derivatives of a KChIP1 polypeptide. Such variants can be naturally occurring, such as in the case of allelic variation or single nucleotide polymorphisms, or non-naturally-occurring, such as those induced by various mutagens and mutagenic processes. Intended variations include, but are not limited to, addition, deletion and substitution of one or more  
15 nucleotides that can result in conservative or non-conservative amino acid changes, including additions and deletions. Preferably the nucleotide (and/or resultant amino acid) changes are silent or conserved; that is, they do not alter the characteristics or activity of a KChIP1 polypeptide. In one embodiment, the nucleic acid sequences are fragments that comprise one or more polymorphic microsatellite markers. In another  
20 embodiment, the nucleotide sequences are fragments that comprise one or more single nucleotide polymorphisms in a KChIP1 gene.

Other alterations of the nucleic acid molecules of the invention can include, for example, labeling, methylation, internucleotide modifications such as uncharged linkages (*e.g.*, methyl phosphonates, phosphotriesters, phosphoamidates, carbamates),  
25 charged linkages (*e.g.*, phosphorothioates, phosphorodithioates), pendent moieties (*e.g.*, polypeptides), intercalators (*e.g.*, acridine, psoralen), chelators, alkylators, and modified linkages (*e.g.*, alpha anomeric nucleic acids). Also included are synthetic molecules that mimic nucleic acid molecules in the ability to bind to a designated sequence via hydrogen bonding and other chemical interactions. Such molecules  
30 include, for example, those in which peptide linkages substitute for phosphate linkages in the backbone of the molecule.

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The invention also pertains to nucleic acid molecules that hybridize under high stringency hybridization conditions, such as for selective hybridization, to a nucleotide sequence described herein (e.g., nucleic acid molecules which specifically hybridize to a nucleotide sequence encoding polypeptides described herein, and, optionally, have an activity of the polypeptide). In one embodiment, the invention includes variants described herein which hybridize under high stringency hybridization conditions (e.g., for selective hybridization) to a nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 114-258. In another embodiment, the invention includes variants described herein that hybridize under high stringency hybridization conditions (e.g., for selective hybridization) to a nucleotide sequence encoding an amino acid sequence or a polymorphic variant thereof. In another embodiment, the variant that hybridizes under high stringency hybridizations has an activity of a KChIP1 polypeptide.

Such nucleic acid molecules can be detected and/or isolated by specific hybridization (e.g., under high stringency conditions). "Specific hybridization," as used herein, refers to the ability of a first nucleic acid to hybridize to a second nucleic acid in a manner such that the first nucleic acid does not hybridize to any nucleic acid other than to the second nucleic acid (e.g., when the first nucleic acid has a higher similarity to the second nucleic acid than to any other nucleic acid in a sample wherein the hybridization is to be performed). "Stringency conditions" for hybridization is a term of art which refers to the incubation and wash conditions, e.g., conditions of temperature and buffer concentration, which permit hybridization of a particular nucleic acid to a second nucleic acid; the first nucleic acid may be perfectly (i.e., 100%) complementary to the second, or the first and second may share some degree of complementarity which is less than perfect (e.g., 70%, 75%, 85%, 90%, 95%). For example, certain high stringency conditions can be used which distinguish perfectly complementary nucleic acids from those of less complementarity. "High stringency conditions", "moderate stringency conditions" and "low stringency conditions" for nucleic acid hybridizations are explained on pages 2.10.1-2.10.16 and pages 6.3.1-6.3.6 in *Current Protocols in Molecular Biology* (Ausubel, F.M. et al., "Current Protocols in Molecular Biology", John Wiley & Sons, (2001)), the entire

5 teachings of which are incorporated by reference herein). The exact conditions which determine the stringency of hybridization depend not only on ionic strength (*e.g.*, 0.2X SSC, 0.1X SSC), temperature (*e.g.*, room temperature, 42°C, 68°C) and the concentration of destabilizing agents such as formamide or denaturing agents such as SDS, but also on factors such as the length of the nucleic acid sequence, base composition, percent mismatch between hybridizing sequences and the frequency of occurrence of subsets of that sequence within other non-identical sequences. Thus, equivalent conditions can be determined by varying one or more of these parameters while maintaining a similar degree of identity or similarity between the two nucleic acid molecules. Typically, conditions are used such that sequences at least about 10 60%, at least about 70%, at least about 80%, at least about 90%, or at least about 95% or more identical to each other remain hybridized to one another. By varying hybridization conditions from a level of stringency at which no hybridization occurs to a level at which hybridization is first observed, conditions which will allow a given sequence to hybridize (*e.g.*, selectively) with the most similar sequences in the sample 15 can be determined.

Exemplary conditions are described in Krause, M.H. and S.A. Aaronson, *Methods in Enzymology* 200:546-556 (1991), and in, Ausubel, *et al.*, "*Current Protocols in Molecular Biology*", John Wiley & Sons, (2001), which describes the determination of washing conditions for moderate or low stringency conditions. 20 Washing is the step in which conditions are usually set so as to determine a minimum level of complementarity of the hybrids. Generally, starting from the lowest temperature at which only homologous hybridization occurs, each °C by which the final wash temperature is reduced (holding SSC concentration constant) allows an increase by 1% in the maximum extent of mismatching among the sequences that 25 hybridize. Generally, doubling the concentration of SSC results in an increase in  $T_m$  of -17°C. Using these guidelines, the washing temperature can be determined empirically for high, moderate or low stringency, depending on the level of mismatch sought.

30 For example, a low stringency wash can comprise washing in a solution containing 0.2X SSC/0.1% SDS for 10 minutes at room temperature; a moderate

stringency wash can comprise washing in a pre-warmed solution (42°C) solution containing 0.2X SSC/0.1% SDS for 15 minutes at 42°C; and a high stringency wash can comprise washing in pre-warmed (68°C) solution containing 0.1X SSC/0.1%SDS for 15 minutes at 68°C. Furthermore, washes can be performed repeatedly or sequentially to obtain a desired result as known in the art. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleic acid molecule and the primer or probe used.

The percent homology or identity of two nucleotide or amino acid sequences can be determined by aligning the sequences for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first sequence for optimal alignment).

The nucleotides or amino acids at corresponding positions are then compared, and the percent identity between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % identity = # of identical positions/total # of positions x 100). When a position in one sequence is occupied by the same nucleotide or amino acid residue as the corresponding position in the other sequence, then the molecules are homologous at that position. As used herein, nucleic acid or amino acid "homology" is equivalent to nucleic acid or amino acid "identity". In certain embodiments, the length of a sequence aligned for comparison purposes is at least 30%, for example, at least 40%, in certain embodiments at least 60%, and in other embodiments at least 70%, 80%, 90% or 95% of the length of the reference sequence.

The actual comparison of the two sequences can be accomplished by well-known methods, for example, using a mathematical algorithm. A preferred, non-limiting example of such a mathematical algorithm is described in Karlin *et al.*, *Proc. Natl.*

*Acad. Sci. USA* 90:5873-5877 (1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) as described in Altschul *et al.*, *Nucleic Acids Res.* 25:389-3402 (1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.*, NBLAST) can be used. In one embodiment, parameters for sequence comparison can be set at score=100, wordlength=12, or can be varied (*e.g.*, W=5 or W=20).

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Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, *CABIOS* 4(1): 11-17 (1988). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package (Accelrys, Cambridge, UK). When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art and include ADVANCE and ADAM as described in Torellis and Robotti, *Comput. Appl. Biosci.* 10:3-5 (1994); and FASTA described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-8 (1988).

In another embodiment, the percent identity between two amino acid sequences can be accomplished using the GAP program in the GCG software package using either a BLOSUM63 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. In yet another embodiment, the percent identity between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package using a gap weight of 50 and a length weight of 3.

The present invention also provides isolated nucleic acid molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 114-258, or the complement of such a sequence, and also provides isolated nucleic acid molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleotide sequence encoding an amino acid sequence or polymorphic variant thereof. The nucleic acid fragments of the invention are at least about 15, preferably at least about 18, 20, 23 or 25 nucleotides, and can be 30, 40, 50, 100, 200 or more nucleotides in length. Longer fragments, for example, 30 or more nucleotides in length, that encode antigenic polypeptides described herein are particularly useful, such as for the generation of antibodies as described below.

30

### *Probes and Primers*

In a related aspect, the nucleic acid fragments of the invention are used as probes or primers in assays such as those described herein. "Probes" or "primers" are oligonucleotides that hybridize in a base-specific manner to a complementary strand  
5 of nucleic acid molecules. Such probes and primers include polypeptide nucleic acids, as described in Nielsen *et al.*, *Science* 254:1497-1500 (1991).

A probe or primer comprises a region of nucleotide sequence that hybridizes to at least about 15, for example about 20-25, and in certain embodiments about 40, 50 or 75, consecutive nucleotides of a nucleic acid molecule comprising a contiguous  
10 nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 114-258 or polymorphic variant thereof. In other embodiments, a probe or primer comprises 100 or fewer nucleotides, in certain embodiments from 6 to 50 nucleotides, for example from 12 to 30 nucleotides. In other embodiments, the probe or primer is at least 70% identical to the contiguous nucleotide sequence or to the complement of the  
15 contiguous nucleotide sequence, for example at least 80% identical, in certain embodiments at least 90% identical, and in other embodiments at least 95% identical, or even capable of selectively hybridizing to the contiguous nucleotide sequence or to the complement of the contiguous nucleotide sequence. Often, the probe or primer further comprises a label, *e.g.*, radioisotope, fluorescent compound, enzyme, or  
20 enzyme co-factor.

The nucleic acid molecules of the invention such as those described above can be identified and isolated using standard molecular biology techniques and the sequence information provided herein. For example, nucleic acid molecules can be amplified and isolated by the polymerase chain reaction using synthetic  
25 oligonucleotide primers designed based on one or more of the sequences selected from the group consisting of SEQ ID NOs: 1, 114-258 or the complement of such a sequence, or designed based on nucleotides based on sequences encoding one or more of the amino acid sequences provided herein. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press,  
30 NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (Eds. Innis *et al.*, Academic Press, San Diego, CA, 1990); Mattila *et al.*, *Nucl. Acids Res.* 19: 4967

(1991); Eckert *et al.*, *PCR Methods and Applications* 1:17 (1991); PCR (eds. McPherson *et al.*, IRL Press, Oxford); and U.S. Patent 4,683,202. The nucleic acid molecules can be amplified using cDNA, mRNA or genomic DNA as a template, cloned into an appropriate vector and characterized by DNA sequence analysis.

5 Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4:560 (1989), Landegren *et al.*, *Science* 241:1077 (1988), transcription amplification (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86:1173 (1989)), and self-sustained sequence replication (Guatelli *et al.*, *Proc. Nat. Acad. Sci. USA* 87:1874 (1990)) and nucleic acid based sequence amplification (NASBA). The  
10 latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

The amplified DNA can be labeled, for example, radiolabeled, and used as a  
15 probe for screening a cDNA library derived from human cells, mRNA in zap express, ZIPLOX or other suitable vector. Corresponding clones can be isolated, DNA can be obtained following *in vivo* excision, and the cloned insert can be sequenced in either or both orientations by art recognized methods to identify the correct reading frame encoding a polypeptide of the appropriate molecular weight. For example, the direct  
20 analysis of the nucleotide sequence of nucleic acid molecules of the present invention can be accomplished using well-known methods that are commercially available. See, for example, Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind *et al.*, *Recombinant DNA Laboratory Manual*, (Acad. Press, 1988)). Additionally, fluorescence methods are also available for  
25 analyzing nucleic acids (Chen *et al.*, *Genome Res.* 9, 492 (1999)) and polypeptides. Using these or similar methods, the polypeptide and the DNA encoding the polypeptide can be isolated, sequenced and further characterized.

Antisense nucleic acid molecules of the invention can be designed using the nucleotide sequences of one or more of SEQ ID NOs: 1, 114-258 and/or the  
30 complement of one or more of SEQ ID NOs: 1, 114-258 and/or a portion of one or more of SEQ ID NOs: 1, 114-258 or the complement of one or more of SEQ ID NOs:



1, 114-258 and constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid molecule (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used. Alternatively, the antisense nucleic acid molecule can be produced biologically using an expression vector into which a nucleic acid molecule has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid molecule will be of an antisense orientation to a target nucleic acid of interest).

The nucleic acid sequences can also be used to compare with endogenous DNA sequences in patients to identify one or more of the disorders described above, and as probes, such as to hybridize and discover related DNA sequences or to subtract out known sequences from a sample. The nucleic acid sequences can further be used to derive primers for genetic fingerprinting, to raise anti-polypeptide antibodies using DNA immunization techniques, and as an antigen to raise anti-DNA antibodies or elicit immune responses. Portions or fragments of the nucleotide sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample. Additionally, the nucleotide sequences of the invention can be used to identify and express recombinant polypeptides for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding polypeptide is expressed, either constitutively, during tissue differentiation, or in diseased states. The nucleic acid sequences can additionally be used as reagents in the screening and/or diagnostic assays described herein, and can also be included as components of kits (e.g., reagent kits) for use in the screening and/or diagnostic assays described herein.

### *Vectors and Host Cells*

Another aspect of the invention pertains to nucleic acid constructs containing a nucleic acid molecule selected from the group consisting of SEQ ID NOs: 1, 114-258 and the complements thereof (or a portion thereof). The constructs comprise a vector (e.g., an expression vector) into which a sequence of the invention has been inserted in a sense or antisense orientation. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Expression vectors are capable of directing the expression of genes to which they are operably linked. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses) that serve equivalent functions.

In certain embodiments, recombinant expression vectors of the invention comprise a nucleic acid molecule of the invention in a form suitable for expression of the nucleic acid molecule in a host cell. This means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" or "operatively linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (e.g., in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence"

is intended to include promoters, enhancers and other expression control elements (e.g., polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, "Gene Expression Technology", *Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct  
5 constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed and the level of expression of polypeptide desired. The  
10 expression vectors of the invention can be introduced into host cells to thereby produce polypeptides, including fusion polypeptides, encoded by nucleic acid molecules as described herein.

The recombinant expression vectors of the invention can be designed for expression of a polypeptide of the invention in prokaryotic or eukaryotic cells, e.g.,  
15 bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors), yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, *supra*. Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

20 Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding  
25 generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, a nucleic acid molecule of the invention can be expressed in bacterial cells (e.g., *E. coli*), insect  
30 cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing a foreign nucleic acid molecule (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.*, (*supra*), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, for resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid molecules encoding a selectable marker can be introduced into a host cell on the same vector as the nucleic acid molecule of the invention or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid molecule can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) a polypeptide of the invention. Accordingly, the invention further provides methods for producing a polypeptide using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding a polypeptide of the invention has been introduced) in a suitable medium such that the polypeptide is produced. In another embodiment, the method further comprises isolating the polypeptide from the medium or the host cell.

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which a nucleic acid molecule of the

invention has been introduced (e.g., an exogenous KChIP1 gene, or an exogenous nucleic acid encoding a KChIP1 polypeptide). Such host cells can then be used to create non-human transgenic animals in which exogenous nucleotide sequences have been introduced into the genome or homologous recombinant animals in which  
5 endogenous nucleotide sequences have been altered. Such animals are useful for studying the function and/or activity of the nucleotide sequence and polypeptide encoded by the sequence and for identifying and/or evaluating modulators of their activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of  
10 the cells of the animal include a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens and amphibians. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types  
15 or tissues of the transgenic animal. As used herein, an "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, e.g., an embryonic cell of the animal, prior to development of the animal.

20 Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, U.S. Pat. NO: 4,873,191 and in Hogan, *Manipulating the Mouse Embryo* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). Methods for constructing  
25 homologous recombination vectors and homologous recombinant animals are described further in Bradley, *Current Opinion in BioTechnology* 2:823-829 (1991) and in PCT Publication Nos. WO 90/11354, WO 91/01140, WO 92/0968, and WO 93/04169. Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.*, *Nature* 385:810-813  
30 (1997) and PCT Publication Nos. WO 97/07668 and WO 97/07669.

## POLYPEPTIDES OF THE INVENTION

The present invention also pertains to isolated polypeptides encoded by KChIP1 nucleic acids ("KChIP1 polypeptides," or "KChIP1 proteins," such as the protein shown in SEQ ID NO: 2) and fragments and variants thereof, as well as polypeptides encoded by nucleotide sequences described herein (e.g., other splicing variants). The term "polypeptide" refers to a polymer of amino acids, and not to a specific length; thus, peptides, oligopeptides and proteins are included within the definition of a polypeptide. As used herein, a polypeptide is said to be "isolated" or "purified" when it is substantially free of cellular material when it is isolated from recombinant and non-recombinant cells, or free of chemical precursors or other chemicals when it is chemically synthesized. A polypeptide, however, can be joined to another polypeptide with which it is not normally associated in a cell (e.g., in a "fusion protein") and still be "isolated" or "purified."

The polypeptides of the invention can be purified to homogeneity. It is understood, however, that preparations in which the polypeptide is not purified to homogeneity are useful. The critical feature is that the preparation allows for the desired function of the polypeptide, even in the presence of considerable amounts of other components. Thus, the invention encompasses various degrees of purity. In one embodiment, the language "substantially free of cellular material" includes preparations of the polypeptide having less than about 30% (by dry weight) other proteins (i.e., contaminating protein), less than about 20% other proteins, less than about 10% other proteins, or less than about 5% other proteins.

When a polypeptide is recombinantly produced, it can also be substantially free of culture medium, i.e., culture medium represents less than about 20%, less than about 10%, or less than about 5% of the volume of the polypeptide preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of the polypeptide in which it is separated from chemical precursors or other chemicals that are involved in its synthesis. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of the polypeptide having less than about 30% (by dry weight) chemical precursors or other chemicals, less than about 20% chemical precursors or other chemicals, less

than about 10% chemical precursors or other chemicals, or less than about 5% chemical precursors or other chemicals.

In one embodiment, a polypeptide of the invention comprises an amino acid sequence encoded by a nucleic acid molecule comprising a nucleotide sequence of SEQ ID NO: 1, optionally additionally comprising one or more of SEQ ID NOs: 114-258; or the complement of such a nucleic acid, or portions thereof, or a portion or polymorphic variant thereof. However, the polypeptides of the invention also encompass fragment and sequence variants. Variants include a substantially homologous polypeptide encoded by the same genetic locus in an organism, *i.e.*, an allelic variant, as well as other splicing variants. Variants also encompass polypeptides derived from other genetic loci in an organism, but having substantial homology to a polypeptide encoded by a nucleic acid molecule comprising a nucleotide of SEQ ID NO: 1, optionally additionally one or more of SEQ ID NOs: 114-258; or a complement of such a sequence, or portions thereof or polymorphic variants thereof. Variants also include polypeptides substantially homologous or identical to these polypeptides but derived from another organism, *i.e.*, an ortholog. Variants also include polypeptides that are substantially homologous or identical to these polypeptides that are produced by chemical synthesis. Variants also include polypeptides that are substantially homologous or identical to these polypeptides that are produced by recombinant methods.

As used herein, two polypeptides (or a region of the polypeptides) are substantially homologous or identical when the amino acid sequences are at least about 45-55%, in certain embodiments at least about 70-75%, and in other embodiments at least about 80-85%, and in other embodiments greater than about 90% or more homologous or identical. A substantially homologous amino acid sequence, according to the present invention, will be encoded by a nucleic acid molecule hybridizing to of SEQ ID NO: 1 or any one of 114-258 or portion thereof, under stringent conditions as more particularly described above, or will be encoded by a nucleic acid molecule hybridizing to a nucleic acid sequence encoding SEQ ID NO: 1 or any one of 114-258 or a portion thereof or polymorphic variant thereof, under stringent conditions as more particularly described thereof.

The invention also encompasses polypeptides having a lower degree of identity but having sufficient similarity so as to perform one or more of the same functions performed by a polypeptide encoded by a nucleic acid molecule of the invention.

5 Similarity is determined by conserved amino acid substitution where a given amino acid in a polypeptide is substituted by another amino acid of like characteristics. Conservative substitutions are likely to be phenotypically silent. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl  
10 residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe and Tyr. Guidance concerning which amino acid changes are likely to be phenotypically silent are found in Bowie *et al.*, *Science* 247:1306-1310 (1990).

15 A variant polypeptide can differ in amino acid sequence by one or more substitutions, deletions, insertions, inversions, fusions, and truncations or a combination of any of these. Further, variant polypeptides can be fully functional or can lack function in one or more activities. Fully functional variants typically contain only conservative variation or variation in non-critical residues or in non-critical  
20 regions. Functional variants can also contain substitution of similar amino acids that result in no change or an insignificant change in function. Alternatively, such substitutions may positively or negatively affect function to some degree. Non-functional variants typically contain one or more non-conservative amino acid substitutions, deletions, insertions, inversions, or truncation or a substitution,  
25 insertion, inversion, or deletion in a critical residue or critical region.

Amino acids that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham *et al.*, *Science* 244:1082-1185 (1989)). The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant  
30 molecules are then tested for biological activity *in vitro*, or *in vitro* proliferative activity. Sites that are critical for polypeptide activity can also be determined by



structural analysis such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith *et al.*, *J. Mol. Biol.* 224:899-904 (1992); de Vos *et al.*, *Science* 255:306-312 (1992)).

The invention also includes polypeptide fragments of the polypeptides of the invention. Fragments can be derived from a polypeptide encoded by a nucleic acid molecule comprising SEQ ID NO: 1 and optionally comprising one or more of SEQ ID NOs: 114-258; or a complement of such a nucleic acid or other variants.

However, the invention also encompasses fragments of the variants of the polypeptides described herein. As used herein, a fragment comprises at least 6 contiguous amino acids. Useful fragments include those that retain one or more of the biological activities of the polypeptide as well as fragments that can be used as an immunogen to generate polypeptide-specific antibodies.

Biologically active fragments (peptides which are, for example, 6, 9, 12, 15, 16, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) can comprise a domain, segment, or motif that has been identified by analysis of the polypeptide sequence using well-known methods, *e.g.*, signal peptides, extracellular domains, one or more transmembrane segments or loops, ligand binding regions, zinc finger domains, DNA binding domains, acylation sites, glycosylation sites, or phosphorylation sites.

Fragments can be discrete (not fused to other amino acids or polypeptides) or can be within a larger polypeptide. Further, several fragments can be comprised within a single larger polypeptide. In one embodiment a fragment designed for expression in a host can have heterologous pre- and pro-polypeptide regions fused to the amino terminus of the polypeptide fragment and an additional region fused to the carboxyl terminus of the fragment.

The invention thus provides chimeric or fusion polypeptides. These comprise a polypeptide of the invention operatively linked to a heterologous protein or polypeptide having an amino acid sequence not substantially homologous to the polypeptide.

"Operatively linked" indicates that the polypeptide and the heterologous protein are fused in-frame. The heterologous protein can be fused to the N-terminus

or C-terminus of the polypeptide. In one embodiment the fusion polypeptide does not affect function of the polypeptide *per se*. For example, the fusion polypeptide can be a GST-fusion polypeptide in which the polypeptide sequences are fused to the C-terminus of the GST sequences. Other types of fusion polypeptides include, but are not limited to, enzymatic fusion polypeptides, for example beta-galactosidase fusions, yeast two-hybrid GAL fusions, poly-His fusions and Ig fusions. Such fusion polypeptides, particularly poly-His fusions, can facilitate the purification of recombinant polypeptide. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of a polypeptide can be increased using a heterologous signal sequence. Therefore, in another embodiment, the fusion polypeptide contains a heterologous signal sequence at its N-terminus.

EP-A-O 464 533 discloses fusion proteins comprising various portions of immunoglobulin constant regions. The Fc is useful in therapy and diagnosis and thus results, for example, in improved pharmacokinetic properties (EP-A 0232 262). In drug discovery, for example, human proteins have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists. Bennett *et al.*, *Journal of Molecular Recognition*, 8:52-58 (1995) and Johanson *et al.*, *The Journal of Biological Chemistry*, 270,16:9459-9471 (1995). Thus, this invention also encompasses soluble fusion polypeptides containing a polypeptide of the invention and various portions of the constant regions of heavy or light chains of immunoglobulins of various subclasses (IgG, IgM, IgA, IgE).

A chimeric or fusion polypeptide can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of nucleic acid fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive nucleic acid fragments which can subsequently be annealed and re-amplified to generate a chimeric nucleic acid sequence (see Ausubel *et al.*, *Current Protocols in Molecular Biology*, 1992).

Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST protein). A nucleic acid molecule encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the polypeptide.

5        The isolated polypeptide can be purified from cells that naturally express it, can be purified from cells that have been altered to express it (recombinant), or synthesized using known protein synthesis methods. In one embodiment, the polypeptide is produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the polypeptide is cloned into an expression vector, the  
10       expression vector introduced into a host cell and the polypeptide expressed in the host cell. The polypeptide can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques.

      The polypeptides of the present invention can be used to raise antibodies or to elicit an immune response. The polypeptides can also be used as a reagent, *e.g.*, a  
15       labeled reagent, in assays to quantitatively determine levels of the polypeptide or a molecule to which it binds (*e.g.*, a ligand) in biological fluids. The polypeptides can also be used as markers for cells or tissues in which the corresponding polypeptide is preferentially expressed, either constitutively, during tissue differentiation, or in a diseased state. The polypeptides can be used to isolate a corresponding binding agent,  
20       *e.g.*, ligand or receptor, such as, for example, in an interaction trap assay, and to screen for peptide or small molecule antagonists or agonists of the binding interaction.

#### ANTIBODIES OF THE INVENTION

      Polyclonal antibodies and/or monoclonal antibodies that specifically bind one  
25       form of the gene product but not to the other form of the gene product are also provided. Antibodies are also provided which bind a portion of either the variant or the reference gene product that contains the polymorphic site or sites. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen  
30       binding site that specifically bind an antigen. A molecule that specifically binds to a polypeptide of the invention is a molecule that binds to that polypeptide or a fragment

thereof, but does not substantially bind other molecules in a sample, *e.g.*, a biological sample, which naturally contains the polypeptide. Examples of immunologically active portions of immunoglobulin molecules include F(ab) and F(ab')<sub>2</sub> fragments which can be generated by treating the antibody with an enzyme such as pepsin. The invention provides polyclonal and monoclonal antibodies that bind to a polypeptide of the invention. The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of a polypeptide of the invention. A monoclonal antibody composition thus typically displays a single binding affinity for a particular polypeptide of the invention with which it immunoreacts.

Polyclonal antibodies can be prepared as described above by immunizing a suitable subject with a desired immunogen, *e.g.*, polypeptide of the invention or a fragment thereof. The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized polypeptide. If desired, the antibody molecules directed against the polypeptide can be isolated from the mammal (*e.g.*, from the blood) and further purified by well-known techniques, such as protein A chromatography to obtain the IgG fraction. At an appropriate time after immunization, *e.g.*, when the antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein, *Nature* 256:495-497 (1975), the human B cell hybridoma technique (Kozbor *et al.*, *Immunol. Today* 4: 72 (1983)), the EBV-hybridoma technique (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, 1985, Inc., pp. 77-96) or trioma techniques. The technology for producing hybridomas is well known (see generally *Current Protocols in Immunology* (1994) Coligan *et al.*, (eds.) John Wiley & Sons, Inc., New York, NY). Briefly, an immortal cell line (typically a myeloma) is fused to lymphocytes (typically splenocytes) from a mammal immunized with an immunogen as described above, and the culture supernatants of the resulting hybridoma cells are screened to

identify a hybridoma producing a monoclonal antibody that binds a polypeptide of the invention.

Any of the many well known protocols used for fusing lymphocytes and immortalized cell lines can be applied for the purpose of generating a monoclonal antibody to a polypeptide of the invention (see, e.g., *Current Protocols in Immunology*, *supra*; Galfre *et al.*, *Nature* 266:55052 (1977); R.H. Kenneth, in *Monoclonal Antibodies: A New Dimension In Biological Analyses*, Plenum Publishing Corp., New York, New York (1980); and Lerner, *Yale J. Biol. Med.* 54:387-402 (1981)). Moreover, the ordinarily skilled worker will appreciate that there are many variations of such methods that also would be useful.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody to a polypeptide of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (e.g., an antibody phage display library) with the polypeptide to thereby isolate immunoglobulin library members that bind the polypeptide. Kits for generating and screening phage display libraries are commercially available (e.g., the Pharmacia *Recombinant Phage Antibody System*, Catalog NO: 27-9400-01; and the Stratagene *SurfZAP™* Phage Display Kit, Catalog NO: 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent NO: 5,223,409; PCT Publication NO: WO 92/18619; PCT Publication NO: WO 91/17271; PCT Publication NO: WO 92/20791; PCT Publication NO: WO 92/15679; PCT Publication NO: WO 93/01288; PCT Publication NO: WO 92/01047; PCT Publication NO: WO 92/09690; PCT Publication NO: WO 90/02809; Fuchs *et al.*, *Bio/Technology* 9: 1370-1372 (1991); Hay *et al.*, *Hum. Antibod. Hybridomas* 3:81-85 (1992); Huse *et al.*, *Science* 246: 1275-1281 (1989); and Griffiths *et al.*, *EMBO J.* 12:725-734 (1993).

Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art.

In general, antibodies of the invention (e.g., a monoclonal antibody) can be used to isolate a polypeptide of the invention by standard techniques, such as affinity chromatography or immunoprecipitation. A polypeptide-specific antibody can facilitate the purification of natural polypeptide from cells and of recombinantly produced polypeptide expressed in host cells. Moreover, an antibody specific for a polypeptide of the invention can be used to detect the polypeptide (e.g., in a cellular lysate, cell supernatant, or tissue sample) in order to evaluate the abundance and pattern of expression of the polypeptide. Antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, e.g., to, for example, determine the efficacy of a given treatment regimen. The antibody can be coupled to a detectable substance to facilitate its detection. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{35}\text{S}$  or  $^3\text{H}$ .

## DIAGNOSTIC ASSAYS

The nucleic acids, probes, primers, polypeptides and antibodies described herein can be used in methods of diagnosis of Type II diabetes; of a susceptibility to Type II diabetes; or of a condition associated with a KChIP1 gene, as well as in kits (e.g., useful for diagnosis of Type II diabetes; a susceptibility to Type II diabetes; or a condition associated with a KChIP1 gene). In one embodiment, the kit comprises primers which contain one or more of the SNP's identified in Table 10.

In one embodiment of the invention, diagnosis of a disease or condition associated with a KChIP1 gene (e.g., diagnosis of Type II diabetes, or of a

susceptibility to Type II diabetes) is made by detecting a polymorphism in a KChIP1 nucleic acid as described herein. The polymorphism can be a change in a KChIP1 nucleic acid, such as the insertion or deletion of a single nucleotide, or of more than one nucleotide, resulting in a frame shift; the change of at least one nucleotide, resulting in a change in the encoded amino acid; the change of at least one nucleotide, resulting in the generation of a premature stop codon; the deletion of several nucleotides, resulting in a deletion of one or more amino acids encoded by the nucleotides; the insertion of one or several nucleotides, such as by unequal recombination or gene conversion, resulting in an interruption of the coding sequence of the gene; duplication of all or a part of the gene; transposition of all or a part of the gene; or rearrangement of all or a part of the gene. More than one such change may be present in a single gene. Such sequence changes cause a difference in the polypeptide encoded by a KChIP1 nucleic acid. For example, if the difference is a frame shift change, the frame shift can result in a change in the encoded amino acids, and/or can result in the generation of a premature stop codon, causing generation of a truncated polypeptide. Alternatively, a polymorphism associated with a disease or condition or a susceptibility to a disease or condition associated with a KChIP1 nucleic acid can be a synonymous alteration in one or more nucleotides (*i.e.*, an alteration that does not result in a change in the polypeptide encoded by a KChIP1 nucleic acid). Such a polymorphism may alter splicing sites, affect the stability or transport of mRNA, or otherwise affect the transcription or translation of the gene. A KChIP1 nucleic acid that has any of the changes or alterations described above is referred to herein as an "altered nucleic acid."

In a first method of diagnosing Type II diabetes or a susceptibility to Type II diabetes, or another disease or condition associated with a KChIP1 gene, hybridization methods, such as Southern analysis, Northern analysis, or *in situ* hybridizations, can be used (see *Current Protocols in Molecular Biology*, Ausubel, F. *et al.*, eds, John Wiley & Sons, including all supplements through 1999). For example, a biological sample (a "test sample") from a test subject (the "test individual") of genomic DNA, RNA, or cDNA, is obtained from an individual, such as an individual suspected of having, being susceptible to or predisposed for, or

carrying a defect for, the disease or condition, or the susceptibility to the disease or condition, associated with a KChIP1 gene (*e.g.*, Type II diabetes). The individual can be an adult, child, or fetus. The test sample can be from any source which contains genomic DNA, such as a blood sample, sample of amniotic fluid, sample of  
5 cerebrospinal fluid, or tissue sample from skin, muscle, buccal or conjunctival mucosa, placenta, gastrointestinal tract or other organs. A test sample of DNA from fetal cells or tissue can be obtained by appropriate methods, such as by amniocentesis or chorionic villus sampling. The DNA, RNA, or cDNA sample is then examined to determine whether a polymorphism in a KChIP1 nucleic acid is present, and/or to  
10 determine which splicing variant(s) encoded by the KChIP1 is present. The presence of the polymorphism or splicing variant(s) can be indicated by hybridization of the gene in the genomic DNA, RNA, or cDNA to a nucleic acid probe. A "nucleic acid probe", as used herein, can be a DNA probe or an RNA probe; the nucleic acid probe can contain, for example, at least one polymorphism in a KChIP1 nucleic acid (*e.g.*,  
15 as set forth in Table 10) and/or contain a nucleic acid encoding a particular splicing variant of a KChIP1 nucleic acid. The probe can be any of the nucleic acid molecules described above (*e.g.*, the gene or nucleic acid, a fragment, a vector comprising the gene or nucleic acid, a probe or primer, etc.).

To diagnose Type II diabetes, or a susceptibility to Type II diabetes, or  
20 another condition associated with a KChIP1 gene, a hybridization sample is formed by contacting the test sample containing a KChIP1 nucleic acid with at least one nucleic acid probe. A preferred probe for detecting mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to mRNA or genomic DNA sequences described herein. The nucleic acid probe can be, for example, a full-length  
25 nucleic acid molecule, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to appropriate mRNA or genomic DNA. For example, the nucleic acid probe can be all or a portion of one of SEQ ID NOs: 114-258 or the complement thereof, or a portion thereof. Other suitable probes for use in the  
30 diagnostic assays of the invention are described above (see *e.g.*, probes and primers discussed under the heading, "Nucleic Acids of the Invention").



The hybridization sample is maintained under conditions that are sufficient to allow specific hybridization of the nucleic acid probe to a KChIP1 nucleic acid.

"Specific hybridization", as used herein, indicates exact hybridization (e.g., with no mismatches). Specific hybridization can be performed under high stringency conditions or moderate stringency conditions, for example, as described above. In a particularly preferred embodiment, the hybridization conditions for specific hybridization are high stringency.

Specific hybridization, if present, is then detected using standard methods. If specific hybridization occurs between the nucleic acid probe and KChIP1 nucleic acid in the test sample, then the KChIP1 has the polymorphism, or is the splicing variant, that is present in the nucleic acid probe. More than one nucleic acid probe can also be used concurrently in this method. Specific hybridization of any one of the nucleic acid probes is indicative of a polymorphism in the KChIP1 nucleic acid, or of the presence of a particular splicing variant encoding the KChIP1 nucleic acid and is therefore diagnostic for a susceptibility to a disease or condition associated with a KChIP1 nucleic acid (e.g., Type II diabetes).

In Northern analysis (see *Current Protocols in Molecular Biology*, Ausubel, F. et al., eds., John Wiley & Sons, *supra*) the hybridization methods described above are used to identify the presence of a polymorphism or a particular splicing variant, associated with a susceptibility to a disease or condition associated with a KChIP1 gene (e.g., Type II diabetes). For Northern analysis, a test sample of RNA is obtained from the individual by appropriate means. Specific hybridization of a nucleic acid probe, as described above, to RNA from the individual is indicative of a polymorphism in a KChIP1 nucleic acid, or of the presence of a particular splicing variant encoded by a KChIP1 nucleic acid and is therefore diagnostic for Type II diabetes or a susceptibility to Type II diabetes or a condition associated with a KChIP1 nucleic acid (e.g., Type II diabetes).

For representative examples of use of nucleic acid probes, see, for example, U.S. Patents NO: 5,288,611 and 4,851,330.

Alternatively, a peptide nucleic acid (PNA) probe can be used instead of a nucleic acid probe in the hybridization methods described above. PNA is a DNA

mimic having a peptide-like, inorganic backbone, such as N-(2-aminoethyl)glycine units, with an organic base (A, G, C, T or U) attached to the glycine nitrogen via a methylene carbonyl linker (see, for example, Nielsen, P.E. *et al.*, *Bioconjugate Chemistry* 5, American Chemical Society, p. 1 (1994). The PNA probe can be  
5 designed to specifically hybridize to a gene having a polymorphism associated with a susceptibility to a disease or condition associated with a KChIP1 nucleic acid (*e.g.*, Type II diabetes). Hybridization of the PNA probe to a KChIP1 gene is diagnostic for Type II diabetes or a susceptibility to Type II diabetes or a condition associated with a KChIP1 nucleic acid.

10 In another method of the invention, alteration analysis by restriction digestion can be used to detect an altered gene, or genes containing a polymorphism(s), if the alteration (mutation) or polymorphism in the gene results in the creation or elimination of a restriction site. A test sample containing genomic DNA is obtained from the individual. Polymerase chain reaction (PCR) can be used to amplify a  
15 KChIP1 nucleic acid (and, if necessary, the flanking sequences) in the test sample of genomic DNA from the test individual. RFLP analysis is conducted as described (see *Current Protocols in Molecular Biology*, *supra*). The digestion pattern of the relevant DNA fragment indicates the presence or absence of the alteration or polymorphism in the KChIP1 nucleic acid, and therefore indicates the presence or absence of Type II  
20 diabetes or the susceptibility to a disease or condition associated with a KChIP1 nucleic acid.

Sequence analysis can also be used to detect specific polymorphisms in a KChIP1 nucleic acid. A test sample of DNA or RNA is obtained from the test individual. PCR or other appropriate methods can be used to amplify the gene or  
25 nucleic acid, and/or its flanking sequences, if desired. The sequence of a KChIP1 nucleic acid, or a fragment of the nucleic acid, or cDNA, or fragment of the cDNA, or mRNA, or fragment of the mRNA, is determined, using standard methods. The sequence of the nucleic acid, nucleic acid fragment, cDNA, cDNA fragment, mRNA, or mRNA fragment is compared with the known nucleic acid sequence of the gene or  
30 cDNA (*e.g.*, one or more of SEQ ID NOs: 114-258 or a complement thereof) or

mRNA, as appropriate. The presence of a polymorphism in the KChIP1 indicates that the individual has Type II diabetes or a susceptibility to Type II diabetes.

Allele-specific oligonucleotides can also be used to detect the presence of a polymorphism in a KChIP1 nucleic acid, through the use of dot-blot hybridization of amplified oligonucleotides with allele-specific oligonucleotide (ASO) probes (see, for example, Saiki, R. *et al.*, *Nature* 324:163-166 (1986)). An "allele-specific oligonucleotide" (also referred to herein as an "allele-specific oligonucleotide probe") is an oligonucleotide of approximately 10-50 base pairs, preferably approximately 15-30 base pairs, that specifically hybridizes to a KChIP1 nucleic acid, and that contains a polymorphism associated with a susceptibility to a disease or condition associated with a KChIP1 nucleic acid. An allele-specific oligonucleotide probe that is specific for particular polymorphisms in a KChIP1 nucleic acid can be prepared, using standard methods (see *Current Protocols in Molecular Biology*, *supra*). To identify polymorphisms in the gene that are associated with a disease or condition associated with a KChIP1 nucleic acid or a susceptibility to a disease or condition associated with a KChIP1 nucleic acid a test sample of DNA is obtained from the individual. PCR can be used to amplify all or a fragment of a KChIP1 nucleic acid and its flanking sequences. The DNA containing the amplified KChIP1 nucleic acid (or fragment of the gene or nucleic acid) is dot-blotted, using standard methods (see *Current Protocols in Molecular Biology*, *supra*), and the blot is contacted with the oligonucleotide probe. The presence of specific hybridization of the probe to the amplified KChIP1 nucleic acid is then detected. Hybridization of an allele-specific oligonucleotide probe to DNA from the individual is indicative of a polymorphism in the KChIP1 nucleic acid, and is therefore indicative of a disease or condition associated with a KChIP1 nucleic acid or susceptibility to a disease or condition associated with a KChIP1 nucleic acid (e.g., Type II diabetes).

The invention further provides allele-specific oligonucleotides that hybridize to the reference or variant allele of a gene or nucleic acid comprising a single nucleotide polymorphism or to the complement thereof. These oligonucleotides can be probes or primers.

An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in conjunction with a second primer, which hybridizes at a distal site. Amplification proceeds from the two primers, resulting in a detectable product, which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, *e.g.*, WO 93/22456).

With the addition of such analogs as locked nucleic acids (LNAs), the size of primers and probes can be reduced to as few as 8 bases. LNAs are a novel class of bicyclic DNA analogs in which the 2' and 4' positions in the furanose ring are joined via an O-methylene (oxy-LNA), S-methylene (thio-LNA), or amino methylene (amino-LNA) moiety. Common to all of these LNA variants is an affinity toward complementary nucleic acids, which is by far the highest reported for a DNA analog. For example, particular all oxy-LNA nonamers have been shown to have melting temperatures of 64°C and 74°C when in complex with complementary DNA or RNA, respectively, as opposed to 28°C for both DNA and RNA for the corresponding DNA nonamer. Substantial increases in  $T_m$  are also obtained when LNA monomers are used in combination with standard DNA or RNA monomers. For primers and probes, depending on where the LNA monomers are included (*e.g.*, the 3' end, the 5' end, or in the middle), the  $T_m$  could be increased considerably.

In another embodiment, arrays of oligonucleotide probes that are complementary to target nucleic acid sequence segments from an individual, can be used to identify polymorphisms in a KChIP1 nucleic acid. For example, in one embodiment, an oligonucleotide array can be used. Oligonucleotide arrays typically comprise a plurality of different oligonucleotide probes that are coupled to a surface of a substrate in different known locations. These oligonucleotide arrays, also

described as "Genechips™," have been generally described in the art, for example, U.S. Pat. NO: 5,143,854 and PCT patent publication Nos. WO 90/15070 and 92/10092. These arrays can generally be produced using mechanical synthesis methods or light directed synthesis methods that incorporate a combination of photolithographic methods and solid phase oligonucleotide synthesis methods. See 5 Fodor *et al.*, *Science* 251:767-777 (1991), Pirrung *et al.*, U.S. Pat. NO: 5,143,854 (see also PCT Application NO: WO 90/15070) and Fodor *et al.*, PCT Publication NO: WO 92/10092 and U.S. Pat. NO: 5,424,186, the entire teachings of each of which are incorporated by reference herein. Techniques for the synthesis of these arrays using 10 mechanical synthesis methods are described in, *e.g.*, U.S. Pat. NO: 5,384,261; the entire teachings of which are incorporated by reference herein. In another example, linear arrays can be utilized.

Once an oligonucleotide array is prepared, a nucleic acid of interest is hybridized with the array and scanned for polymorphisms. Hybridization and 15 scanning are generally carried out by methods described herein and also in, *e.g.*, published PCT Application Nos. WO 92/10092 and WO 95/11995, and U.S. Pat. NO: 5,424,186, the entire teachings of which are incorporated by reference herein. In brief, a target nucleic acid sequence that includes one or more previously identified polymorphic markers is amplified by well-known amplification techniques, *e.g.*, PCR. 20 Typically, this involves the use of primer sequences that are complementary to the two strands of the target sequence both upstream and downstream from the polymorphism. Asymmetric PCR techniques may also be used. Amplified target, generally incorporating a label, is then hybridized with the array under appropriate conditions. Upon completion of hybridization and washing of the array, the array is 25 scanned to determine the position on the array to which the target sequence hybridizes. The hybridization data obtained from the scan is typically in the form of fluorescence intensities as a function of location on the array.

Although primarily described in terms of a single detection block, *e.g.*, for detection of a single polymorphism, arrays can include multiple detection blocks, and 30 thus be capable of analyzing multiple, specific polymorphisms. In alternative arrangements, it will generally be understood that detection blocks may be grouped

within a single array or in multiple, separate arrays so that varying, optimal conditions may be used during the hybridization of the target to the array. For example, it may often be desirable to provide for the detection of those polymorphisms that fall within G-C rich stretches of a genomic sequence, separately from those falling in A-T rich segments. This allows for the separate optimization of hybridization conditions for each situation.

Additional uses of oligonucleotide arrays for polymorphism detection can be found, for example, in U.S. Patents Nos. 5,858,659 and 5,837,832, the entire teachings of which are incorporated by reference herein. Other methods of nucleic acid analysis can be used to detect polymorphisms in a Type II diabetes gene or variants encoding by a Type II diabetes gene. Representative methods include direct manual sequencing (Church and Gilbert, *Proc. Natl. Acad. Sci. USA* 81:1991-1995 (1988); Sanger, F. *et al.*, *Proc. Natl. Acad. Sci. USA* 74:5463-5467 (1977); Beavis *et al.*, U.S. Pat. NO: 5,288,644); automated fluorescent sequencing; single-stranded conformation polymorphism assays (SSCP); clamped denaturing gel electrophoresis (CDGE); denaturing gradient gel electrophoresis (DGGE) (Sheffield, V.C. *et al.*, *Proc. Natl. Acad. Sci. USA* 86:232-236 (1989)), mobility shift analysis (Orita, M. *et al.*, *Proc. Natl. Acad. Sci. USA* 86:2766-2770 (1989)), restriction enzyme analysis (Flavell *et al.*, *Cell* 15:25 (1978); Geever, *et al.*, *Proc. Natl. Acad. Sci. USA* 78:5081 (1981)); heteroduplex analysis; chemical mismatch cleavage (CMC) (Cotton *et al.*, *Proc. Natl. Acad. Sci. USA* 85:4397-4401 (1985)); RNase protection assays (Myers, R.M. *et al.*, *Science* 230:1242 (1985)); use of polypeptides which recognize nucleotide mismatches, such as *E. coli* mutS protein; allele-specific PCR, for example.

In one embodiment of the invention, diagnosis of a disease or condition associated with a KChIP1 nucleic acid (*e.g.*, Type II diabetes) or a susceptibility to a disease or condition associated with a KChIP1 nucleic acid (*e.g.*, Type II diabetes) can also be made by expression analysis by quantitative PCR (kinetic thermal cycling). This technique, utilizing TaqMan<sup>®</sup>, can be used to allow the identification of polymorphisms and whether a patient is homozygous or heterozygous. The technique can assess the presence of an alteration in the expression or composition of the

polypeptide encoded by a KChIP1 nucleic acid or splicing variants encoded by a KChIP1 nucleic acid. Further, the expression of the variants can be quantified as physically or functionally different.

In another embodiment of the invention, diagnosis of Type II diabetes or a susceptibility to Type II diabetes 5 or a condition associated with a KChIP1 gene) can be made by examining expression and/or composition of a KChIP1 polypeptide, by a variety of methods, including enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. A test sample from an individual is assessed for the presence of an alteration in the expression and/or an alteration in composition of the polypeptide encoded by a KChIP1 nucleic acid, or for 10 the presence of a particular variant encoded by a KChIP1 nucleic acid. An alteration in expression of a polypeptide encoded by a KChIP1 nucleic acid can be, for example, an alteration in the quantitative polypeptide expression (*i.e.*, the amount of polypeptide produced); an alteration in the composition of a polypeptide encoded by a KChIP1 nucleic acid is an alteration in the qualitative polypeptide expression (*e.g.*, 15 expression of an altered KChIP1 polypeptide or of a different splicing variant). In a preferred embodiment, diagnosis of the disease or condition associated with KChIP1 nucleic acid or a susceptibility to a disease or condition associated with a KChIP1 nucleic acid is made by detecting a particular splicing variant encoded by that KChIP1 nucleic acid, or a particular pattern of splicing variants. 20

Both such alterations (quantitative and qualitative) can also be present. The term "alteration" in the polypeptide expression or composition, as used herein, refers to an alteration in expression or composition in a test sample, as compared with the expression or composition of polypeptide by a KChIP1 nucleic acid in a control 25 sample. A control sample is a sample that corresponds to the test sample (*e.g.*, is from the same type of cells), and is from an individual who is not affected by a susceptibility to a disease or condition associated with a KChIP1 nucleic acid. An alteration in the expression or composition of the polypeptide in the test sample, as compared with the control sample, is indicative of a susceptibility to a disease or 30 condition associated with a KChIP1 nucleic acid. Similarly, the presence of one or more different splicing variants in the test sample, or the presence of significantly

different amounts of different splicing variants in the test sample, as compared with the control sample, is indicative of a disease or condition associated with a KChIP1 nucleic acid or a susceptibility to a disease or condition associated with a KChIP1 nucleic acid. Various means of examining expression or composition of the polypeptide encoded by a KChIP1 nucleic acid can be used, including: spectroscopy, colorimetry, lectrophoresis, isoelectric focusing, and immunoassays (*e.g.*, David *et al.*, U.S. Pat. 4,376,110) such as immunoblotting (see also *Current Protocols in Molecular Biology*, particularly Chapter 10). For example, in one embodiment, an antibody capable of binding to the polypeptide (*e.g.*, as described above), preferably an antibody with a detectable label, can be used. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')<sub>2</sub>) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin.

Western blotting analysis, using an antibody as described above that specifically binds to a polypeptide encoded by an altered KChIP1 nucleic acid (*e.g.*, a KChIP1 nucleic acid having one or more alterations as shown in Table 10), or an antibody that specifically binds to a polypeptide encoded by a non-altered nucleic acid, or an antibody that specifically binds to a particular splicing variant encoded by a nucleic acid, can be used to identify the presence in a test sample of a particular splicing variant or of a polypeptide encoded by a polymorphic or altered KChIP1 nucleic acid, or the absence in a test sample of a particular splicing variant or of a polypeptide encoded by a non-polymorphic or non-altered nucleic acid. The presence of a polypeptide encoded by a polymorphic or altered nucleic acid, or the absence of a polypeptide encoded by a non-polymorphic or non-altered nucleic acid, is diagnostic for a disease or condition associated with a KChIP1 nucleic acid or a susceptibility to a disease or condition associated with a KChIP1 nucleic acid (*e.g.*, Type II diabetes),



as is the presence (or absence) of particular splicing variants encoded by the KChIP1 nucleic acid.

In one embodiment of this method, the level or amount of polypeptide encoded by a KChIP1 nucleic acid in a test sample is compared with the level or amount of the polypeptide encoded by the KChIP1 in a control sample. A level or amount of the polypeptide in the test sample that is higher or lower than the level or amount of the polypeptide in the control sample, such that the difference is statistically significant, is indicative of an alteration in the expression of the polypeptide encoded by the KChIP1 nucleic acid, and is diagnostic for a disease or condition associated with a KChIP1 nucleic acid or a susceptibility to a disease or condition associated with that KChIP1 nucleic acid (*e.g.*, Type II diabetes). Alternatively, the composition of the polypeptide encoded by a KChIP1 nucleic acid in a test sample is compared with the composition of the polypeptide encoded by the KChIP1 nucleic acid in a control sample (*e.g.*, the presence of different splicing variants). A difference in the composition of the polypeptide in the test sample, as compared with the composition of the polypeptide in the control sample, is diagnostic for a disease or condition associated with a KChIP1 nucleic acid or a susceptibility to a disease or condition associated with that KChIP1 nucleic acid (*e.g.*, Type II diabetes). In another embodiment, both the level or amount and the composition of the polypeptide can be assessed in the test sample and in the control sample. A difference in the amount or level of the polypeptide in the test sample, compared to the control sample; a difference in composition in the test sample, compared to the control sample; or both a difference in the amount or level, and a difference in the composition, is indicative of a disease or condition associated with a KChIP1 nucleic acid or a susceptibility to a disease or condition associated with that KChIP1 nucleic acid.

The invention further pertains to a method for the diagnosis or identification of a susceptibility to Type II diabetes in an individual, by identifying an at-risk haplotype (*e.g.*, a haplotype comprising a KChIP1 nucleic acid). The KChIP1-associated haplotypes, *e.g.*, those described in Table 2 and Table 5, describe a set of genetic markers ("alleles"). In a certain embodiment, the haplotype can comprise one

or more alleles, two or more alleles, three or more alleles, four or more alleles, or five or more alleles. The genetic markers are particular "alleles" at "polymorphic sites" associated with KChIP1. A nucleotide position at which more than one sequence is possible in a population (either a natural population or a synthetic population, *e.g.*, a library of synthetic molecules), is referred to herein as a "polymorphic site". Where a polymorphic site is a single nucleotide in length, the site is referred to as a single nucleotide polymorphism ("SNP"). For example, if at a particular chromosomal location, one member of a population has an adenine and another member of the population has a thymine at the same position, then this position is a polymorphic site, and, more specifically, the polymorphic site is a SNP. Polymorphic sites can allow for differences in sequences based on substitutions, insertions or deletions. Each version of the sequence with respect to the polymorphic site is referred to herein as an "allele" of the polymorphic site. Thus, in the previous example, the SNP allows for both an adenine allele and a thymine allele.

Typically, a reference sequence is referred to for a particular sequence. Alleles that differ from the reference are referred to as "variant" alleles. For example, the reference KChIP1 sequence is described herein by SEQ ID NO: 1. The term, "variant KChIP1", as used herein, refers to a sequence that differs from SEQ ID NO: 1, but is otherwise substantially similar. The genetic markers that make up the haplotypes described herein are KChIP1 variants. The variants of KChIP1 that are used to determine the haplotypes disclosed herein of the present invention are associated with Type II diabetes or a susceptibility to Type II diabetes.

Additional variants can include changes that affect a polypeptide, *e.g.*, the KChIP1 polypeptide. These sequence differences, when compared to a reference nucleotide sequence, can include the insertion or deletion of a single nucleotide, or of more than one nucleotide, resulting in a frame shift; the change of at least one nucleotide, resulting in a change in the encoded amino acid; the change of at least one nucleotide, resulting in the generation of a premature stop codon; the deletion of several nucleotides, resulting in a deletion of one or more amino acids encoded by the nucleotides; the insertion of one or several nucleotides, such as by unequal recombination or gene conversion, resulting in an interruption of the coding sequence

of a reading frame; duplication of all or a part of a sequence; transposition; or a rearrangement of a nucleotide sequence, as described in detail above. Such sequence changes alter the polypeptide encoded by a KChIP1 nucleic acid. For example, if the change in the nucleic acid sequence causes a frame shift, the frame shift can result in a change in the encoded amino acids, and/or can result in the generation of a premature stop codon, causing generation of a truncated polypeptide. Alternatively, a polymorphism associated with Type II diabetes or a susceptibility to Type II diabetes can be a synonymous change in one or more nucleotides (*i.e.*, a change that does not result in a change in the amino acid sequence). Such a polymorphism can, for example, alter splice sites, affect the stability or transport of mRNA, or otherwise affect the transcription or translation of the polypeptide. The polypeptide encoded by the reference nucleotide sequence is the "reference" polypeptide with a particular reference amino acid sequence, and polypeptides encoded by variant alleles are referred to as "variant" polypeptides with variant amino acid sequences.

Haplotypes are a combination of genetic markers, *e.g.*, particular alleles at polymorphic sites. The haplotypes described herein, *e.g.*, having markers such as those shown in Table 10, Table 11, Table 12 or Table 13, are found more frequently in individuals with Type II diabetes than in individuals without Type II diabetes. Therefore, these haplotypes have predictive value for detecting Type II diabetes or a susceptibility to Type II diabetes in an individual. The haplotypes described herein are a combination of various genetic markers, *e.g.*, SNPs and microsatellites. Therefore, detecting haplotypes can be accomplished by methods known in the art for detecting sequences at polymorphic sites, such as the methods described above.

## HAPLOTYPE SCREENING

In the methods for the diagnosis and identification of susceptibility to Type II diabetes or Type II diabetes in an individual, an at-risk haplotype is identified. In one embodiment, the at-risk haplotype is one which confers a significant risk of Type II diabetes. In one embodiment, significance associated with a haplotype is measured by an odds ratio. In a further embodiment, the significance is measured by a percentage. In one embodiment, a significant risk is measured as an odds ratio of at

least about 1.2, including by not limited to: 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, and 1.9. In a further embodiment, an odds ratio of at least 1.2 is significant. In a further embodiment, an odds ratio of at least about 1.5 is significant. In a further embodiment, a significant increase in risk is at least about 1.7 is significant. In a further embodiment, a significant increase in risk is at least about 20%, including but not limited to about 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% and 98%. In a further embodiment, a significant increase in risk is at least about 50%. It is understood however, that identifying whether a risk is medically significant may also depend on a variety of factors, including the specific disease, the haplotype, and often, environmental factors.

The invention also pertains to methods of diagnosing Type II diabetes or a susceptibility to Type II diabetes in an individual, comprising screening for an at-risk haplotype in, or comprising portions of, the KChIP1 gene, where the haplotype is more frequently present in an individual susceptible to Type II diabetes (affected), compared to the frequency of its presence in a healthy individual (control), and wherein the presence of the haplotype is indicative of Type II diabetes or susceptibility to Type II diabetes. Standard techniques for genotyping for the presence of SNPs and/or microsatellite markers can be used, such as fluorescent based techniques (Chen, *et al.*, *Genome Res.* 9, 492 (1999)), PCR, LCR, Nested PCR and other techniques for nucleic acid amplification. In a preferred embodiment, the method comprises assessing in an individual the presence or frequency of SNPs and/or microsatellites in, comprising portions of, the KChIP1 gene, wherein an excess or higher frequency of the SNPs and/or microsatellites compared to a healthy control individual is indicative that the individual has Type II diabetes or is susceptible to Type II diabetes. See, for example, Tables 6, 7, 9, 11 and 13 (below) for SNPs and markers that can form haplotypes that can be used as screening tools. These markers and SNPs can be used to design diagnostic tests for determining Type II diabetes or a susceptibility to Type II diabetes. For example, an at-risk haplotype can include microsatellite markers and/or SNPs such as those set forth in Table 10, Table 11, Table 12 and/or Table 13. The presence of the haplotype is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes. Haplotype analysis involves

defining a candidate susceptibility locus using LOD scores. The defined regions are then ultra-fine mapped with microsatellite markers with an average spacing between markers of less than 100kb. All usable microsatellite markers that found in public databases and mapped within that region can be used. In addition, microsatellite markers identified within the deCODE genetics sequence assembly of the human genome can be used.

The frequencies of haplotypes in the patient and the control groups using an expectation-maximization algorithm can be estimated (Dempster A. *et al.*, 1977. *J. R. Stat. Soc. B*, 39:1-389). An implementation of this algorithm that can handle missing genotypes and uncertainty with the phase can be used. Under the null hypothesis, the patients and the controls are assumed to have identical frequencies. Using a likelihood approach, an alternative hypothesis where a candidate at-risk-haplotype, which can include the markers described herein, is allowed to have a higher frequency in patients than controls, while the ratios of the frequencies of other haplotypes are assumed to be the same in both groups is tested. Likelihoods are maximized separately under both hypotheses and a corresponding 1-df likelihood ratio statistics is used to evaluate the statistic significance.

To look for at-risk-haplotypes in the 1-lod drop, for example, association of all possible combinations of genotyped markers is studied, provided those markers span a practical region. The combined patient and control groups can be randomly divided into two sets, equal in size to the original group of patients and controls. The haplotype analysis is then repeated and the most significant p-value registered is determined. This randomization scheme can be repeated, for example, over 100 times to construct an empirical distribution of p-values.

The at-risk haplotypes identified in Table 2 (haplotypes identified as A1, A2, A3, A4, A5, A6, B1, B2, B3, B4 and B5) or Table 5 (haplotypes identified as D1, D2, D3, D4 and D5) are associated with Type II diabetes or a susceptibility to Type II diabetes. In certain embodiments, a haplotype associated with Type II diabetes or a susceptibility to Type II diabetes comprises markers DG5S879, DG5S881, D5S2075, DG5S883 and DG5S38 at the 5q35 locus; or DG5S1058 and DG5S37 at the 5q35 locus; or DG5S1058, DG5S37 and DG5S101 at the 5q35 locus; or DG5S881,

DG5S1058, D5S2075, DG5S883 and DG5S38 at the 5q35 locus; or DG5S879, DG5S1058 and DG5S37; or DG5S881, D5S2075, DG5S883 and DG5S38 at the 5q35 locus; DG5S953, DG5S955, DG5S13 and DG5S959 at the 5q35 locus; or DG5S888 and DG5S953 at the 5q35 locus; or DG5S953, DG5S955 and DG5S124 at the 5q35 locus; or DG5S888, DG5S44 and DG5S953 at the 5q35 locus; or DG5S953, DG5S955, DG5S13, DG5S123, and DG5S959 at the 5q35 locus. The presence of the haplotype is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes.

Also described herein is a haplotype associated with Type II diabetes or a

susceptibility to Type II diabetes comprising markers DG5S13, KCP\_1152, and

D5S625 at the 5q35 locus; the presence of the haplotype is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes. In one particular embodiment, the presence of the -4, 1, 0 haplotype at DG5S13, KCP\_1152, and D5S625 is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes. In another embodiment, a haplotype associated with Type II diabetes or a susceptibility to Type II diabetes in an individual, comprises markers DG5S124, KCP\_1152, KCP\_2649, KPC\_4976 and KPC-16152 at the 5q35 locus. In one particular embodiment, the presence of the 0, 1, 1, 3 and 0 haplotype at DG5S124, KCP\_1152, KCP\_2649, KPC\_4976 and KPC-16152 is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes. In another embodiment, a haplotype associated with Type II diabetes or a susceptibility to Type II diabetes in an individual, comprises markers KCP\_173982, KCP\_15400, and KCP\_18069. In one particular embodiment, the presence of the 0, 1, 1 haplotype at KCP\_173982, KCP\_15400, and KCP\_18069 is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes.

In additional embodiments, a haplotype associated with Type II diabetes or a susceptibility to Type II diabetes comprises markers DG5S124, KCP\_1152, KCP\_2649, KCP\_4976, and KCP\_16152 at the 5q35 locus, as well as one of the following 3 markers: KCP\_197678, KCP\_197775, and KCP\_202795 at the 5q35 locus; the presence of the haplotype is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes. In particular embodiments, the presence of the 0, 3, 1, 1, 3, 0 haplotype at DG5S124, KCP\_197679, KCP\_1152, KCP\_2649, KCP\_4976, and KCP\_16152; the presence of the 0, 3, 1, 1, 3, 0 haplotype at DG5S124,

KCP\_197775, KCP\_1152, KCP\_2649, KCP\_4976, and KCP\_16152; or the presence of the 0, 1, 1, 1, 3, 0 haplotype at DG5S124, KCP\_202795, KCP\_1152, KCP\_2649, KCP\_4976, and KCP\_16152; is diagnostic of Type II diabetes or of a susceptibility to Type II diabetes.

5       Kits (*e.g.*, reagent kits) useful in the methods of diagnosis comprise components useful in any of the methods described herein, including for example, hybridization probes or primers as described herein (*e.g.*, labeled probes or primers), reagents for detection of labeled molecules, restriction enzymes (*e.g.*, for RFLP analysis), allele-specific oligonucleotides, antibodies which bind to altered or to non-  
10       altered (native) KChIP1 polypeptide, means for amplification of nucleic acids comprising a KChIP1 nucleic acid, or means for analyzing the nucleic acid sequence of a KChIP1 nucleic acid or for analyzing the amino acid sequence of a KChIP1 polypeptide as described herein, etc. In one embodiment, the kit for diagnosing a Type II diabetes or a susceptibility to Type II diabetes can comprise primers for  
15       nucleic acid amplification of a region in the KChIP1 nucleic acid comprising an at-risk haplotype that is more frequently present in an individual having Type II diabetes or who is susceptible to Type II diabetes. The primers can be designed using portions of the nucleic acids flanking SNPs that are indicative of Type II diabetes. In a certain embodiment, the primers are designed to amplify regions of the KChIP1 gene  
20       associated with an at-risk haplotype for Type II diabetes, as shown in Table 10 and 13, or more particularly the haplotypes described in Tables 2 and 5.

#### SCREENING ASSAYS AND AGENTS IDENTIFIED THEREBY

      The invention provides methods (also referred to herein as "screening assays")  
25       for identifying the presence of a nucleotide that hybridizes to a nucleic acid of the invention, as well as for identifying the presence of a polypeptide encoded by a nucleic acid of the invention. In one embodiment, the presence (or absence) of a nucleic acid molecule of interest (*e.g.*, a nucleic acid that has significant homology with a nucleic acid of the invention) in a sample can be assessed by contacting the  
30       sample with a nucleic acid comprising a nucleic acid of the invention (*e.g.*, a nucleic acid having the sequence of one of SEQ ID NOs: 1, 114-258, or the complement

thereof, or a nucleic acid encoding an amino acid having the sequence of one of SEQ ID NOs: 2, or a fragment or variant of such nucleic acids), under stringent conditions as described above, and then assessing the sample for the presence (or absence) of hybridization. In one embodiment, high stringency conditions are conditions  
5 appropriate for selective hybridization. In another embodiment, a sample containing the nucleic acid molecule of interest is contacted with a nucleic acid containing a contiguous nucleotide sequence (*e.g.*, a primer or a probe as described above) that is at least partially complementary to a part of the nucleic acid molecule of interest (*e.g.*, a KChIP1 nucleic acid), and the contacted sample is assessed for the presence or  
10 absence of hybridization. In another embodiment, the nucleic acid containing a contiguous nucleotide sequence is completely complementary to a part of the nucleic acid molecule of interest.

In any of these embodiments, all or a portion of the nucleic acid of interest can be subjected to amplification prior to performing the hybridization.

15 In another embodiment, the presence (or absence) of a polypeptide of interest, such as a polypeptide of the invention or a fragment or variant thereof, in a sample can be assessed by contacting the sample with an antibody that specifically hybridizes to the polypeptide of interest (*e.g.*, an antibody such as those described above), and then assessing the sample for the presence (or absence) of binding of the antibody to  
20 the polypeptide of interest.

In another embodiment, the invention provides methods for identifying agents (*e.g.*, fusion proteins, polypeptides, peptidomimetics, prodrugs, receptors, binding agents, antibodies, small molecules or other drugs, or ribozymes) which alter (*e.g.*, increase or decrease) the activity of the polypeptides described herein, or which  
25 otherwise interact with the polypeptides herein. For example, such agents can be agents which bind to polypeptides described herein (*e.g.*, KChIP1 binding agents); which have a stimulatory or inhibitory effect on, for example, activity of polypeptides of the invention; or which change (*e.g.*, enhance or inhibit) the ability of the polypeptides of the invention to interact with KChIP1 binding agents (*e.g.*, receptors  
30 or other binding agents); or which alter posttranslational processing of the KChIP1 polypeptide (*e.g.*, agents that alter proteolytic processing to direct the polypeptide



from where it is normally synthesized to another location in the cell, such as the cell surface; agents that alter proteolytic processing such that more polypeptide is released from the cell, etc.

In one embodiment, the invention provides assays for screening candidate or test agents that bind to or modulate the activity of polypeptides described herein (or biologically active portion(s) thereof), as well as agents identifiable by the assays. Test agents can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to polypeptide libraries, while the other four approaches are applicable to polypeptide, non-peptide oligomer or small molecule libraries of compounds (Lam, K.S., *Anticancer Drug Des.* 12:145 (1997)).

In one embodiment, to identify agents which alter the activity of a KChIP1 polypeptide, a cell, cell lysate, or solution containing or expressing a KChIP1 polypeptide, or another splicing variant encoded by a KChIP1 gene (such as comprising a SNP as shown in Table 10 and/or 3), or a fragment or derivative thereof (as described above), can be contacted with an agent to be tested; alternatively, the polypeptide can be contacted directly with the agent to be tested. The level (amount) of KChIP1 activity is assessed (e.g., the level (amount) of KChIP1 activity is measured, either directly or indirectly), and is compared with the level of activity in a control (i.e., the level of activity of the KChIP1 polypeptide or active fragment or derivative thereof in the absence of the agent to be tested). If the level of the activity in the presence of the agent differs, by an amount that is statistically significant, from the level of the activity in the absence of the agent, then the agent is an agent that alters the activity of a KChIP1 polypeptide. An increase in the level of KChIP1 activity relative to a control, indicates that the agent is an agent that enhances (is an agonist of) KChIP1 activity. Similarly, a decrease in the level of KChIP1 activity relative to a control, indicates that the agent is an agent that inhibits (is an antagonist of) KChIP1 activity. In another embodiment, the level of activity of a KChIP1

polypeptide or derivative or fragment thereof in the presence of the agent to be tested, is compared with a control level that has previously been established. A level of the activity in the presence of the agent that differs from the control level by an amount that is statistically significant indicates that the agent alters KChIP1 activity.

5       The present invention also relates to an assay for identifying agents which alter the expression of a KChIP1 nucleic acid (*e.g.*, antisense nucleic acids, fusion proteins, polypeptides, peptidomimetics, prodrugs, receptors, binding agents, antibodies, small molecules or other drugs, or ribozymes) which alter (*e.g.*, increase or decrease) expression (*e.g.*, transcription or translation) of the gene or which  
10       otherwise interact with the nucleic acids described herein, as well as agents identifiable by the assays. For example, a solution containing a nucleic acid encoding a KChIP1 polypeptide (*e.g.*, a KChIP1 gene or nucleic acid) can be contacted with an agent to be tested. The solution can comprise, for example, cells containing the nucleic acid or cell lysate containing the nucleic acid; alternatively, the solution can  
15       be another solution that comprises elements necessary for transcription/translation of the nucleic acid. Cells not suspended in solution can also be employed, if desired. The level and/or pattern of KChIP1 expression (*e.g.*, the level and/or pattern of mRNA or of protein expressed, such as the level and/or pattern of different splicing variants) is assessed, and is compared with the level and/or pattern of expression in a  
20       control (*i.e.*, the level and/or pattern of the KChIP1 expression in the absence of the agent to be tested). If the level and/or pattern in the presence of the agent differs, by an amount or in a manner that is statistically significant, from the level and/or pattern in the absence of the agent, then the agent is an agent that alters the expression of a Type II diabetes gene. Enhancement of KChIP1 expression indicates that the agent is  
25       an agonist of KChIP1 activity. Similarly, inhibition of KChIP1 expression indicates that the agent is an antagonist of KChIP1 activity. In another embodiment, the level and/or pattern of KChIP1 polypeptide(s) (*e.g.*, different splicing variants) in the presence of the agent to be tested, is compared with a control level and/or pattern that have previously been established. A level and/or pattern in the presence of the agent  
30       that differs from the control level and/or pattern by an amount or in a manner that is statistically significant indicates that the agent alters KChIP1 expression.

In another embodiment of the invention, agents which alter the expression of a KChIP1 nucleic acid or which otherwise interact with the nucleic acids described herein, can be identified using a cell, cell lysate, or solution containing a nucleic acid encoding the promoter region of the KChIP1 gene or nucleic acid operably linked to a reporter gene. After contact with an agent to be tested, the level of expression of the reporter gene (*e.g.*, the level of mRNA or of protein expressed) is assessed, and is compared with the level of expression in a control (*i.e.*, the level of the expression of the reporter gene in the absence of the agent to be tested). If the level in the presence of the agent differs, by an amount or in a manner that is statistically significant, from the level in the absence of the agent, then the agent is an agent that alters the expression of the KChIP1, as indicated by its ability to alter expression of a gene that is operably linked to the KChIP1 gene promoter. Enhancement of the expression of the reporter indicates that the agent is an agonist of KChIP1 activity. Similarly, inhibition of the expression of the reporter indicates that the agent is an antagonist of KChIP1 activity. In another embodiment, the level of expression of the reporter in the presence of the agent to be tested is compared with a control level that has previously been established. A level in the presence of the agent that differs from the control level by an amount or in a manner that is statistically significant indicates that the agent alters expression.

Agents which alter the amounts of different splicing variants encoded by a KChIP1 nucleic acid (*e.g.*, an agent which enhances activity of a first splicing variant, and which inhibits activity of a second splicing variant), as well as agents which are agonists of activity of a first splicing variant and antagonists of activity of a second splicing variant, can easily be identified using these methods described above.

In other embodiments of the invention, assays can be used to assess the impact of a test agent on the activity of a polypeptide in relation to a KChIP1 binding agent. For example, a cell that expresses a compound that interacts with a KChIP1 polypeptide (herein referred to as a "KChIP1 binding agent", which can be a polypeptide or other molecule that interacts with a KChIP1 polypeptide, such as a receptor) is contacted with a KChIP1 in the presence of a test agent, and the ability of the test agent to alter the interaction between the KChIP1 and the KChIP1 binding

agent is determined. Alternatively, a cell lysate or a solution containing the KChIP1 binding agent, can be used. An agent which binds to the KChIP1 or the KChIP1 binding agent can alter the interaction by interfering with, or enhancing the ability of the KChIP1 to bind to, associate with, or otherwise interact with the KChIP1 binding agent. Determining the ability of the test agent to bind to a KChIP1 nucleic acid or a KChIP1 binding agent can be accomplished, for example, by coupling the test agent with a radioisotope or enzymatic label such that binding of the test agent to the polypeptide can be determined by detecting the labeled with  $^{125}\text{I}$ ,  $^{35}\text{S}$ ,  $^{14}\text{C}$  or  $^3\text{H}$ , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test agents can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. It is also within the scope of this invention to determine the ability of a test agent to interact with the polypeptide without the labeling of any of the interactants. For example, a microphysiometer can be used to detect the interaction of a test agent with a KChIP1 polypeptide or a KChIP1 binding agent without the labeling of either the test agent, KChIP1 polypeptide, or the KChIP1 binding agent. McConnell, H.M. *et al.*, *Science* 257:1906-1912 (1992). As used herein, a "microphysiometer" (*e.g.*, Cytosensor<sup>TM</sup>) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate can be used as an indicator of the interaction between ligand and polypeptide.

Thus, these receptors can be used to screen for compounds that are agonists or antagonists, for use in treating a susceptibility to a disease or condition associated with a KChIP1 gene or nucleic acid; or for studying a susceptibility to a disease or condition associated with a KChIP1 (*e.g.*, Type II diabetes). Drugs could be designed to regulate KChIP1 activation that in turn can be used to regulate signaling pathways and transcription events of genes downstream.

In another embodiment of the invention, assays can be used to identify polypeptides that interact with one or more KChIP1 polypeptides, as described herein.

For example, a yeast two-hybrid system such as that described by Fields and Song (Fields, S. and Song, O., *Nature* 340:245-246 (1989)) can be used to identify polypeptides that interact with one or more KChIP1 polypeptides. In such a yeast two-hybrid system, vectors are constructed based on the flexibility of a transcription factor that has two functional domains (a DNA binding domain and a transcription activation domain). If the two domains are separated but fused to two different proteins that interact with one another, transcriptional activation can be achieved, and transcription of specific markers (e.g., nutritional markers such as His and Ade, or color markers such as lacZ) can be used to identify the presence of interaction and transcriptional activation. For example, in the methods of the invention, a first vector is used which includes a nucleic acid encoding a DNA binding domain and also a KChIP1 polypeptide, splicing variant, or fragment or derivative thereof, and a second vector is used which includes a nucleic acid encoding a transcription activation domain and also a nucleic acid encoding a polypeptide which potentially may interact with the KChIP1 polypeptide, splicing variant, or fragment or derivative thereof (e.g., a KChIP1 polypeptide binding agent or receptor). Incubation of yeast containing the first vector and the second vector under appropriate conditions (e.g., mating conditions such as used in the Matchmaker™ system from Clontech (Palo Alto, California, USA)) allows identification of colonies that express the markers of interest. These colonies can be examined to identify the polypeptide(s) that interact with the KChIP1 polypeptide or fragment or derivative thereof. Such polypeptides may be useful as agents that alter the activity of expression of a KChIP1 polypeptide, as described above.

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either the KChIP1 gene or nucleic acid, the KChIP1 polypeptide, the KChIP1 binding agent, or other components of the assay on a solid support, in order to facilitate separation of complexed from uncomplexed forms of one or both of the polypeptides, as well as to accommodate automation of the assay. Binding of a test agent to the polypeptide, or interaction of the polypeptide with a binding agent in the presence and absence of a test agent, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include

microtitre plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein (*e.g.*, a glutathione-S-transferase fusion protein) can be provided which adds a domain that allows a KChIP1 nucleic acid, KChIP1 polypeptide, or a KChIP1 binding agent to be bound to a matrix or other solid support.

5 In another embodiment, modulators of expression of nucleic acid molecules of the invention are identified in a method wherein a cell, cell lysate, or solution containing a KChIP1 nucleic acid is contacted with a test agent and the expression of appropriate mRNA or polypeptide (*e.g.*, splicing variant(s)) in the cell, cell lysate, or solution, is determined. The level of expression of appropriate mRNA or  
10 polypeptide(s) in the presence of the test agent is compared to the level of expression of mRNA or polypeptide(s) in the absence of the test agent. The test agent can then be identified as a modulator of expression based on this comparison. For example, when expression of mRNA or polypeptide is greater (statistically significantly greater) in the presence of the test agent than in its absence, the test agent is identified  
15 as a stimulator or enhancer of the mRNA or polypeptide expression. Alternatively, when expression of the mRNA or polypeptide is less (statistically significantly less) in the presence of the test agent than in its absence, the test agent is identified as an inhibitor of the mRNA or polypeptide expression. The level of mRNA or polypeptide expression in the cells can be determined by methods described herein for detecting  
20 mRNA or polypeptide.

This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein (*e.g.*, a test agent that is a  
25 modulating agent, an antisense nucleic acid molecule, a specific antibody, or a polypeptide-binding agent) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the mechanism of action of such an agent.

30 Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein. In addition, an

agent identified as described herein can be used to alter activity of a polypeptide encoded by a KChIP1 nucleic acid, or to alter expression of a KChIP1 nucleic acid, by contacting the polypeptide or the nucleic acid (or contacting a cell comprising the polypeptide or the nucleic acid) with the agent identified as described herein.

5

## PHARMACEUTICAL COMPOSITIONS

The present invention also pertains to pharmaceutical compositions comprising nucleic acids described herein, particularly nucleotides encoding the polypeptides described herein (*e.g.*, a KChIP1 polypeptide); comprising polypeptides described herein and/or comprising other splicing variants encoded by a KChIP1 nucleic acid; and/or an agent that alters (*e.g.*, enhances or inhibits) KChIP1 nucleic acid expression or KChIP1 polypeptide activity as described herein. For instance, a polypeptide, protein (*e.g.*, a KChIP1 nucleic acid receptor), an agent that alters KChIP1 nucleic acid expression, or a KChIP1 binding agent or binding partner, fragment, fusion protein or pro-drug thereof, or a nucleotide or nucleic acid construct (vector) comprising a nucleotide of the present invention, or an agent that alters KChIP1 polypeptide activity, can be formulated with a physiologically acceptable carrier or excipient to prepare a pharmaceutical composition. The carrier and composition can be sterile. The formulation should suit the mode of administration.

20 Suitable pharmaceutically acceptable carriers include but are not limited to water, salt solutions (*e.g.*, NaCl), saline, buffered saline, alcohols, glycerol, ethanol, gum arabic, vegetable oils, benzyl alcohols, polyethylene glycols, gelatin, carbohydrates such as lactose, amylose or starch, dextrose, magnesium stearate, talc, silicic acid, viscous paraffin, perfume oil, fatty acid esters, hydroxymethylcellulose, polyvinyl pyrrolidone, etc., as well as combinations thereof. The pharmaceutical preparations can, if desired, be mixed with auxiliary agents, *e.g.*, lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, coloring, flavoring and/or aromatic substances and the like which do not deleteriously react with the active agents.

30 The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. The composition can be a liquid solution,

suspension, emulsion, tablet, pill, capsule, sustained release formulation, or powder.

The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, polyvinyl  
5 pyrollidone, sodium saccharine, cellulose, magnesium carbonate, etc.

Methods of introduction of these compositions include, but are not limited to, intradermal, intramuscular, intraperitoneal, intraocular, intravenous, subcutaneous, topical, oral and intranasal. Other suitable methods of introduction can also include gene therapy (as described below), rechargeable or biodegradable devices, particle  
10 acceleration devises ("gene guns") and slow release polymeric devices. The pharmaceutical compositions of this invention can also be administered as part of a combinatorial therapy with other agents.

The composition can be formulated in accordance with the routine procedures as a pharmaceutical composition adapted for administration to human beings. For  
15 example, compositions for intravenous administration typically are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a  
20 hermetically sealed container such as an ampule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water, saline or dextrose/water. Where the composition is administered by injection, an ampule of sterile water for injection or saline can be provided so that the ingredients may be  
25 mixed prior to administration.

For topical application, nonsprayable forms, viscous to semi-solid or solid forms comprising a carrier compatible with topical application and having a dynamic viscosity preferably greater than water, can be employed. Suitable formulations include but are not limited to solutions, suspensions, emulsions, creams, ointments,  
30 powders, enemas, lotions, sols, liniments, salves, aerosols, etc., which are, if desired, sterilized or mixed with auxiliary agents, e.g., preservatives, stabilizers, wetting



agents, buffers or salts for influencing osmotic pressure, etc. The agent may be incorporated into a cosmetic formulation. For topical application, also suitable are sprayable aerosol preparations wherein the active ingredient, preferably in combination with a solid or liquid inert carrier material, is packaged in a squeeze  
5 bottle or in admixture with a pressurized volatile, normally gaseous propellant, *e.g.*, pressurized air.

Agents described herein can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with free amino groups such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., and  
10 those formed with free carboxyl groups such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

The agents are administered in a therapeutically effective amount. The amount of agents which will be therapeutically effective in the treatment of a  
15 particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the symptoms, and should be decided according  
20 to the judgment of a practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical  
25 compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use of sale for human administration. The pack or kit can be labeled with information regarding mode of administration, sequence of drug  
30 administration (*e.g.*, separately, sequentially or concurrently), or the like. The pack or kit may also include means for reminding the patient to take the therapy. The pack or

kit can be a single unit dosage of the combination therapy or it can be a plurality of unit dosages. In particular, the agents can be separated, mixed together in any combination, present in a single vial or tablet. Agents assembled in a blister pack or other dispensing means is preferred. For the purpose of this invention, unit dosage is  
5 intended to mean a dosage that is dependent on the individual pharmacodynamics of each agent and administered in FDA approved dosages in standard time courses.

## METHODS OF THERAPY

The present invention also pertains to methods of treatment (prophylactic  
10 and/or therapeutic) for certain diseases and conditions associated with KChIP1. In particular, the invention relates to methods of treatment for Type II diabetes or a susceptibility to Type II diabetes, using a Type II diabetes therapeutic agent. A "Type II diabetes therapeutic agent" is an agent that alters (*e.g.*, enhances or inhibits) KChIP1 polypeptide activity and/or KChIP1 nucleic acid expression, as described  
15 herein (*e.g.*, a Type II diabetes nucleic acid agonist or antagonist). In certain embodiments, the Type II diabetes therapeutic agent alters activity and/or nucleic acid expression of KChIP1.

Type II diabetes therapeutic agents can alter KChIP1 polypeptide activity or nucleic acid expression by a variety of means, such as, for example, by providing  
20 additional KChIP1 polypeptide or by upregulating the transcription or translation of the KChIP1 nucleic acid; by altering posttranslational processing of the KChIP1 polypeptide; by altering transcription of KChIP1 splicing variants; or by interfering with KChIP1 polypeptide activity (*e.g.*, by binding to a KChIP1 polypeptide), or by binding to another polypeptide that interacts with KChIP1, by altering (*e.g.*,  
25 downregulating) the expression, transcription or translation of a KChIP1 nucleic acid, or by altering (*e.g.*, agonizing or antagonizing) activity.

Representative Type II diabetes therapeutic agents include the following:

nucleic acids or fragments or derivatives thereof described herein, particularly  
30 nucleotides encoding the polypeptides described herein and vectors comprising such nucleic acids (*e.g.*, a gene, cDNA, and/or mRNA, such as a

nucleic acid encoding a KChIP1 polypeptide or active fragment or derivative thereof, or an oligonucleotide; or a complement thereof, or fragments or derivatives thereof, and/or other splicing variants encoded by a Type II diabetes nucleic acid, or fragments or derivatives thereof);

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polypeptides described herein and/ or splicing variants encoded by the KChIP1 nucleic acid or fragments or derivatives thereof;

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other polypeptides (*e.g.*, KChIP1 receptors); KChIP1 binding agents; or agents that affect (*e.g.*, increase or decrease) activity,

antibodies, such as an antibody to an altered KChIP1 polypeptide, or an antibody to a non-altered KChIP1 polypeptide, or an antibody to a particular splicing variant encoded by a KChIP1 nucleic acid as described above;

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peptidomimetics; fusion proteins or prodrugs thereof; ribozymes; other small molecules; and

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other agents that alter (*e.g.*, enhance or inhibit) expression of a KChIP1 nucleic acid, or that regulate transcription of KChIP1 splicing variants (*e.g.*, agents that affect which splicing variants are expressed, or that affect the amount of each splicing variant that is expressed).

More than one Type II diabetes therapeutic agent can be used concurrently, if desired.

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A Type II diabetes nucleic acid therapeutic agent that is a nucleic acid is used in the treatment of Type II diabetes or in the treatment for a susceptibility to Type II diabetes. The term, "treatment" as used herein, refers not only to ameliorating symptoms associated with the disease or condition, but also preventing or delaying the onset of the disease or condition, and also lessening the severity or frequency of symptoms of the disease or condition. The therapy is designed to alter (*e.g.*, inhibit or enhance), replace or supplement activity of a KChIP1 polypeptide in an individual.

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For example, a Type II diabetes therapeutic agent can be administered in order to upregulate or increase the expression or availability of the KChIP1 nucleic acid or of specific splicing variants of KChIP1 nucleic acid, or, conversely, to downregulate or decrease the expression or availability of the KChIP1 nucleic acid or specific splicing variants of the KChIP1 nucleic acid. Upregulation or increasing expression or availability of a native KChIP1 gene or nucleic acid or of a particular splicing variant could interfere with or compensate for the expression or activity of a defective gene or another splicing variant; downregulation or decreasing expression or availability of a native KChIP1 gene or of a particular splicing variant could minimize the expression or activity of a defective gene or the particular splicing variant and thereby minimize the impact of the defective gene or the particular splicing variant.

The Type II diabetes therapeutic agent(s) are administered in a therapeutically effective amount (*i.e.*, an amount that is sufficient to treat the disease, such as by ameliorating symptoms associated with the disease, preventing or delaying the onset of the disease, and/or also lessening the severity or frequency of symptoms of the disease). The amount which will be therapeutically effective in the treatment of a particular individual's disorder or condition will depend on the symptoms and severity of the disease, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of a practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

In one embodiment, a nucleic acid of the invention (*e.g.*, a nucleic acid encoding a KChIP1 polypeptide, such as one of SEQ ID NO: 1 or a complement thereof); or another nucleic acid that encodes a KChIP1 polypeptide or a splicing variant, derivative or fragment thereof (*e.g.*, comprising any one or more of SEQ ID NO: 114-258), can be used, either alone or in a pharmaceutical composition as described above. For example, a KChIP1 gene or nucleic acid or a cDNA encoding a KChIP1 polypeptide, either by itself or included within a vector, can be introduced

into cells (either *in vitro* or *in vivo*) such that the cells produce native KChIP1 polypeptide. If necessary, cells that have been transformed with the gene or cDNA or a vector comprising the gene, nucleic acid or cDNA can be introduced (or re-introduced) into an individual affected with the disease. Thus, cells which, in nature, lack native KChIP1 expression and activity, or have altered KChIP1 expression and activity, or have expression of a disease-associated KChIP1 splicing variant, can be engineered to express the KChIP1 polypeptide or an active fragment of the KChIP1 polypeptide (or a different variant of the KChIP1 polypeptide). In certain embodiments, nucleic acids encoding a KChIP1 polypeptide, or an active fragment or derivative thereof, can be introduced into an expression vector, such as a viral vector, and the vector can be introduced into appropriate cells in an animal. Other gene transfer systems, including viral and nonviral transfer systems, can be used. Alternatively, nonviral gene transfer methods, such as calcium phosphate coprecipitation, mechanical techniques (e.g., microinjection); membrane fusion-mediated transfer via liposomes; or direct DNA uptake, can also be used.

Alternatively, in another embodiment of the invention, a nucleic acid of the invention; a nucleic acid complementary to a nucleic acid of the invention; or a portion of such a nucleic acid (e.g., an oligonucleotide as described below), can be used in "antisense" therapy, in which a nucleic acid (e.g., an oligonucleotide) which specifically hybridizes to the mRNA and/or genomic DNA of a Type II diabetes gene is administered or generated *in situ*. The antisense nucleic acid that specifically hybridizes to the mRNA and/or DNA inhibits expression of the KChIP1 polypeptide, e.g., by inhibiting translation and/or transcription. Binding of the antisense nucleic acid can be by conventional base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interaction in the major groove of the double helix.

An antisense construct of the present invention can be delivered, for example, as an expression plasmid as described above. When the plasmid is transcribed in the cell, it produces RNA that is complementary to a portion of the mRNA and/or DNA which encodes the KChIP1 polypeptide. Alternatively, the antisense construct can be an oligonucleotide probe that is generated *ex vivo* and introduced into cells; it then

inhibits expression by hybridizing with the mRNA and/or genomic DNA of the polypeptide. In one embodiment, the oligonucleotide probes are modified oligonucleotides, which are resistant to endogenous nucleases, *e.g.*, exonucleases and/or endonucleases, thereby rendering them stable *in vivo*. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphothioate and methylphosphonate analogs of DNA (see also U.S. Pat. Nos. 5,176,996; 5,264,564; and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy are also described, for example, by Van der Krol *et al.*, (*BioTechniques* 6:958-976 (1988)); and Stein *et al.*, (*Cancer Res.* 48:2659-2668 (1988)). With respect to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site are preferred.

To perform antisense therapy, oligonucleotides (mRNA, cDNA or DNA) are designed that are complementary to mRNA encoding the KChIP1. The antisense oligonucleotides bind to KChIP1 mRNA transcripts and prevent translation. Absolute complementarity, although preferred, is not required. A sequence "complementary" to a portion of an RNA, as referred to herein, indicates that a sequence has sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid, as described in detail above. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures.

The oligonucleotides used in antisense therapy can be DNA, RNA, or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotides can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotides can include other appended groups such as peptides (*e.g.* for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, *Proc. Natl. Acad. Sci. USA*

86:6553-6556 (1989); Lemaitre *et al.*, *Proc. Natl. Acad. Sci. USA* 84:648-652 (1987); PCT International Publication NO: WO 88/09810) or the blood-brain barrier (see, *e.g.*, PCT International Publication NO: WO 89/10134), or hybridization-triggered cleavage agents (see, *e.g.*, Krol *et al.*, *BioTechniques* 6:958-976 (1988)) or  
5 intercalating agents. (See, *e.g.*, Zon, *Pharm. Res.* 5:539-549 (1988)). To this end, the oligonucleotide may be conjugated to another molecule (*e.g.*, a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent).

The antisense molecules are delivered to cells that express KChIP1 *in vivo*. A number of methods can be used for delivering antisense DNA or RNA to cells; *e.g.*,  
10 antisense molecules can be injected directly into the tissue site, or modified antisense molecules, designed to target the desired cells (*e.g.*, antisense linked to peptides or antibodies that specifically bind receptors or antigens expressed on the target cell surface) can be administered systematically. Alternatively, in a preferred embodiment, a recombinant DNA construct is utilized in which the antisense  
15 oligonucleotide is placed under the control of a strong promoter (*e.g.*, pol III or pol II). The use of such a construct to transfect target cells in the patient results in the transcription of sufficient amounts of single stranded RNAs that will form complementary base pairs with the endogenous KChIP1 transcripts and thereby prevent translation of the KChIP1 mRNA. For example, a vector can be introduced *in*  
20 *vivo* such that it is taken up by a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art and described above. For example, a plasmid, cosmid, YAC or viral vector can be used to  
25 prepare the recombinant DNA construct that can be introduced directly into the tissue site. Alternatively, viral vectors can be used which selectively infect the desired tissue, in which case administration may be accomplished by another route (*e.g.*, systemically).

Endogenous KChIP1 polypeptide expression can also be reduced by  
30 inactivating or "knocking out" the gene, nucleic acid or its promoter using targeted homologous recombination (*e.g.*, see Smithies *et al.*, *Nature* 317:230-234 (1985);

Thomas & Capecchi, *Cell* 51:503-512 (1987); Thompson *et al.*, *Cell* 5:313-321 (1989)). For example, an altered, non-functional gene or nucleic acid (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous gene or nucleic acid (either the coding regions or regulatory regions of the nucleic acid) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express the gene or nucleic acid *in vivo*. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the gene or nucleic acid. The recombinant DNA constructs can be directly administered or targeted to the required site *in vivo* using appropriate vectors, as described above. Alternatively, expression of non-altered genes or nucleic acids can be increased using a similar method: targeted homologous recombination can be used to insert a DNA construct comprising a non-altered functional gene or nucleic acid, *e.g.*, a nucleic acid comprising one or more of SEQ ID NOs: 114-258 or the complement thereof, or a portion thereof, in place of an altered KChIP1 in the cell, as described above. In another embodiment, targeted homologous recombination can be used to insert a DNA construct comprising a nucleic acid that encodes a Type II diabetes polypeptide variant that differs from that present in the cell.

Alternatively, endogenous KChIP1 nucleic acid expression can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of a KChIP1 nucleic acid (*i.e.*, the KChIP1 promoter and/or enhancers) to form triple helical structures that prevent transcription of the KChIP1 nucleic acid in target cells in the body. (See generally, Helene, C., *Anticancer Drug Des.*, 6(6):569-84 (1991); Helene, C. *et al.*, *Ann. N.Y. Acad. Sci.* 660:27-36 (1992); and Maher, L. J., *Bioassays* 14(12):807-15 (1992)). Likewise, the antisense constructs described herein, by antagonizing the normal biological activity of one of the KChIP1 proteins, can be used in the manipulation of tissue, *e.g.*, tissue differentiation, both *in vivo* and *for ex vivo* tissue cultures. Furthermore, the anti-sense techniques (*e.g.*, microinjection of antisense molecules, or transfection with plasmids whose transcripts are anti-sense with regard to a Type II diabetes gene mRNA or gene sequence) can be used to investigate the role of KChIP1 or the interaction of KChIP1 and its binding agents in developmental events; as well as the normal cellular function of KChIP1 or of the



interaction of KChIP1 and its binding agents in adult tissue. Such techniques can be utilized in cell culture, but can also be used in the creation of transgenic animals.

In yet another embodiment of the invention, other Type II diabetes therapeutic agents as described herein can also be used in the treatment or prevention of a susceptibility to a disease or condition associated with a Type II diabetes gene. The therapeutic agents can be delivered in a composition, as described above, or by themselves. They can be administered systemically, or can be targeted to a particular tissue. The therapeutic agents can be produced by a variety of means, including chemical synthesis; recombinant production; *in vivo* production (e.g., a transgenic animal, such as U.S. Pat. NO: 4,873,316 to Meade *et al.*), for example, and can be isolated using standard means such as those described herein.

A combination of any of the above methods of treatment (e.g., administration of non-altered polypeptide in conjunction with antisense therapy targeting altered mRNA of KChIP1; administration of a first splicing variant encoded by a KChIP1 nucleic acid in conjunction with antisense therapy targeting a second splicing encoded by a KChIP1 nucleic acid) can also be used.

The present invention is now illustrated by the following Exemplification, which is not intended to be limiting in any way. All references cited herein are incorporated by reference in their entirety.

#### EXEMPLIFICATION

The study was done in collaboration with the Icelandic Heart Association, who provided an encrypted list of 1350 diabetic patients. In 1967-1991 the Heart Association started a study of cardiovascular disease and its complications. Measurements of blood sugar were included in a thorough check-up of the participants which results led to many individuals being diagnosed with diabetes. The list of participants is an unbiased sample of about a third of the Icelandic nation. Individuals diagnosed in the years following 1991 were either diagnosed at the Icelandic Heart Association or at one of two major hospitals in Reykjavik, Iceland.

All participants in the Type II diabetes study visited the Icelandic Heart Association where each answered a questionnaire, had blood drawn, a blood sugar

assessment, and measurements taken. Height (m) and weight (kg) were measured to calculate the body mass index. In serum, the fasting blood glucose and triglyceride levels were measured as well. Diagnoses of Type II diabetes were based on the diagnostic criteria set by the World Health Organization (1999). All patients with  
5 fasting glucose above 7 mM were diagnosed as having Type II diabetes and individuals with fasting blood sugar between 6.1 – 6.9 mM were diagnosed with impaired fasting glucose. If the participants had no prior history of diabetes, they were requested to come in for another test to have their diagnosis confirmed. All individuals on diabetic medication were classified as Type II. The questionnaire  
10 included questions regarding age at diagnosis and type of medication. All patients were requested to bring two relatives who's DNA was used to confirm the genotypes of the patients.

Since the patients had participated in a study that was conducted between 1967-1991 a considerable time had passed, in some instances, since they had visited  
15 the Heart Association. Therefore, all the patients were required to have another fasting blood glucose test to check on their blood sugar level at the time of participation in the study. Thus, all patients were labeled unconfirmed, meaning that results of blood glucose levels were pending, for this particular study. A label of confirmed diabetic was given to the patient when the measurements were received.  
20 Linkage analyses were done with confirmed patients and unconfirmed patients were included only if they were close relatives of a confirmed index patient. The initial list of patients included 1350 Type II diabetics, but during this study new patients were diagnosed who were relatives of the index patients. All participants with no previous history of diabetes but with elevated fasting glucose were diagnosed according to the  
25 WHO criteria as described above. At present date, 1406 Type II diabetics and 266 patients with impaired fasting glucose have participated in the study, together with 3972 of their close relatives.

This study was approved by the Data Protection Commission of Iceland and the National Bioethics Committee of Iceland. All patients and their relatives who  
30 participated in the Study gave informed consents.

*Outline of the study*

This particular genetic study, which has the aim of identifying a genetic variant or a gene that may contribute to type II diabetes by using a positional cloning approach, can be divided into three steps:

- 5           i.   *Genome-wide linkage study*, where excess allele sharing among related type II diabetics is used to identify a chromosomal segment, typically 2 – 8 Megabases long, that may harbor a disease susceptibility gene/genes.
- 10           ii. *Locus-wide association study*, where a high-density of microsatellite markers is typed in a large patient and control cohort. By comparing the frequencies of individual alleles or haplotypes between the two cohorts, the location of the putative disease gene/genes is narrowed down to a few hundred kilobases.
- 15           iii. *Candidate gene assessment*, where additional microsatellites and/or SNPs are typed in all genes that are identified within the smaller candidate region and further association analysis is used to identify which of the genes shows strong association to the disease.

## 20   **Linkage analysis**

### *Pedigree Construction*

For the linkage analysis, blood samples were obtained from 964 Type II diabetics and 203 individuals with impaired fasting glucose. The patients were clustered into families such that each patient is related to (within and including six  
25   meiotic events) at least one other patient. In this manner, 772 patients fell into families - 705 Type II diabetics and 67 with impaired fasting glucose. The confirmed Type II patients were treated as probands and clustered into families that each proband is related to, within and including six meiotic events. The other patients, unconfirmed Type II and IFG patients, were added to the families if they were related  
30   to a proband within and including three meiotic events. The rationale behind this was to include as many patients as possible in the study. Impaired fasting glucose is an

immediate diagnosis, and we assumed that the more closely related these patients are to the confirmed diabetics, the likelier they are to have or to develop the disease.

The families were checked for relationship errors by comparing the identity-by-state (IBS) distribution for the set of 906 markers, for each pair of related and genotyped individuals, to a reference distribution corresponding to the particular degree of relatedness. The reference distributions were constructed from a large subset of the Icelandic population. Individuals were excluded from the study if their relationship with the rest of the family was inconsistent with the relationship specified in the geneology database.

The remaining material that was available for the study was the following: 763 now confirmed Type II patients in 227 families together with 764 genotyped relatives. Of the patients, 667 were confirmed Type II patients, 35 unconfirmed Type II patients, 52 confirmed patients with impaired fasting glucose (IFG) and 9 unconfirmed patients with IFG.

#### *Stratification of the Patient Material*

The patients were classified into two sub-phenotypes based on their BMI: non-obese Type II diabetes are patients who have BMI less than 30, and obese Type II diabetes are patients who have BMI at or above 30. The reason for fractionating the diabetics into non-obese and obese groups is that other factors may be influencing the pathogenesis of disease in these two groups. Obesity alone could be contributing to the diabetic phenotype. Therefore, this factor was separated. Obesity is most likely due to a combination of environmental and genetic factors. This fractionation into non-obese and obese diabetics practically separates the material into two halves; 60% of the patients are in the non-obese category (20% with BMI below 25 (lean) and 40% with BMI between 25-30 (overweight)), and 40% of the patients are in the obese category (BMI above 30).

An affected-only linkage analysis for each of those sub-phenotypes was performed, using the same set of families as above, but classifying patients not belonging to the particular sub-group as having an unknown disease status. Restricted to a particular sub-phenotype, some families no longer contain a pair of related

patients classified as affecteds and hence do not contribute in the linkage analysis. Such families were excluded from the analysis of the particular sub-phenotype. The number of patients and families used in the linkage analysis is summarized in Table 1 below.

- 5 Table 1: The number of patients and families that contribute to the genome-wide linkage scan, both when all the patients are used, and when the analysis is restricted to obese or non-obese diabetic patients, respectively.

Table 1: Phenotype and Patients

Phenotype	Total Number of Patients	NO: of families contributing to the analysis	NO: of patients contributing to the analysis
All diabetics	763	227	763
Obese	296	92	219
Non-obese	467	154	413

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#### *Genome wide scan*

- A genome wide scan was performed on 772 patients and their relatives. Nine patients were excluded due to inheritance errors so the linkage analysis was performed with 763 patients and 764 relatives. The procedure was as described in Gretarsdóttir, *et al.*, *Am J Hum Genet.*, 70(3):593-603 (2002). In short, the DNA was genotyped with a framework marker set of 906 microsatellite markers with an average resolution of 4cM. Alleles were called automatically with the TrueAllele program (Cybergenetics, Co., Pittsburgh, PA), and the program DecodeGT (deCODE genetics, ehf., Iceland), was used to fractionate according to quality and edit the called genotypes (Palsson, B., *et al.*, *Genome Res.*, 9(10):1002-1012 (1999)). The population allele frequencies for the markers were constructed from a cohort of more than 30,000 Icelanders that have participated in genome-wide studies of various disease projects at deCODE genetics. Additional markers were genotyped within the locus on chromosome 5q, where we observed the strongest linkage signal, to increase the information on identity by descent (IBD) sharing within the families. For those
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- 25

markers, at least 180 Icelandic controls were genotyped to derive the population allele frequencies.

The additional microsatellite markers that were genotyped within the locus were either publicly available or designed at deCODE genetics; those markers are indicated with a DG designation. Repeats within the DNA sequence were identified that allowed us to choose or design primers that were evenly spaced across the locus. The identification of the repeats and location with respect to other markers was based on the work of the physical mapping team at deCODE genetics.

For the markers used in the genomewide scan, the genetic positions were taken from the recently published high-resolution genetic map (HRGM), constructed at deCODE genetics (Kong A., *et al.*, *Nat Genet.*, 31: 241-247 (2002)). The genetic position of the additional markers are either taken from the HRGM, when available, or by applying the same genetic mapping methods as were used in constructing the HRGM map to the family material genotyped for this particular linkage study.

#### *Statistical Methods for Linkage Analysis*

The linkage analysis is done using the software Allegro (Gudbjartsson *et al.*, *Nat. Genet.* 25:12-3, (2000)) that determines the statistical significance of excess sharing among related patients by applying non-parametric affected-only allele-sharing methods (without any particular disease inheritance model being specified). Allegro, a linkage program developed at deCODE genetics, calculates LOD scores based on multipoint calculations. Our baseline linkage analysis uses the  $S_{\text{pairs}}$  scoring function (Whittemore, A.S. and Halpern, J., *Biometrics* 50:118-27 (1994); Kruglyak L., *et al.*, *Am J Hum Genet* 58:1347-63, (1996)), the exponential allele-sharing model (Kong, A. and Cox, N.J., *Am. J. Hum. Genet.*, 61:1179 (1997)), and a family weighting scheme which is halfway on a log scale between weighting each affected pair equally and weighting each family equally. In the analysis, all genotyped individuals who are not affected are treated as "unknown". Because of concern with small sample behavior, we usually compute corresponding P-values in two different ways for comparison. The first P-value is computed based on large sample theory;  $Z_{1\tau} = \sqrt{(2 \log_e (10) \text{ LOD})}$  and is approximately distributed as a standard normal

distribution under the null hypothesis of no linkage. A second P-value is computed by comparing the observed LOD score to its complete data sampling distribution under the null hypothesis. When a data set consists of more than a handful of families, these two P-values tend to be very similar.

5 All suggestive loci with LOD scores greater than 2 are followed up with some extra markers to increase the information on the IBD-sharing within the families and to decrease the chance that a LOD score represents a false-positive linkage. The information measure we use was defined by Nicolae (D. L. Nicolae, Thesis, University of Chicago (1999)) and is a part of the Allegro program output. This  
10 measure is closely related to a classical measure of information as previously described by Dempster *et al.* (Dempster, A.P., *et al.*, *J. R. Statist. Soc. B*, 39:1 (1977)); the information equals zero if the marker genotypes are completely uninformative and equals one if the genotypes determine the exact amount of allele sharing by descent among the affected relatives. Using the framework marker set  
15 with average marker spacing of 4 cM typically results in information content of about 0.7 in the families used in our linkage analysis. Increasing the marker density to one marker every centimorgan usually increases the information content above 0.85.

### Results

20 The results of the genome-wide linkage analysis with the framework marker set are shown in FIG. 4 which depicts the allele-sharing LOD-score versus the genetic distance from the p-terminus in centimorgan (cM) for each of the 23 chromosomes. The analysis was performed with the three phenotypes: all Type II diabetics (solid lines), non-obese diabetics (dashed lines) and obese diabetics (dotted lines). A LOD-  
25 score of 1.84 is observed on chromosome 5q34-q35.2 with the framework marker set when we use all Type II diabetics in the analysis. When the linkage analysis is restricted to non-obese diabetics, this LOD-score increases to 2.81. The obese diabetics do not show linkage in this region.

Additional markers were genotyped in this area to increase the information  
30 content and to confirm the linkage. The information on the IBD-sharing at this locus was about 78% with the framework marker set. In order to increase the information

content, another 38 microsatellite markers were genotyped within a 40 cM region that includes the observed signal. Repeating the linkage analysis including the additional markers increased the LOD-score to 3.64 ( $P$ -value =  $3.18 \times 10^{-5}$ ) for the non-obese diabetics. For all patients, the peak LOD-score increased to 2.9 ( $P$ -value =  $1.22 \times 10^{-4}$ ).

5 This is shown in FIG. 5.

The peak of the LOD-score is centered on marker D5S625 and the region determined by a drop of one in the LOD is from marker DG5S5 to marker D5S429, centromeric and telomeric respectively. The one-LOD-drop is about 9 cM and estimated to be about 3.5 Mb. This 1-LOD-drop roughly corresponds to the 80-90%  
10 confidence interval for the location of a putative disease associated gene.

### Locus-wide association study

#### *Genotyping to Narrow Down the Region of Linkage*

In order to narrow down the region of interest, the linkage analysis is followed  
15 by a comprehensive association study of the 1-LOD-drop. This is necessary as the linkage analysis has limited resolution; it compares sharing among closely related individuals that share on average large chromosomal segments. For the association analysis, we identified a large number of additional microsatellite markers located in the 1-LOD-drop and typed those markers in both our patient cohort and in a large  
20 number of unrelated controls randomly selected from the Icelandic population.

We identified and typed 67 markers in the 1-LOD-drop in addition to the 17 markers already typed and used in the linkage analysis (locus-wide association micorsatellites; Table 6). The new polymorphic repeats (dinucleotide or trinucleotide repeats) were identified with the Sputnik program. We subtracted the smaller allele of  
25 CEPH sample 1347-02 (CEPH genomics repository) from the alleles of the microsatellites and used it as a reference. A total of 84 markers were available for the association analysis, *i.e.*, an average density of one marker every 42kb or one marker every 0.107 cM. All those markers were typed for 590 non-obese diabetics and 477 unrelated controls.



*Statistical Methods for Association and Haplotype Analysis*

For single marker association to the disease, we use Fisher exact test to calculate a two-sided P-value for each individual allele. When presenting the results, we use allelic frequencies rather than carrier frequencies for microsatellites, SNPs and haplotypes. Haplotype analyses are performed using a computer program we developed at deCODE called NEMO (NEsted MOdels) (Gretarsdóttir, *et al.*, *Nat Genet.* 2003 Oct;35(2):131-8). We use NEMO both to study marker-marker association and to calculate linkage disequilibrium (LD) between markers, and for case-control haplotype analysis. With NEMO, haplotype frequencies are estimated by maximum likelihood and the differences between patients and controls are tested using a generalized likelihood ratio test. The maximum likelihood estimates, likelihood ratios and P-values are computed with the aid of the EM-algorithm directly for the observed data, and hence the loss of information due to the uncertainty with phase and missing genotypes is automatically captured by the likelihood ratios, and under most situations, large sample theory can be used to reliably determine statistical significance. The relative risk (RR) of an allele or a haplotype, *i.e.*, the risk of an allele compared to all other alleles of the same marker, is calculated assuming the multiplicative model (Terwilliger, J.D. & Ott, J. A haplotype-based 'haplotype relative risk' approach to detecting allelic associations. *Hum Hered* 42, 337-46 (1992) and Falk, C.T. & Rubinstein, P. Haplotype relative risks: an easy reliable way to construct a proper control sample for risk calculations. *Ann Hum Genet* 51 ( Pt 3), 227-33 (1987)), together with the population attributable risk (PAR).

In the haplotype analysis, it may be useful to group haplotypes together and test the group as a whole for association to the disease. This is possible to do with NEMO. A model is defined by a partition of the set of all possible haplotypes, where haplotypes in the same group are assumed to confer the same risk while haplotypes in different groups can confer different risks. A null hypothesis and an alternative hypothesis are said to be nested when the latter corresponds to a finer partition than the former. NEMO provides complete flexibility in the partition of the haplotype space. In this way, it is possible to test multiple haplotypes jointly for association and to test if different at-risk haplotypes confer different risk. As a measure of LD, we use

two standard definitions of LD,  $D'$  and  $R^2$  (Lewontin, R., *Genetics*, 49:49-67 (1964) and Hill, W.G. and A. Robertson, *Theor. Appl. Genet.*, 22:226-231 (1968)) as they provide complementary information on the amount of LD. For the purpose of estimating  $D'$  and  $R^2$ , the frequencies of all two-marker allele combinations are  
5 estimated using maximum likelihood methods and the deviation from linkage disequilibrium is evaluated using a likelihood ratio test. The standard definitions of  $D'$  and  $R^2$  are extended to include microsatellites by averaging over the values for all possible allele combinations of the two markers weighted by the marginal allele probabilities.

10 The number of possible haplotypes that can be constructed out of the dense set of markers genotyped in the 1-LOD-drop is very large and even though the number of haplotypes that are actually observed in the patient and control cohort is much smaller, testing all those haplotypes for association to the disease is a formidable task. Note that we do not restrict our analysis to haplotypes constructed from a set of  
15 consecutive markers, as some markers may be very mutable and might split up an otherwise well conserved haplotype constructed out of surrounding markers.

The approach we take to the problem of identifying those haplotypes in the candidate region that show strongest association to the disease is two-fold. First, we restrict the haplotypes we test to span a sub-region small enough that the included  
20 markers may be expected to be in substantial LD. In this study, we only consider haplotypes that span less than 300kb. Second, we apply an iterative procedure that gradually builds up the most significant haplotypes. Starting with haplotypes constructed out of 3 markers, we select those haplotypes that show strong association to the disease, add other nearby markers to those haplotypes and repeat the association  
25 test. By iterating this procedure, we expect to identify those haplotypes that show strongest association to the disease.

### Results

For the association analysis, we genotyped 590 non-obese Icelandic Type II  
30 diabetes patients and 477 unrelated population controls using a total of 84 microsatellite markers. These markers are distributed evenly across a region of

approximately 3.5 Mb. The region is centered on our linkage peak and corresponds to the 1-LOD-drop. We then applied the procedure described above and looked for single-markers and haplotypes consisting of up to 5 markers that showed association to the disease. The result is summarized in FIG. 6. In FIG. 6, we show the location of a marker or a haplotype on the horizontal axis and the corresponding P-value from the association test on the vertical axis. This is shown for all haplotypes tested that have a P-value less than 0.01. The horizontal bars indicated the size of the corresponding haplotypes and the location of all markers is shown at the bottom of the figure. All locations are in Mb and refer to the NCBI Build33.

We observe a series of correlated haplotypes that show strong association for non-obese diabetics in two locations within the 1-LOD-drop. We denote those regions A (168.37 – 168.83Mb) and B (169.70 – 170.17Mb), and in Table 10 we list the most significant haplotype in each of those regions. For each haplotype, the table includes a two-sided single-test P-value for association, calculated using NEMO, the corresponding relative risk, the estimated frequency of the haplotype in the patient and the control cohorts, the region the haplotype spans, and the markers and alleles (in bold) that define the haplotype.

Note, however, that some of the haplotypes listed within each of the two regions are very correlated and should be considered as a single observation of association to the disease. This is demonstrated for region B in Table 3, which lists the pairwise correlation, both  $D'$  and  $R^2$ , between the haplotypes. Based on the correlation, we observe that haplotypes B2 and B4 are strongly correlated and should be considered as a single observation of association to this region. Likewise, haplotypes B1 and B5 are strongly correlated. However, haplotypes B1, B2 and B3 are all weakly correlated with each other, and in fact, B1 and B2 are mutually exclusive, *i.e.*, never appear jointly on the same chromosome. These three haplotypes hence constitute three almost independent observations of association to non-obese diabetes of this region within the locus. It is possible to test haplotypes B1, B2 and B3 together as a group for association to non-obese diabetes. This test yields a P-value =  $8.5 \times 10^{-8}$  with a corresponding relative risk of 5.2, a population attributable

risk of 13.9%, and an allelic frequency of 0.089 and 0.018 in the patient and the control cohorts, respectively.

Table 2

	P-value	RR	Aff.fr q	Ctrl.fr q	Span (Mb)	Haplotype
A1	0.000005	> 10	0.033	0.000	168.37- 168.72	<b>0</b> DG5S879 <b>4</b> DG5S881 <b>-4</b> D5S2075 <b>0</b> DG5S883 <b>4</b> DG5S38
A2	0.000006	3.81	0.053	0.015	168.55- 168.77	<b>4</b> DG5S1058 <b>-6</b> DG5S37
A3	0.000008	3.64	0.054	0.015	168.55- 168.83	<b>4</b> DG5S1058 <b>-6</b> DG5S37 <b>0</b> DG5S101
A4	0.000015	6.18	0.046	0.008	168.40- 168.72	<b>4</b> DG5S881 <b>4</b> DG5S1058 <b>-4</b> D5S2075 <b>0</b> DG5S883 <b>4</b> DG5S38
A5	0.000015	4.42	0.047	0.011	168.37- 168.77	<b>0</b> DG5S879 <b>4</b> DG5S1058 <b>-6</b> DG5S37
A6	0.000018	6.94	0.045	0.007	168.40- 168.72	<b>4</b> DG5S881 <b>-4</b> D5S2075 <b>0</b> DG5S883 <b>4</b> DG5S38
B1	0.000011	> 10	0.039	0.000	169.87- 170.17	<b>0</b> DG5S953 <b>0</b> DG5S955 <b>0</b> DG5S13 <b>5</b> DG5S959
B2	0.000023	> 10	0.034	0.000	169.65- 169.87	<b>27</b> DG5S888 <b>0</b> DG5S953
B3	0.000023	5.26	0.049	0.010	169.87- 170.04	<b>0</b> DG5S953 <b>0</b> DG5S955 <b>4</b> DG5S124
B4	0.000031	> 10	0.034	0.000	169.65- 169.87	<b>27</b> DG5S888 <b>0</b> DG5S44 <b>0</b> DG5S953
B5	0.000060	> 10	0.034	0.000	169.87- 170.17	<b>0</b> DG5S953 <b>0</b> DG5S955 <b>0</b> DG5S13 <b>0</b> DG5S123 <b>5</b> DG5S959

Table 2: Haplotypes within the 1-LOD-drop that show the strongest association to non-obese diabetes. For each haplotype, we show (i) a two-sided P-value for a single test of association to non-obese diabetes, (ii) the corresponding relative risk (RR), (iii) the estimated allelic frequency of the haplotype in the patient and the control cohort, (iv) the span of the haplotype (referring to NCBI 33) and (v) the alleles (in bold) and markers that define the haplotype. The haplotypes are separated into two groups, A and B, corresponding to two different regions within the 1-LOD-drop.

Table 3

		D'				
		B1	B2	B3	B4	B5
R <sup>2</sup>	B1	-	0	0	0	1
	B2	0	-	0.4	1	0
	B3	0	0.1	-	0.35	0
	B4	0	0.96	0.7	-	0
	B5	0.92	0	0	0	-

Table 3: Pairwise correlation between the five haplotypes in the B-region that show the strongest association to non-obese diabetes. Estimates of D' are shown in the upper right corner, and estimates of R<sup>2</sup> are shown in the lower left corner. The haplotypes are labelled B1, ..., B5 as in Table 2.

### Investigation of Region B

#### 10 Genes in Region B

We next identified all genes in and around region B (UCSC). In the region defined by the five most significant haplotypes, 169.70 – 170.17 Mb, there are four genes, *LCP2* (lymphocyte cytosolic protein 2), *KCNMB1* (potassium large conductance calcium-activated channel, subfamily M, beta member 1), *KCHIP1* (Kv channel interacting protein 1) and *GABRP* (gamma-aminobutyric acid (GABA) A receptor, pi). Of those genes, *KCHIP1* is by far the largest, stretching from 169.7 to 170.1 MB, or almost the entire span of the observed haplotype association. The other three genes are small. In addition, there is a big gene, *RANBP17* (RAN binding protein 17), just telomeric of the location of the observed association signal. The relative location of all the genes is shown in FIG. 7, which shows the location of the exons of *KCHIP1* as solid bars, and the location of the other genes as shaded boxes. In addition, FIG. 7 shows the location of the microsatellites (filled boxes) that we have typed in this region and the location of the at-risk haplotypes B1, ..., B5 (gray horizontal lines).

25

*Description of new Splice Variants of KChIP1 Identified by RACE and PCR*

The published sequence for KChIP1 comprises exons 1 to 8. New exons belonging to the KChIP1 gene and four different splice variants were discovered by performing RACE or PCR (primers within the exons) using as template human  
5 Marathon cDNA and cDNA prepared from rat pancreatic INS1 beta cells. In all, 6 new exons located in the 5' region of the gene were discovered.. An alternative exon 1 was found that we call exon 1a. Here, we label the published sequence for exon 1 with a "b" to distinguish it from the alternative exon 1, exon 1a. Four exons are called UTR 1, UTR 2, UTR 3 and UTR 4, or untranslated region 1 - 4, because they  
10 lie upstream of exon 1b and they are not translated. The last exon to be identified is called Ins-r, or insert rodent, because it was known to be present in mouse and rat, and has recently been demonstrated by others to be present in humans as well (Boland *et al.*, *Am J Physiol Cell Physiol* 285, C161-170. (2003)). See nucleotide sequences of the new exons below, as well as their location in the genomic sequence of NCBI build  
15 33. Even if not mentioned, all new variants of KChIP1 found and described below include exons 2 - 8 of the published sequence.

Splice variant 1 consists of exon 1a, UTR1, UTR2, UTR3, UTR4 and exon 1b. Exon 1a is untranslated and the resulting protein is identical in amino acid sequence to KChIP1 described by An *et al.* (*Nature* 430, 553-556 (2000), see also FIG.2). This  
20 variant was observed in human heart and testis and the rat INS1 cell line.

Splice variant 2 consists of exon 1b and the Ins-r exon giving rise to a protein that is identical in amino acid sequence to KChIP1 described by Boland *et al.*. This variant was observed in human brain, heart, pancreas and the rat INS1 cell line.

Splice variant 3 consists of exon 1a and is identical in nucleotide sequence to  
25 AL538404, an EST in NCBI. The amino acid sequence of the N-terminus coded by exon 1a is unique (see sequence below) but the amino acid sequence coded by exons 2 - 8 is that of the published sequence. This variant was observed in human brain, heart, pancreas, skeletal muscle, adipose tissue, liver, hypothalamus, small intestine, testis and the rat INS1 cell line.

Splice variant 4 consists of exons 1a and UTR1, which would result in a protein translated from exons 2 - 8. The second methionine in exon 2 has a Kozak sequence. This variant was observed in human heart.

The nucleotide sequences of the new exons are as follows (the genomic locations given are from NCBI build 33, see also Table 8):

Exon 1a: 169716298 - 169716511 (Build 33)

GGCTTCAGGGGTGCATCCGTCACCTCAGGGTTCATTCACCCAGGCAGGCTCCAAGT  
TCCTGGGGTGCACAAGGTGGGCACTGTCCCTTCTGGGTGCTGACAGCAGAGCCTG  
GCTCCCCTCCGCCACCATGAGCGGCTGCTCCAAAAGATGCAAGCTTGGGTTCGTG  
AAATTGCCCAGACCATCTTTAAGCTCATCACTGGGACCCTCAGCAAAG (SEQ ID  
NO: 4)

UTR 1: 169848417-169848523 (Build 33)

ACTCAGCATCATCAAGACTGGAGGGACAGAGCATTGAATCATCAGACGCTGGGC  
CAGACGTCACCCACGCGTTTCTCATTTTATC GTCCTAAGAAGCCCAGAAG (SEQ  
ID NO: 5)

UTR 2: 169861083-169861154 (Build 33)

CCTGAATGCAATTTGCAATGAGGAGATGATTTGATTTTCTTCAGCCCTAGACCTCC  
AGCTTCCTGAGAGCAG (SEQ ID NO: 6)

UTR 3: 169864589-169864679 (Build 33)

GGGTTCCCCAGGAGACCACGACAGAGGCCTGGAACCCAAGTTCTAATCCACATC  
CTGGCTGGGCAACTTCAGGCAAATTTCTAACACAAG (SEQ ID NO: 7)

UTR 4: 169867066-169867173 (Build 33)

GGTAGGGGAGGGGCGGGCCCGGGTCCCAACTCGCACTCAAGTCTTCGCTGCCA  
TGGGGGCCGTCATGGGCACCTTCTCATCTCTGC<sub>2</sub>AACCAAACAAAGGCGACCC  
(SEQ ID NO: 8)

Ins-r 170075401-170075433

ACATCGCCTGGTGGTATTACCAGTATCAGAGAG (SEQ ID NO: 9)

The nucleotide sequence derived from splice variant 4 (KChIP1.4) with the ATG and a Kozak sequence ((G/ANNATGG) underlined is as follows:

ATAAGATTGAAGATGAGCTGGAGATGACCATGGTTTGCCATCGGCCCCGAGGGACT  
GGAGCAGCTCGAGGCCAGACCAACTTCACCAAGAGGGAGCTGCAGGTCTTTTAT  
CGAGGCTTCAAAAATGAGTGCCCCAGTGGTGTGGTCAACGAAGACACATTCAAGC  
AGATCTATGCTCAGTTTTTCCCTCATGGAGATGCCAGCACGTATGCCATTACCTC  
TTCAATGCCTTCGACACCACTCAGACAGGCTCCGTGAAGTTCGAGGACTTTGTAAC  
CGCTCTGTCTGATTTTATTGAGAGGAACTGTCCACGAGAACTAAGGTGGACATTT  
AATTTGTATGACATCAACAAGGACGGATACATAAACAAAGAGGAGATGATGGAC  
ATTGTCAAAGCCATCTATGACATGATGGGGAAATACACATATCCTGTGCTCAAAG  
AGGACACTCCAAGGCAGCATGTGGACGTCTTCTTCCAGAAAATGGACAAAAATAA  
AGATGGCATCGTAACCTTTAGATGAATTTCTTGAATCATGTTCAGGAGGACGACAAC  
ATCATGAGGTCTCTCCAGCTGTTTCAAAATGTCATGTAAGTGGTGACACTCAGCCA  
TTCAGCTCTCAGAGACATTGTAATAACAACCACTTAACACCCTGATCTGCCCTT  
GTTCTGATTTTACACACCAACTCTTGGGACAGAAACACCTTTTACACTTTGGAAGA

ATTCTCTGCTGAAGACTTTCTATGGAACCCAGCATCATGTGGCTCAGTCTCTGATT  
GCCAACTCTTCCYCTTTCTTCTTCTTGAGAGAGA (SEQ ID NO: 10)

5 The protein sequences resulting from the splice variants are as follows:

#### KChIP1.3

(The amino acid sequence derived from splice variant 3 (KChIP1.3), the underlined amino acids are coded by exon 1a.)

10 MSGCSKRCKLGFVKFAQTIFKLITGTLSKDKIEDELEMTMVCHRPEGLEQLEAQTNFT  
KRELQVLYRGFKNECPSGVVNEDTFKQIYAQFFPHGDASTYAHYLFNAFDTTQTGSV  
KFEDFVTALSILLRGTVHEKLRWTFNLYDINKDGYINKEEMMDIVKAIYDMMGKYTY  
PVLKEDTPRQHVDVFFQKMDKNKDGIVTLDEFLESCQEDDNIMRSLQLFQNV (SEQ  
ID NO: 11)

#### KChIP1.2

(The amino acid sequence derived from splice variant 2 (KChIP1.2), the underlined amino acids are coded by exon Ins-r.)

20 MGAVMGTFSSLQTKQRRPSKDIAWWYYQYORDKIEDELEMTMVCHRPEGLEQLEA  
QTNFTKRELQVLYRGFKNECPSGVVNEDTFKQIYAQFFPHGDASTYAHYLFNAFDTT  
QTGSVKFEDFVTALSILLRGTVHEKLRWTFNLYDINKDGYINKEEMMDIVKAIYDMM  
GKYTYTPVLKEDTPRQHVDVFFQKMDKNKDGIVTLDEFLESCQEDDNIMRSLQLFQNV  
M (SEQ ID NO: 12)

#### KChIP1.4

(The amino acid sequence derived from splice variant 4 (KChIP1.4).)

25 MVCHRPEGLEQLEAQTNFTKRELQVLYRGFKNECPSGVVNEDTFKQIYAQFFPHGDA  
STYAHYLFNAFDTTQTGSVKFEDFVTALSILLRGTVHEKLRWTFNLYDINKDGYINKE  
EMMDIVKAIYDMMGKYTYTPVLKEDTPRQHVDVFFQKMDKNKDGIVTLDEFLESCQE  
30 DDNIMRSLQLFQNV (SEQ ID NO: 13)

### Identification of SNPs and Microsatellites

35 In order to identify SNPs across KChIP1, all exons of KChIP1 and their  
flanking regions were sequenced on 94 non-obese diabetic patients. As a  
consequence, 31 SNPs were identified (Table 9). Additional SNPs were identified  
across the gene by selecting SNPs from the public domain (US National Center for  
Biotechnology Information's SNP database) and designing SNP assays for them.  
(Table 10).

40 We genotyped SNPs on 470 non-obese diabetics and 658 population-based  
controls using a method for detecting SNPs with fluorescent polarization template-  
directed dye-terminator incorporation (SNP-FP-TDI assay) (Chen, X., Zehnauer, B.,  
Gnirke, A. & Kwok, P.Y. *Proc. Natl. Acad. Sci. USA* 94, 10756-10761 (1997)).



### Association Study of Genes in Region B

We tested all the genes in and around Region B (*LCP2*, *KCNMB1*, *KChIP1*, *GABRP* and *RANBP17*) individually for association to non-obese diabetes. In the analysis of each gene, we included all SNPs identified, and previously typed

5 microsatellites, in and close to that gene. The association analysis was carried out in the same way as the locus-wide association, i.e., using the iterative approach, we search for haplotypes, shorter than 300kb, that showed strongest association to the disease.

The strongest association observed was for *KChIP1*. For *KChIP1*, we tested  
10 25 markers, 7 microsatellites and 18 SNPs, for association (Table 11). The strongest association signal was observed in the 3'-end of the gene; a three marker haplotype with a P-value =  $9.2 \times 10^{-5}$ , relative risk 12, and allelic frequency 3.6% and 0.3% in the patient and control cohorts, respectively. This haplotype, which extends over the last 8 exons of *KChIP1*, from 169.96 to 170.11 Mb, is listed in Table 4 as D1. We also  
15 observed another haplotype in the same region that showed association to non-obese diabetes, albeit less significant than D1, with a P-value = 0.037, relative risk 1.69 and allelic frequency 7.8% and 4.8% in the patient and the control cohorts, respectively. This haplotype is labelled D2 in Table 4. For risk haplotypes, the corresponding population attributable risk is PAR = 4.9% for D1 and PAR = 4.7% for D2. However,  
20 as D1 and D2 are independent haplotypes, i.e., they do not appear jointly on the same chromosome, their population attributable risk can be added together.

Table 4

	P-Value	RR	Aff.frq.	Ctrl.frq	Haplotype
<b>Icelandic</b>					
<b>D1</b>	9.20E-05	12	0.036	0.003	-4 DG5S13 C KCP_1152
<b>D2</b>					0 D5S625
	0.037	1.69	0.078	0.048	0 DG5S124 C KCP_1152 C
					KCP_2649 T KCP_4976 A
					KCP_16152
<b>Danish</b>					
<b>D1</b>	0.052*	2.98	0.031	0.011	-4 DG5S13 C KCP_1152 0
<b>D2</b>					D5S625
	0.002*	2.74	0.098	0.038	0 DG5S124 C KCP_1152 C
					KCP_2649 T KCP_4976 A
					KCP_16152

\* One-sided P-value

Table 4: *Microsatellite* and SNP haplotype association within *KChIP1*. The two independent haplotypes D1 and D2 are located in the 3'-end of the gene, from 169.96 - 170.11 Mb. Shown are results of a test of association for non-obese diabetics vs population controls for both haplotypes in a cohort of Icelandic diabetics (top) and a replication in a cohort of Danish diabetics (bottom). Note that we report one-sided P-values for the test on the Danish cohort as that is a replication of association results previously observed in the Icelandic cohort.

#### *Replication in a Cohort of Danish Diabetics*

We typed the markers that define the two at-risk haplotypes, D1 and D2, in a cohort of 149 non-obese Danish females that have been diagnosed with diabetes and/or measured >7mM glucose who participated in a Danish PERF (Prospective Epidemiological Risk Factors) study. As controls, we used 346 females from the same study that answered no to a question about their diabetes status and/or measured <7mM glucose.

The results of the association test for the two at-risk haplotypes, identified in the Icelandic diabetes cohort, are listed in Table 4. Both haplotypes appear in higher frequency in the non-obese Danish diabetics than in the control cohort. For haplotype D1, the association to non-obese diabetes is only marginally significant, with a one-sided P-value = 0.05, and the relative risk of the at-risk haplotype is  $RR = 3.0$ , somewhat less than is observed for the Icelandic non-obese diabetics. Note, however, that the estimated frequency of haplotype D1 is very low, especially in the control cohorts, hence the estimates of the relative risk are not very reliable. For haplotype D2, on the other hand, we do observe a statistically significant association with a one-sided P-value = 0.002 and relative risk = 2.74. Note that as the test of association of haplotypes D1 and D2 are attempts to replicate the association we have observed for Icelandic non-obese diabetics, it is appropriate to report one-sided P-values for those tests.

#### *Additional SNP Genotyping for KChIP1*

Having observed association to the 3'-end of *KChIP1*, both in Icelandic and Danish non-obese diabetics, we subsequently sequenced 94 Icelandic individuals, 1/3 non-obese type II diabetes patients with the observed haplotype D1, 1/3 additional non-obese type II diabetes patients and 1/3 controls. The purpose of the sequencing

was to identify additional SNPs. We identified 725 SNPs (Table 12). Many of those SNPs were completely correlated so we removed several redundant SNPs from further genotyping. Some SNPs with very low minor allele frequencies were also ignored. Of the 725 identified SNPs plus what was originally identified, 108 were  
5 selected for further genotyping in the Icelandic cohort (Table 13).

We performed a single-marker test of association to non-obese diabetes for each of the additional SNPs we typed, although none of the SNPs showed a strong association. We did, however, observe that three of the SNPs, KCP\_197678, KCP\_197775 and KCP\_202795, increased the specificity of haplotype D2, if added to  
10 that haplotype, while still retaining most of its sensitivity. This is shown in Table 5, both for the association in the Icelandic and in the Danish cohorts. This increases the value of the at-risk haplotype as a diagnostic tool. Note that the three SNPs are very correlated to each other, with pairwise correlation coefficients  $D' \approx 0.96$  and  $R^2 \approx 0.9$ , hence the association of haplotypes D3, D4 and D5 to non-obese diabetes should be  
15 considered as a single observation.

In addition to the refinement of the at-risk haplotype D2, we observed another refinement of the at-risk haplotype, consisting of three SNPs only, that was very correlated with the three at-risk haplotypes, D3, D4 and D5, with pairwise correlation coefficients  $D' \approx 0.83$  and  $R^2 \approx 0.59$ . This haplotype is included in Table  
20 5 as D6.

25

30

Table 5

	P-Value	RR	PAR	Aff.frq.	Ctrl.f rq	Haplotype
<b>Icelandic</b>						
D2	0.037	1.69	6.3%	0.078	0.048	0 DG5S124 C KCP_1152 C KCP_2649 T KCP_4976 A KCP_16152
D3	0.022	2.19	5.5%	0.052	0.024	0 DG5S124 C KCP_1152 C KCP_2649 T KCP_4976 A KCP_16152 T KCP_197678
D4	0.052	2.03	4.6%	0.046	0.023	0 DG5S124 C KCP_1152 C KCP_2649 T KCP_4976 A KCP_16152 T KCP_197775
D5	0.023	2.14	5.5%	0.052	0.025	0 DG5S124 C KCP_1152 C KCP_2649 T KCP_4976 A KCP_16152 C KCP_202795
D6	0.054	1.77	4.0%	0.046	0.027	A KCP_173982 C KCP_15400 C KCP_18069
<b>Danish</b>						
D2	0.002*	2.74	12.0%	0.098	0.038	0 DG5S124 C KCP_1152 C KCP_2649 T KCP_4976 A KCP_16152
D3	0.0046	2.60	9.0%	0.076	0.030	0 DG5S124 C KCP_1152 C KCP_2649 T KCP_4976 A KCP_16152 T KCP_197678
D4	0.0004	3.69	11.3%	0.078	0.023	0 DG5S124 C KCP_1152 C KCP_2649 T KCP_4976 A KCP_16152 T KCP_197775
D5	0.0002	3.67	11.7%	0.084	0.024	0 DG5S124 C KCP_1152 C KCP_2649 T KCP_4976 A KCP_16152 C KCP_202795

\* One-sided P-value

**Table 5:** Microsatellite and SNP haplotype association within *KChIP1*. Shown is association of the at-risk haplotype D2, and of further refinements of that haplotype; haplotypes D3, D4 and D5, to non-obese diabetes. This is shown both for the Icelandic and the Danish cohorts and, as in Table 4, we report one-sided P-values for the association test in the Danish cohort. Finally, we include the result of association to non-obese diabetes, in the Icelandic cohort, of a 3 SNP haplotype, D6, that is strongly correlated with the at-risk haplotypes D3, D4 and D5.

#### Allele Numbering System

SNP alleles are indicated by the letters found in the DNA sequence. In general the alleles can be references by A=0, C=1, G=2 and T=3. For microsatellite alleles, the CEPH sample (Centre d'Etudes du Polymorphisme Humain, genomics repository) is used as a reference, the lower allele of each microsatellite in this sample is set at 0 and all other alleles in other samples are numbered according in relation to this reference. Thus allele 1 is 1 bp longer than the lower allele in the CEPH sample, allele 2 is 2 bp longer than the lower allele in the CEPH sample, allele 3 is 3 bp longer than the lower allele in the CEPH sample, allele 4 is 4 bp longer than the lower allele

in the CEPH sample, allele -1 is 1 bp shorter than the lower allele in the CEPH sample, allele -2 is 2 bp shorter than the lower allele in the CEPH sample, and so on.

Table 6:

- 5 The DNA sequence of the microsatellites employed for the C05 locus wide association (including Build 33 locations).

Y = C or T; S = C or G; R = A or G; W = A or T; M = A or C; K = G or T.

TABLE 6

Name	Position	Nucleic Acid Sequence	SEQ ID NO:
DG5S5	167638990 - 167639163	TCCTCAGAACAGGTGCAACACAGTGTGTTTTGCTGGGG AAAAGGGATGTCAAGCAATCTATGACGGGGGTGCAGG GAGTCTGGGGAGAAACACAAGGAAGTGTGTGTGTGTG TGTGTGTGTGTGTGTGTGAATGTGTGTGTGTGTGAGAG AGAGAGCTGGTGTTTGTGTTCCA	SEQ ID NO: 14
D5S671	167657904 - 167658237	GGAATGTGCCAAGACATTCTTTAGGGTTGGTAACCAG AGACGCTATTTTGTCTTGGTGGCTAAGAAATCACTTT TCTGACTGAAGGNCCATTTGACTTACTTCTTTTAAATT CAGGGGAATGGGTGGGCATCTCCATGATTCAGGTAAG GAAAAATCCAAGGNAAATAAACACACACACACACAC ACACACACACACACACACACGGAGTAGAAATTTTTAG TGCAATTTTTTGTCTCACAGCATTAAATTAATTGCAGGG ATATAACTACCTTGGCAGAATTTTTTCTCCCCAACCCA CCACCCCCCGGAATAAGTTTGGCTCTTTTCAGCT	SEQ ID NO: 15
DG5S870	167719773 - 167719939	TGCCCACTCATAAGATGCTGAGGTTACAACGTGTTAATA AGATATTAAGATACTGTCTTTTTCTTCTCTCTCTCTCT TACACACACACACACACACACACACACACTTTTTG GGCCAACTGGAAATTCATACATTCTCCCCAGCACTGGA GCTCAAAGCGTCTG	SEQ ID NO: 16
D5S671	167657904 - 167658237	GGAATGTGCCAAGACATTCTTTAGGGTTGGTAACCAG AGACGCTATTTTGTCTTGGTGGCTAAGAAATCACTTT TCTGACTGAAGGNCCATTTGACTTACTTCTTTTAAATT CAGGGGAATGGGTGGGCATCTCCATGATTCAGGTAAG GAAAAATCCAAGGNAAATAAACACACACACACACAC ACACACACACACACACACACGGAGTAGAAATTTTTAG TGCAATTTTTTGTCTCACAGCATTAAATTAATTGCAGGG ATATAACTACCTTGGCAGAATTTTTTCTCCCCAACCCA CCACCCCCCGGAATAAGTTTGGCTCTTTTCAGCT	SEQ ID NO: 17
DG5S870	167719773 - 167719939	TGCCCACTCATAAGATGCTGAGGTTACAACGTGTTAATA AGATATTAAGATACTGTCTTTTTCTTCTCTCTCTCTCT TACACACACACACACACACACACACACACTTTTTG GGCCAACTGGAAATTCATACATTCTCCCCAGCACTGGA GCTCAAAGCGTCTG	SEQ ID NO: 18

DG5S85	167721558 - 167721918	TTGTTGTTGTTGGTGGTGGTGGGGTGTGTGTGTGTGTG TGTGTGTGTGTGTGTGTGTGTGTGTTTCGAGACAGACTCTC ACTCTGTCACCCAGGCTGGAGTGCAGTGGCAGCATCT GGGTTCACTGCAACCTCTACTTCCTCAGCTCCAAGGAT CCTCTCACCTCCACCTCCCAAGTAGCTGGGACTACAGG TACGCGCCACCATGTCTGGCTAATTTTTTTGTATTGGA GAGACAGGGTTCCACCATGTTGCCCCGGGCTAGTGTTCG ACTCCTGAGCTCAGGTGATCCACCCACCTCAACGTCCC CAAGTGCTGGGATTAGAGGCGTGAGCCACCACGTCTG GCCTATACACTATAGAGTTT	SEQ ID NO: 19
DG5S90	167766290 - 167766502	TCTGGACAGGACCAGGAGTTGGCTGCTGTCAGCCTTTG CCCCACCTCTCTGTGGCTACTGGGTATGTGAATCTCTC AAGGCCTGAAGAGAGGACAGCTGAGGAATTTGGAAAT CCTAAAACACATGCATACACACACACACACACACACA CACACACACACACACACACTTTTCTTTCCCTTAAAAAA AAAAAGATTTCATTACCCGTGTGCA	SEQ ID NO: 20
DG5S874	167846718 - 167847065	CTGTCTACACTACCCACCCATTAGTCACTTATTAGCCC TCTGAATTACTGGATTGAAAAAACATAGTATATATATA GGGCTTGGTACTATTACGGTTTCAGGCATCCACTGAG GGGTGTTGCAATGTATCTCCACGGATAAGGAAGGAC TGGTATATTAACACTTTTATTTGATTTACAAAAATAAG GATAGTTTATATAGTTCTGGGTAAAATTAATTAATTA TTTAAAAGGAAAAAAGATAAAGGCAAACCTTTAAGCTT GTTAAAATTAAGTAAAATAATTTGGATTATTTAATTG GACAAAGAGGACTGGCTTTGCCAATGAAACAATATGG CCGACATG	SEQ ID NO: 21
DG5S88	167864864 - 167865059	GGACCTTCTTTCTGCCCTAAAACCGCAATATCATTATA ATAACAAATATATATATATATATATATATATTTTTTTT TTTAAAACAATCTTGCTATGTTGCCTAGGCTGGTGTGG AACTCCTGGCCTCAAGTGATCCTCCACCTCGGCCTCC CAGAGTGCTGGGATTATAGACATGAACTACCATACCC AGCCA	SEQ ID NO: 22
DG5S7	167910343 - 167910651	CACAGCCATCAAGTTTCCAACCTTACTGCCTCACATATT AAGATGATTTTTTTTAAACAACTTAACAGGCGATGGAT ACTCCATTCTCCATGATGTGCTTAATTCACATGCATGC TTGTATCAAAACATCTCACATACTCCATAAAGCCTGTA ATCCCAACACTTTGGGATGCCAAGGTGGGTGGATCAC TTGAGCCCAGGAGTTTGAGAACAGCCTGGACAACATG GCGAAACCCCATTTACACACACACACACACACACACA CACACACACCACACAAACAAAATGAAACAAACACCTA ACCAACAA	SEQ ID NO: 23
DG5S6	167952553 - 167952858	TCCTAACGGCTGCTACCACTAAAGATCTTAGCATGGTG TGTGTGTGCGTGTGTGTGTGTGTGTGTGTGTGTGTG TGTGTGGTGGGGCTATTCAGTAAGGCTAGAAGTGAAA AAGCTAGTAGAAAGCCCATGGTGATGGAGAATGGAGG AAGACTGATTAGGGAGCTCCTCAGCAGTATAAGGAAG GACTAAGAGCACATAAGGACAGGATCATAGAATTCCG CATCTCAGGATTTTTGAGGCTGCCACTGCCTTAGCTGT GAGGCCAGTGCATATAAGAATAGTTTGCACAGTTCTG CTGTGG	SEQ ID NO: 24
DG5S87	167992779 - 167993149	CCTCTGGGATTAGCCTCTCAGGGTACAGATATAACGAT GATTGAGTTGGCTTATGTATGTGTGTGTGTGTGTGTG TCTGTGTGTGTGTGTGTGAGAGAGAGAGAGAGAGAGA GAGAGAGTGACAGAGAGAGAATGAGAGAGAACTGGA AGTTGTCAACAAGAAGAGTCAAACCTCTGTAAATATT TGAAGAGATTTATTCTGAGCCAAATAGGAGTGCCACA	SEQ ID NO: 25

		GCCCCGGGAGATCCTAAGAACATGTGCCAGAGTAGT CAAGCTATAGTTTGGTTTTATACATTTTAGGGAGACAT AAGACATCAGTCAATACATGTAAGATGCACATTGATA CACTGGTTTAGTAGGGAAAGGTGGGACAACTCGAA	
DG5S91	168014827 - 168015078	GGTGCCAATTAAATCCAACAAGGTAGCTGAGTGTGGT GGTGCACGCCTGTAGTCTAGCTATGCAGGAGGCTGA GGTGGGAGGATCACTTGAGCCTGGGAGGTCGAGGCTG CTGTGAGCTGTGATTGCACCGCTGCATTCCAGCCTGGG AGACAGAGCAAGATCCTGACACACACACACACACACA CACACACACACACACACACACACACATTCCAACAAGG TAATGTGTAGGAGGAAGTACCCGAGCTT	SEQ ID NO: 26
DG5S92	168065529 - 168065864	CAACTCCTGCAGCCCTTTACGCCAAGCACAGAAATCC AGGAGGCAGAGCCTAGCGCTTGATGACATGGTAATTG GGCCTGGAAGTGGGGATTTCTGTCACTTACCTCTCCTT GAAAAATAATCACTATTGCCAACGCCTGGTTAATTAGC CTGATTCAATTCTCTTCAGCCTCATTITGCTCAAATCTA CCAGATTTGTGGTGTCTCCTTGGTCCTCCACCACACTTT CTACCCCTCATCCCCTTTGTGTGTGTGTGTGTGTGTGT GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT TGGCCAGGAATCCTGACTGGCTTCCTTTAAA	SEQ ID NO: 27
DG5S491	168081175 - 168081342	AAGACCACCCTCCTGTTGTGTCTCTCCTGAAATGTATTC ATATCCACCCATACACACACACACACACACACACACA CACACACACACACACACACACACACACATTCTCTCTCT CTCTCTCTTTCTCTCTCTCTCTTAAATGTCAGTTTTCTCT TCCTGCTTTCCAGA	SEQ ID NO: 28
DG5S9	168139425 - 168139680	CTTGACATTGAGGGCCTTCTGAGTACATCATCTTGTCA AGAAACACTGAACTATTTCAGTACACAACAGGTGAGAG GTGCCCATTTGATAGCCTGAGGATGGAATCCTTATTGC AGCATTTTGCATGATGCCACATATATGTGTTTTTCAAT CCTCCTCTGTTTTAAAAATTGGAAAATTTTATACAACA CACACACACACACACACACACACACACACACACACAC ACCCCCCATACACACCACACCACATCA	SEQ ID NO: 29
DG5S876	168266982 - 168267134	AGCCTCTGACTCTCCTCTGTGGGGCTAATCCAGAAAAT CTTACTTTAGAAATAACAATAATAATAATAATAAT AATAATACCTCATTATCTTTACTTATCATGTGCTAGT ATGTTTCTAAGCCTTTTGGCATAGCCTTCAATGTCCCT	SEQ ID NO: 30
DG5S97	168286866 - 168287096	CTCTTCCCATGTCTGCTTCTCTCCTTCCCTGCGGGTTGG GACCCAGTACCCTCCATCTCTCTCACTCCTCCCCTCTCA AACCCTTCTTTTAGGAAAGGAGTCCAAATCGACCACTT ACACCTCAGTTCAATGCAAGCCAGTATAATTAATAAG GAACATTTAAGGGTGTGTAAAGGGTGTGTGTGTGTGTAT GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT C	SEQ ID NO: 31
D5S2052	168324273 - 168324633	GATCACCAGGGAATCTAGATGGAATCCATAGTNCNCTNC CCTGCAAGAAATGCTGCAATTCTGTACCGTGGAGGNGC CAACAGAATCACCAGGCTCTGTGACTCAGTCACAACA CCCTGACCTGCCCTGTCCATTCTCCATATCATACCCA GAGTGGTCTTTTCAAAGCACAGCTTTGACCAATTCTCT GTCTTTTACACATACACACACACACACACACACACAC ACATGCGTGCATGCATGCCTGAAATAGTATAGTATTGC TCTTAAGATAAACATTAAANGTTCTACCATGGTACAGA AAATATATGTNGTTAGGCCCGTGGCTCTTTCTTTTCC AGACTCCTCTTACCCCTTTGTG	SEQ ID NO: 32
DG5S879	168369069 - 168369202	AAATCTTCCATTGCAGACCAATTAATAATTAAAGATTT TCTCTCTCTTTCCCTCTCTCTCTCTCTCTCTCTCTCT CTCTCTCACACACACACACACACACACACACAACTCTC	SEQ ID NO: 33

[illegible]



		TCACCTCTTGGGCCGTGATGATGATGAGGGAGAGGAGC AGT	
DG5S38	168715977 - 168716367	TATTTGCCTGCCTGGGTTAGATGATTCTCCAGGCTTCT ACACAATTTTATGTTTATATGAAAATAGCCACAAAGG GAAAAGAGGACAATAAAACAAGAGATATGAATAATA ATGTATTGTATACCTTGAAATTTGCTAAAAGAGTAGATC TCAAGTGTCTACATACACACACACACACACACACAC ACACAAAGGTAATGAATGAGATGATAGGTGTTAATTA ACTTGATTGTGGTAATCACTTCACAATGTATACATATA AAAACATCATGTTTTACAACCTACATTTATACAATTCC TCAATTATATATCAATAAACCTGGAAAAATAAAGATG TATAAAAAAGATTTACAAATAAGATTTTAAAAAAGG ATTGTGAGGAAACAAAG	SEQ ID NO: 41
DG5S37	168770226 - 168770418	ACCAGCTAACCTGCCATGAGACTGTTGTGTAGCCATCT TCACCTCCTCATCTTCAGGGAAGGGGATGAAAATATCT GTGCACTGCAAATGTTAACTATATATACACACACACAC ACACACACACACACGTACAGTAGGCCCTCCATAACCT GAGGTTCCACATCTGCATATTTTACCAACTCTGGTCCC TGC	SEQ ID NO: 42
DG5S886	168803195 - 168803445	TTGTTCTGAATGGGAGGAGGACTGGTGAGTGAGGGG GAAAGAATGGAGACAGGACTGAGAAGAACCAGAAAT TAAAATAATAGTAGTAATAGCCTAACATGTACACGTA TATGAGATCTATCTATCTATCTATCTATCTATCTATCTA TCTATCTATCTATCATCTATATATCTATCATCCATCATG TATCTATCTATTTGCATATATAAGCTATAATATCTGGC TCTGTTCTAATTGTTT	SEQ ID NO: 43
DG5S101	168833451 - 168833700	CCAGGCTTGGATGAGAGAATAATCTTAAGGAAGTCAG CATATGTTCTAGAAACATTGAGAAGACAAAAGAGTCT GTTATGAAAGAACAAGTATTTGTAATAATAAATTGA ATGTTACATGGACACACCCAGACATACACACACAGAC ACACACACACACAGTTTTTCTTCTCTCTCTCTCTCCC CACTCCCCTCTCTCATACCTTGCAAACAAGCTCCTCAG CAGCTGGTAAGCTGTTCCCTGTCC	SEQ ID NO: 44
DG5S102	168895047 - 168895352	TCCTGACTGCTCAAAGCTCAAGGTGTTGCCTTTTTCAA ATGGGATGCAATAGCCTACTCATTTTCCAAGATTAAAG CTAGAGAGAAGAATGAATGAATGAATAAATAAATAAA TAAATAAATAAATAAATAAATAAATGAGCAAAGTTAA TATTAGCTGGAAAAAATAGGGTACAGGTGGAAGGAAT GAACCCATATTGAGAGTCCACTATGTGTCAAATTCCTT GCATGGAATCTCTAAGGTCTGTCTAGCTTAAAGCAAT GCCAGCCTTGCTATCTGTACTTGATGAGGAGATGGATC GGAA	SEQ ID NO: 45
DG5S39	168920224 - 168920577	CCAAACTGCAAACCCAACTTCTACAATGAATTCATGT GCAACTTATTCTAAAAGATCTATACACACACACACAC ACACACACACACACACACACACACACTTCCTGTCTCT ATTGCTCTTCACTACTTCCTTCATCTCTGTGCTACAATC TGGGTTTCATTTTTCTTCCCCTTGAGTAATTTATTATGTT TTTTACAGTGAGTCTGTTGCTCAAAAATTCCTTTAGTAT TTATTTGTATAAAAAGTCTTAATTTTGTCTTCATATAAA ATTTTGTGTTGACACTCTATTATAAATTGACTGTTATTCT CTTCCATGTTTTCCGGACATAGTTCCATTGTCTTCTGA CTTCCA	SEQ ID NO: 46
D5S1456	168968063 - 168968256	TTCNACCTTATGGGTATATCGAATTGTAACCCCGTTGT AGGTCAAGGAGCATCTNCATATATACATACATAGATG ATAGATAGATAGATAGATAGATAGATAGATAGATAGA TAGATAGATTTAATTCTAAANTTTCCAAATACTCTTTC	SEQ ID NO: 47

		ATTTAAATGATTATAGTTTTACAACAATTTTCATATATT NTATAGGTAGGAGAATTAGGGTTTTCCAGAGAAATAG ANNCAATAGGCTGTGTGTGTATATAANGATTTANTTTN AAGA	
DG5S106	169021310 - 169021609	GTTGGGCATGATGGTGTGTACCTATAGTCCTAGCTACC TGGGAGGCTGAGGCAGGAGGATCCCTTGAGCCCAGGA GTTTAAGACTAACAAGACTCCATCTCTGAAAAATAAG GCAAAAAAAGTATGAAGAATAAAATAACAATCACTTA CATTCCAACCACTATAAATTAATCATTGCCAACACCTG AGGATATTTGCTTCCAATCTACAAGACTGCATTATTAT TATTATTATTATTATTATTATTATTATTATTATTATTATT ATTATTGAGATGGGGGTTTCTCTTTGTTGCCAG	SEQ ID NO: 48
DG5S40	169067041 - 169067434	GCAGACAGGGTTCAAATTCAGCCTCCCTCATATTAG CTGTGTGATCTTAGGCAAGTTTATTCATGTGTAAAAAG AAATAATAACCTCTTCTCGTGGGGTTGCAGGTTAAACA AAAGAGTAGGTATTAACAACAACTAAAAGAGTATGATT GGATTGTTTATAACACAAAGGATAAATGCTTGAGGAC ATGGATCCCCATCTTCCATGATGTGATTTTTATGCATT GTATGCCTCTATCAAAACATCTCATTACTCCATATAT ATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT GTGTGTGTGTATGTGTATGCACACACTATGTGCCACACA AAAATTAAAAATTTTAAAAATTAAAAATTTTAAAAAT AAACATGCTGCTGGGC	SEQ ID NO: 49
D5S504	169142805 - 169143006	AGCTGCCAGCACACAAGGCCAGAGGTACTTTATTGG ATGCCAAATTCTTTTAACACACCATGAGAAAAGAAGT TGACAACTTTCCCATGCATTTTGGAAGGTGTGTTAGAA CGATTCAACACACACACACACACACACACACACACAC ACACACACACACATTTATTGGGTTGGGGGAGCCTT AAAACCTACAAATCT	SEQ ID NO: 50
D5S1961	169173385 - 169173631	AATTTCTTACCCTTTATCCCGTCTTCTACTCCCATTCC ACATGCCCCCACCCTCATGAATGATTGTCTAATGC GTTGAATATGCACGTGTGGTTTTGGGTGCATGTATGTT TACACACACACACACAGACTCTCTCTCTCTCTCTCA CACACACACACACACACACACACACACACACACTCAT GCCTCTCCTTTGAAGAGGATCAGATATGGACAGCAA GGCATTAGCATCTTAGCT	SEQ ID NO: 51
DG5S108	169203019 - 169203370	GCTCCAAAGTTCCTGATTCCAAAGCCTAAGTTAAGCCA TCTTAACTTATATTTCAAGGTGACTAGTGGAATTTTTAT GCCAGTGTAGGTGGTAATGACGATGGAGATATGGCG ATGATGATGATGATGATGATGATGATGATGATGATGA TGGCAGTAGTGGTGGTGGTGTGGTGGTGGTGGTGGTGA GATCACCATGTCTGACCACTGTTGTCTGTGTCCTTTGT ACAATTGTTGAGATGCAGTGTCTGGTGTGCACATAGA TGTCTCTGACTGTTTTACAGGCCTTCACCTACCACCAT ATCCAGGAGATCATGGTCCAGCTGCTGCGGACAGTGA ACCGGACAGTCA	SEQ ID NO: 52
DG5S41	169277936 - 169278300	TTAACCCTGCTCCCATTTTGTGTTGGAAAACTGAA AACCAAAGAGATTAAGTCATTTACCCAAGGTCATGTA ACTAATATATTGAATCTCAGATGTTTTAATGATTTTGA CTCATTTCCAATTTGCCTGGCTATATAGAGAAAAATATT TGAGGAATTGACAGGGAACACACACACACACACACAC ACACACACACACACACACACACACAGAGGGGAGGGAG GGGAGAGAGAGAGACAGAGACAGACAGAGACTGAAC AGATTATTTCTCCACTGATGTTTATTATTAGATCTATT TTCAACATTTAAAGGCAATTGTCAGCATAGTCAATTCA GCCATTTTAAACCATCAAGGGCCAATG	SEQ ID NO: 53

DG5S42	169285983 - 169286144	GCAACCTATTTGTTAGCAGCACATGCGTGCGTGTGCAT GCACGTGGGCACACACACACACACACACACACACA CTCTTTGCAGGGGAATTTTGAGCCAGAAATTTATCTGT AGGCCCATATTCAATTCCTTTTTGCACATTTCTATTGTGA CCTTGGGCA	SEQ ID NO: 54
DG5S10	169356049 - 169356318	CAATTCCACACAGCTGGAGAGTAACAAAGCCAGAAAT CACATCCATTTGTGTGTGTGTGTGTGTGTGTGTGTGTC CAAATCCTGTGATTCCAGTGCCAGGATACACTGTCTTC CGTGTTCAACAGTCATGAAAGTATTTTAATGAACACCT GGCCCTGCAGTGCCTGATGTAGCAAATGCTGCAGATA CTCCACCCACCGACTCTTGGACCACCCAAAATCCACTG GCAGCTTCAGTGAGGCTTTCCTACTTCTTTCTTCCCTG GGCT	SEQ ID NO: 55
DG5S110	169391090 - 169391341	CACTGGACTTGGAGTCAGGACATCATTTTAACAGCTTT ATCGAGATGTAATTTACATGCCATACAATTTACCCAAA GTGTACAATCATTGACTCTTAGTATGTTACAGAGCTA TGTAACCATCACACAATCAATTTTACAACATTTTCAT TACTCCTAAAAAGCAAACCTGCACCCCTTAGCCACTGC TCTGCCAACACACACACACACACACACACACACACGC GTGCGCACACACACCCAAACACTC	SEQ ID NO: 56
DG5S11	169409260 - 169409401	CGCGTGTAACCTCCACATAGATGTTTGCCAATGCCTATG CCCAAGACACACACACATACACACACACACACACACA CAGGATACATTCAAGCACACACTAATGTATGTGCACTT GCCTGCACAGAGTCCACATCACACAGGC	SEQ ID NO: 57
D5S1973	169424532 - 169424861	AGCTTCTAGTCTGCTATGTTGCTAATTGTCTTCTTGGTC ATCTTTTAAACCATTTCTGTGAAATTATAGCCTCCTT ACTCCCTTACCCTGAGTCTGGATGTTTCTGAAGATGAC TGATCTCTACAGTGAGAAGGCCCTGGGAATTGACTGA CTCACTCTCTGTCTCTCTCTCTCTCTCTCTCTCACACAC ACACACACACACACACACACTCATATACATACACA CATAGATACACATATACATGCATCCACACATGCACAC CCTGGGCACACCCACACACCCTACAACCTGCACATGCA TGCACACACATAATGTAACTGAAGG	SEQ ID NO: 58
D5S397	169542970 - 169543287	AGCTTTTGGCTATGGAACCTTAGGCAAGATGTTTCATAA ACCCTTTAATCTCTAGTGCCCTTGTTTCATAAAAAGAAG TGAATCGGATCCCTGCAGGACTGTTTTGTATTCACTG CACAGGTGTGTGTGAAGACACCCAGCATGTTGCCAGG CACACAGAGATGTCTACCTTGATACTTTTCTCTCCTCCT CCCCGCAAATACACACACACACACACACACACACACA CACACTCACACACTCTAATTTTGATCTTGGCCTGAGGC TGACAAGCCCCAGATTAGTGATCAGTGACAATTCGG CTTTATCAGCT	SEQ ID NO: 59
DG5S115	169586308 - 169586550	CGAGGATGCACACCTCATTAATTGAGGAGCTAGGATT TAGATCCAGAGCCTCATGATTCTAAAGCCTGTTTTTG TTGTTTGTGTTGTTGTTTGTGTTTGGCCACACTAGGTT TCTAGAACTTCCAGTTCCTTCTTAAAAGTCCTTTTTGG GCATTCCGGCCTAAATCCCAAAACTGTGGTCTGGGTAC AAGAGAGAATTAGGCCAGTGAGAAAAATTTAAACCAC CCTGCCCTCTAAAT	SEQ ID NO: 60
DG5S888	169653226 - 169653848	CTTGATGTCTTCTTTTACCATCCCCTGGCACCCGCCTAT ACATTTATTACTTGAAACAGACTGACCTTTATTTGGTT AGGCCACTGTGGTCAGGTTTCTGCAACATGGGGTCAC ATGCCCTCCCAACTGACACAAGTCTCAAGCTCCTTTTC TCTTCTTTTTATAACTTCTAGAAGCATAGCTTCTACCAG ATAAGGATCTAACCTTTTCAAGTGGAACAAAAATGG CAAAGAAGTAAAGAAAGAAGAGAGAGAAAGAAGAAA	SEQ ID NO: 61

		GAAAGAAAAGAAAAAGAAAAGAAAAGAAAAGAAAAG AAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAG AGAGAAAAGAAAAGAGAGAAAAGAAAAGAGAGATGGAGAG AGGGAAGGAAGGAAGAAAAGAAAAGAGAGGGGAGAAG AAAGAAGACAGGGAAGGAAAGGGAAAGGGAAAAGAG GGAAGGGGAGAGGGGAGGACAAGGGAAGGGGAGAG GGGAGGACAAGGGAAGGGAGGAAGGAAGAAAGGAA GGAAAGAAGGCAGGAAGGAAGGAAGGAAGGAAGGA. AGAAAGGAAGGAAGGAAGGAAGGAAGGAATAACTAGG GCCTTTCACTTTTGCCTTCAATAGCAGAGTGCCCTGG ATAT	
DG5S44	169661202 - 169661574	TATTGGCAGAGGGTGAGTCCAGTGTATAAAAAGCAACT ATATTTGTGCAATAAGGCCAACCTCTAAACACAAGTTAC TACTTCATCTAATGCCACACACACACACACACACAC ACACACACACACGAGTCATCTGTTCCAAGGCTGTTGCC TTTACTAAGTGATGCTATGTTGGTCCTTGAGGTGGTGC CTTCCTGAGGGTTTTCAAGCATAGCTTTGGCCATGCAC AGTTTTCTTCTTATACACACTCTGAGGAGCCCCGCCGT CACGGTAATGCACCTGCCTCACAAGCTGGTGGGCAGC TTAAATGAAATACACATTTTGCTCCAGGCCCAGCACTA GCTCATCAATGTGAGCTGGTGTTAGCCTCACC	SEQ ID NO: 62
DG5S45	169693772 - 169693912	CAGTAGCCAGGAAGCTGAGGAACACACACACACAC ACACACACACACACACACACAAACACACCCCCTTCC TGGCTCCAGTTCGCCACCACCCCAACCCCCAACCCG GAAGTAGATTTCTCAATAGGCAGGGCTG	SEQ ID NO: 63
DG5S46	169702377 - 169702678	TTTGCCAGAATGTCCTCACACCAAATAGTGGACCCCTT CTTTTGCTGATTTATCTGCTATTGTATAGGTGTATGTGT GTGTGGGTGTGTGTGTGTGTGTGTGTGTTAAGGCAGGT GGTAGTATGTGTAGGGTAGGGTTTCCCCAGTCACCTGG AGCCCTGAGTGCCTGCTTCCCTAAACTAGGCCAGTTTA GCTGACTGGCTTCCTTTGTGTATTGGTCCATTCTGCATC AAAAGCATCTGAATTTTCATTCAATCTCTCTCTGAAT TTTCACTTTTAAAAACCTGACCAGTCCCTTGTG	SEQ ID NO: 64
DG5S47	169788696 - 169788899	CTCCTCCATGGTAGGGACTGGTTCTCTTAGGCCCTGT ATCCTCAGGCCCAGCATGCTTGGGAAAATGTTTGCTAA TGCTTTGTGACTCAAAGGAATCACACACACACACAC ACACACACACAAACACACACACACAGTTTTTAATATT ATCAGTCATATCAGCCCCCTGAGGCAGCTGCTCTGTT CAGACAAACCCTGTT	SEQ ID NO: 65
DG5S119	169843903 - 169844041	GGGTACAGGAGAGTTGTGGTGGGCATTAGTACTACTC CTGCTGCTGCTGCTGCTGCTGCTGCTGTGTCCACTGTT AGTGACAGAAGTGGGAAAATATTTAAGTTGAGTTCAC ATTAGTGTTCAGTTTAGCGTGAGC	SEQ ID NO: 66
DG5S953	169866165 - 169866415	CCATGAGTTCAGGCAGTGGGTTAAATAAGATTTCCTT GAAGTCGAATGAAATCACAATGCACCACACACAGGGA CACACACACACACACACGCACGCACGCACATCACACA CACACACACACACACACACACACACACACACATAC ACACACACAGTCTCCCTGGGGCCAATCTACTGCCCCCT GAACCTCACCCATCAGCCAGGTGCCTGGCCCCGGGTCT GTCTCTTAGGGTTACATGCTCCCGG	SEQ ID NO: 67
DG5S955	169951970 - 169952619	ACTTATGGAACACCTACTCAGTGCCAGGTATTGTTGTA GATGCCAGGAGTACAGCAGGGAATAAAACAACATCCC TGTCCTCGACACAAACACACAAGTAAATAGAGAAGGT CAGAGATAAATGCTGTGCAGGAAAACAAAGCAAAGTG AGGGATGGAGAGTGCGGAAGGTTGGGGCACTTTTGTT TCAGATGAGTGTACAGGGAAGCCCCCTTGGAGGAGGCA	SEQ ID NO: 68

		CTGTAAGGGGCACAGAATCGAATGAAAGGAGTATGTGA AGGTGCTTAAATTGTTTCTGTTTGGTTTGGTGTGGTGT GATGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT GTGGTGTGGTGTGGTGTGGTGTGGTGTGATGTGATGTG GTGTGCGGTGCGGTGCGGTGCGGTGCGGTGCGGTGTG GTGTGGTATGGGTTGAGGCTGGCCTTAGGAGCCTGTTG GCCTTCCAGGCCAGTCCTGAAGCCCAGCCCAGAGCAC CAGACTCTGCAGTCAGTCAGTGGAGGGCCCCACATCTC AGCCAATGCATGGCTTTGGGTGGTGACTTCATCTCCCC TAGTGTTCCTTTCCCCCTCTGCAAAATGGGAATGGGGA TGGCTCAGAACTCCCAGCGGGAGTTAGGAGGAATAAT GTATAGGAAGTATGAGCAGAGTGCCTGG	
DG5S13	169961410 - 169961530	TGATGTGCTCGTTCCCATAGCCCCGCTGTGTGTGTGTG CGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG TGTTTGGTGGGGTGGGAGGGGAGGCAGAAGAGGAAG AGAGGGCA	SEQ ID NO: 69
DG5S123	170015858 - 170015997	TGGTGATCAGCTCAGTGTCTTGGAAAAGAGCAGAAA GTGGTATCACGAACATATCTTCTCCTTTGCTTCCTTCTC CTCACTCTTCATCATCATCATCATCATCAAT ATGGATCTGTGAGGCTACCTCTGGG	SEQ ID NO: 70
DG5S124	170041996 - 170042336	GGAGGAGAGACCAGCATTACATTAGTTATTGTTGTT TTAAATCCATTACGCACATACATAGGAGAAAATTTCA GCAACAGTCACCTCTGAACCCAGTTCCTCAGTTCTCT CCAGAGGCAACTAAAATGCTCAATTATTAGTGTATCCT TTTGAAAATATTTTATGTATATGACAGTGTGTGTGTGT GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT AAATAATATTAACATTGGTAATAGTGGTACTAAACAA CTTAGGGTGTTTTTTTTTTTCATTAAATAGTATATTTTA GTATCTTTCCAGGAAAAGATACATGGATGTGCCACA	SEQ ID NO: 71
D5S625	170105556 - 170105787	TCAATAAATGATTCTGGGGATGTGTCTGTCTGTCCATC TGTCTCTCTCNAGANACANATACACACACACACACAC ACACACACACACACACACATCCTGTTAGTTCTGTTTAC CTGGAGAACCTTGACTAACATACCCATTAAACCAAA ATATGTCCTTCAGGGTGTAAATGTTTGGTTGAAGAAAC ACAGAAAGTTTAACAATTGTATCAGGCTGGGCACGGCC TATAATCCCAGCATTTTGGGAGGCCACAATGAGNGGA TCACTTGAGCCCAGGAGTTCTAGACCAGCCTATGCAAC ATAGTGAGACAAAAAATGAANAAAATTAGGGGTGTG GTGGAGCGCACCTGTAGTCCTAGCT	SEQ ID NO: 72
DG5S959	170167429 - 170167616	GAGTTCTATGGAACAGCATTTATTGAATAATAACATTT CAGGAAAAAATATAAGCTTTACTGTATATTAAAATAC ATATATACGTTTATATATTATATATTATATTATATTATA TATTATATATATTATATATATTATAATTTTATATATTA TATAGATATAAATCAACTACAAGATCCAGTTCAA	SEQ ID NO: 73
DG5S960	170203240 - 170203459	TTGCCTAAGATCTAGGTGTTCAAAAGAATTTCTCCAAT CCACTTCAGCCTGTTATTATGTATGTATTCTGTTTTAAA TGAGAAACAAGAGTCATTTCTCCAGAATAATAGAAC CATAGTGACACTTGAAGTAAGTCCAGTGGTCCTGATAT GATAATAATAATAATAATAATTATTATTATTATTATTA TTATTTTGAGACGAGGTCTGTATCTGTTG	SEQ ID NO: 74
DG5S16	170280782 - 170281084	ATGGAGAGACACGGAGTTGCTTGAGGGTACAGTGCCT GTAGATACTCAATAAATATTTGTTTAATTAAGAAAATT TCTGTTATTTGTGTGCTCATACATACCATTTTCACTCTGG TGAGTATTGTTCTTTCTAGAGTTTACTTTTAATCTTAA GTATTTTCCAGGTCTTTGTTGACTTCTGTTTAAACCAC AGTACACACACACACACACACACACACAACTTTTGTG	SEQ ID NO: 75

		TACTATAATAGCTTCCCCAAAATTATAATTTAGTCATT GTGATGCAGATCTTCTTCCAAGGCCTCTACTTTGG	
DG5S962	170338421 - 170338789	AAACAAACAAACAGAAACACCAAAATGGATTCCAGCA TCTTATAAGTGCTTTCTCTTATGATCGAGAGTAAGACA AGCATGGCTACTCCCTTCTCTCTATTAAATATTGTACT AGGGGTTCTATTGAGATAAATAGGCAAAAAACAAAAC AAAACAAAACAAAAGGCATCCAGATTAAAAAAA AAGGAATCTAGGAATAAAGGGATTACATCTCTACTTG CAGATGACATGATCTTATGTATAGGAAATCCTAAGGA TCCACTGAAAACTGTTAGAACTAATAACATCGTAA GTTTGCAGGATTATAAGATTAAATACAAAAACTCGACT GAATTTCTGTGCACTTGCAATAAACACCCAAA	SEQ ID NO: 76
DG5S132	170442700 - 170442947	TCTGCCCCACACACTTTATGCTTTAAAACAAAAGGCCAT GTTGAACCTGTAGAACCAATGATTGCTAATTACTTGG GGCGATACTAGTGATATATTATCTTACATACACACACA CAAAACACACACACACACACACACACACACACACACG GCTTGAGTCCAGCATGGCCTACTGATTTTAAAAATAGGA AATGACAGTGTAATGCCAGGATAAAGGACAAAGTGC TCTGACCTGTTGCCAAACCTT	SEQ ID NO: 77
DG5S136	170469573 - 170469843	GGGTTTAGGACCCACGTATCTTTTGTGTTGTTGTTGTTG TTGTTGTTGTTTGGAGTTCAACATGTTTATGGTGTGTA GCCATGGTTGAAAGCTTTTATTTTATAAGATAGACAAA GCAGGAATTATTATTCTCATTTTACAGGAGAAAAACA GAAGGGCTATGTGGTTTGTAAAAGGCCACACAGACA GTAAAGAACACAGCCTTTACATGGTCAGCCTCACATTC TAGTACTCATTTTATTACACTGCTCTTCTCTCTGTGTC CTG	SEQ ID NO: 78
DG5S133	170480360 - 170480621	CTGGCCTCTTTGCCCATTTTCTAATTGGATTATATGTGG GGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT TGCTGTTGTGACGTTAGAGTTCCTTGTATATTCTAGAT ATTAATCCCTTGCCAATTAATAGTTTGCCAGTATTTCT CCCATCCTGTAGGTTGTTCACTCTGATGATTGTTCCCT TGCTGTGCAGAAGGTATTTAATTGATATAATCCCATT TATTTACTTTTGTGTTCTGTTGCCTGTGA	SEQ ID NO: 79
DG5S17	170499980 - 170500284	CCATCCAGGGTCTAACTCCAGCATTTGTATAAACTTGG ACAATACTTTTGCTACAGGGTTGTCATTGAAAGTATTG CCTCATTATATTTCTTAGTGGTCCCTGTATGAAGCCAT ATAAGAGAACTTCTTAATTTAGCACTAGGAAATGCTT CTGTTGACTTGAGATGTGTGTGTGTGTGTGTGTGTGT TGTGTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGT GTGTATTCCCTAATTGATAAACTATAAAATAATCTTT CTCTTTTCACTTTGGCCATCTGGAAATTTGCCACCAA	SEQ ID NO: 80
DG5S137	170644993 - 170645364	TGGCTTCCCAATCCTAGAAAAGGAAGAAAGCTGCATG TTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT TGTTAGATGGAGTTTCTGTGCGCCAGGCTGGAGTGCA GTCACATGATCTCAGCTCACTGCAGCCTCTGCCTCCCT GGTTCAAGCAATTCTCCAGTCTCAGCCTCCCAAGTAGC TGGGATTACAGGTGCGCACCACCACTCCAGGCTAATTT TTTGATTTTATAGTAGAGACGGGGTTTCACGATGTTGG CCAGGCTGGTCTTGAATCCTGACCTCAGGTGACCCAC CTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTG AGCCACCGCACCTGGCTGAAAGCTGCAT	SEQ ID NO: 81
DG5S53	170673106 - 170673364	GCCTTCGCAGATTGTACCTCTTCTTTTACCCTTCTCGC TGGCCTGTGCTTCTCTCTCCATCGTGGTCTCCACGCCT TGGTTTCTCCTCCATCCCCATCCCCATCTTTCGTGAGCC CCTCCAACCTCTCTCCCCGTGTTTGTACGGTCTCCTGCG	SEQ ID NO: 82

		TTCAC TTGATTTCTCTCACCCACCCCGCCCCAAACA CACAGGCACACACACACACACACACGCGCACACAC ACGGGCCTCTCGCACTCTCCTTCTCCT	
DG5S968	170675807 - 170676033	TGACTCTTGGCCTCTGTGTGTCTCTGGGTTTCTTTGTCT CCCTCCTCTCCACGGTCTCTTGTCTTTTGTCTTCCCT TTCTTGTTTCTTGAATCTCTTTGCCTTTATGTATCTGTCT TTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT TCTTTCCCTTTCTCCCTGACTCCCTCTCTCCCTCTTCCAG GCCCAGCTCCCGTAGCTCCTAAGGCAA	SEQ ID NO: 83
DG5S904	170735417 - 170735632	CATTTGGGATAAATGTTGTCTTTAGTTTTCAACTACTTT TTCTTTGGCTTATTCTCTCTCTCTCCCTCCCTCCCTCTCT CTCTCTCTCTCTCTCTCTGTGTGTGTGTGTGTGTGTGTG TGTGTATTTCATGTTTTCTTAATCTATCTGAATTGTTGTG TCGGTTTTCCATGCGAATTTCCAGTTACCTCCACAGTA TTCGTTTCAGAATGCTTCT	SEQ ID NO: 84
DG5S906	170820130 - 170820505	TTGCAGTTTCATGAACCAAGTATTACTGCCTCAACAAT TAAAAACAACAGACAAATTATTTAAAAAACCATGAGG CGAGTGGTGGCTGGTGGCTGGTGGCAGGGCGGGGGCA GGGTGGCCTCTGTGTCTCATGCTTTCTGGTTGGTCTGT GGTCTTTGCACTGAGAGCTAGGGCCTTGCACATTCATT CATTCAATTCATTCAATTCATTCTTTGAATTCAACAT TACTATGCACCAGGCGCTGAGAAGGCAGCCTTAGACA GATGGAAATCCTTGCTTTCCGGGAGATTCCATTCTAAT GGGTCAATTGATTCAAGTGGCCTCTTCAGTCATTTGTTCA TATGCATTTACTCGTACCTCTCATGTGCCA	SEQ ID NO: 85
DG5S141	170910447 - 170910786	AACTGAACCTGGGCTGTGTCACTAAGACTTATGCTT GGAACCTGTAAGAAGAACAAGTGTGCGTGCATGCATG TGTGTGTGTGTGTGTGTGTGTGTTTGGAGGGATAGTGA AGTTTTTTCCTACAGCTACAAATAGAACATGCTTTCT ATACAATTGTACTAATCAATATTATTTCTTACATTATC TCCAGCCATTTCCCTATAATTAGACATTCAGATTATTT CAAGGTTGTTATTCCTATAAACAGTGATGTGATGAATT TTTAAAGTTGGTTCTCACAATCCGTCTGTTCTTGTA TGTATCCATCATAGAACTGGACCACAAAGGTTGG	SEQ ID NO: 86
DG5S909	170941109 - 170941259	GGGAGTTCTCTTTCTTCAAGTGCTTAGGGGAGAAAATA AGTGAGAAAAAGAGAGATAGAGGAAGGAAGGAAGGA AGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGA AGAAGAAAAGGAAACGAAAAGGAAAGGAAGGAAG AAAGGA	SEQ ID NO: 87
DG5S910	170946679 - 170947010	TCCATGTTATTCTCTACCTGTTGGTTCCTTCCTCATTGA AAATTGGTGTATAGATGGTAGATAGATAGATAGATAGA TAGATAGGTAGATAGATAGATAGATAGATAGATAGAT AGATAGATAGATAGATAGATAGATTTTATTTTGGTC TATCTCCTTTACTAAACAGTAAGCTCCATGAAAATATG GATCATCACTGTCTTATTCACCATTTATTTCTCAGCAT ATGGTATTGTCCTGGTATAGAATAGATTCTCAATAAAT GCTTGCTAAATGAATGCATTCATGAGTGAGTGAATGA ATGAATATGCGAGTGGATGAGTGTGTGGA	SEQ ID NO: 88
DG5S911	170985696 - 170986066	TGCTTGAGGGCAGGATCTATATGTAATTCCTTTCTGGA AAACCAGGGATTGAAACAGGATCTGGCATGCAATGGG CTGGATGGGTGAATGGAGAAATAGATGAATGACAGAT GGATGGACAAACAGATGGAAGGAAGGATGGATGGAT AGATGGATGGATGGATGGTTGGATGGATGGATGGATG GATGGATGGATGGATGGATGGATGGATGGATGGACAG ATGGATTGGTTGGTAGATGTGTGGATAGATGGATGGG TGAACAAGCGAGTAGATGGATGAGTAAATGGCTAAAT	SEQ ID NO: 89

		CTGGTGCTTTTCTTCCAGAATCCTGGATTCTGAAGGGA GGCTTTGCAGCCCTTCCTCGTGGATCACTTGCTCTG	
DG5S143	171018986 - 171019237	GGCTGAATTACTGGGCATGTTTTCTGAGAAGAAAGAAC TTCTATTTTAATTATATATCTACAGAAACCAAATTGCC TGCTTACAGTTTTACATGTCTGATGATTGGAAGTTTTT GTTTGTTTGTTGTTTGTTTGTTTGTTTCCACAGACTAG CCTCTGACTCCATATATTTCAAACCTTTGTTCTCTTCCA CTACCCACATATTTCTGATGTGAGACATTCTAGAAAAA TTTCATATTGCAAGACGGCTTC	SEQ ID NO: 90
DG5S143	171039003 - 171039366	TTGGCAGGATTTCAGTTCCTCATGGGCACCAGACGGAG AGTCTCAGCAAATCACTAGCTGGTGAAGTGCAGCCACC GCAGTTCTTTATCAGTGGTTCCTCTCCATAGGGCAGTT CACAGTGTGGTAACTTGCTTCATCAGAGCAAGCCAGG AAGAAGACCCAGAGACAGACAGAGAGAGAGAGAGAG AGAGAGAGAGAGAGAGGAGGCCTCTGAAAGAGAGAGAG AAGAGAGAGAGAGGCAAGAGAGAGAATGAGAACTCCAGA AGTCACTGTCTTTTATAGCCTAATCTTGAAAGTGACAT TCATCACTTTCACTACATTTTCTTCCCCAGCAGTGCTCA GTGGGAGGGGATTATACACGGCCATGGAT	SEQ ID NO: 91
DG5S145	171040948 - 171041151	GCACATTTGCAGAGGTTTGAGGTCCCATCATTAGCCAT GCTTCTTGGTTCCTGCACTATGAGTATACGTATGTGGG CTGATGGCCTCATTCACTGGATACACACACACACAC ACACACACACACACACACACACACACCTCACCAGGGA CTTGGGAGTATCTAAATGTTTGAGAATCATAGAGCAG GGAGACATCCAACAC	SEQ ID NO: 92
DG5S146	171073796 - 171074122	GGGCACATACAGCTTTCCTTGCAAGGAAAAAACCTGC TTAACTTTGTTTATTATATATTATTTGATCTGTGCTTCA TATATTATTCATATATTATTTGATCAAGTTGCTTCATGT ATTATTTGATCAAGGAATCATGTGTGTCTACAGCACCT ATTAAAATTCCTGGCACTGAAATTCTGTAGAAAACCA TTTAGGAAAAAGTTGATCTAACTGTATAATTATTAGTAA AACATATACACACACACATACACACACACACACACAC ACACACACACACCACAAGCAAACAAAAAACCAC CTTAATGGTCTCCTAACCAAGGCA	SEQ ID NO: 93
DG5S147	171107565 - 171107831	GCATGTTCCGCACAGAGATTCAATTAATTTAAATAGGT AGAGGACTTGGGGCAGTGCCTAGGACAACATTACACT CAGGGATGGTGATGATGATGATTATAATGATGATGAT GATGTTGATGATGATGATGTTGATAATGATGATGATGA TGATGATGATGATGATCATGATGATAATGGAAAAGAA GATAGAGGAGGTAGAAGAGGAGACAATCATGATGTTG GAGGTAGACTCCAATCTTCAGAATCAGAAGCTCAGGG TTGGA	SEQ ID NO: 94
D5S462	171134297 - 171134396	AGCTTAATCTATTATTTNAGAGGCAGAAAGTTAACTTG CTTATCCTGAAAAGAAAGTGCAAATATATCCCAAAAGT GCCATTCTTTCATTTCATCCACTCAAACAGATACACACA CACACACATACACACACACACACACACACACCCCTTTTC ACCCCTTGGTAGTGACAGTCTCTGAGTTGTAAAAAAT AGTCATTNCTTTCTGCTTGAAAGACTGTATTAGCT	SEQ ID NO: 95
DG5S148	171140975 - 171141303	CCAGCATGATCCTATGAATCCTTATAAAAGGGAGATG GGAAAATTTACACACACACACACACACACACACACA CACACACACACACACACAGATAGAGACAGAGAGAAG AGGATAAGGCAATGTAACCATGGAGGCAGAGATGGG AGTGCTGTAGCCACAAGCTAAGGAATGCTGGCAGCCA CAGATGCTGGAAGAGTTGAAGAATGGGTTCCCCCTGA GGGAGCACAGCCAGATGCATGCTTTGAGAGTTTCAGCC CAGTGCTACTGACTTTAGACTTATGGTTTCCAGAATA	SEQ ID NO: 96



		CAAAAAATTAATTTCTGTCGTTTCAAACCATCC	
DG5S914	171219902 - 171220159	CAAACGTCGCTGACCTGAGTCTGACCTGGGCTGCCTCG TGTTACCAACATGAAAAGGGAGTGAGAAAATCTGAGG CCAATTAACCTCTCTCCCTCTCTCTCTTTTCTCCCCT TGCCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC TCTCTCTCTCTCTTTTCCCCCTCCTCTTCTTGGAGAC ATGATGAAATTTCTGAAACAAAACTCGCAGCCCGT TCAATAAAATGCTTTCGCCTTTGGTG	SEQ ID NO: 97
DG5S150	171232854 - 171233077	ACAGTTGCCATTTGCTCATTTAAAAATGTAGTGAGGTGT TTTAAAGAGGGTTTGTTCATTTACCAAAAAGGGAAA AAAAGGGAAAAGAAGAACTTATTGTTGAACGAACAC ACACACACACACACACACACAAAGAGCCTGGCTTAAT TTAGGGATAAAGCAAAGAAGTCAATACCCCCACATCA ACTATTGAAACCTAAGCTATTGCTGGAGTTGACAGCG	SEQ ID NO: 98
D5S429	171276128 - 171276490	AGCTCTNCCTAGCATTGTTTTCCCTTTGCTTCATTTCTC TTAAATGTGTTGGATGCACTTNGTTCCTGCTAACTAAT CTATCTTNCAGTTTCAAATCAAATGAACCCAGAGAAT TTATTTTACATTATTATCTTCAGATTTAGATTTGTTT GCTTTTAATCCTGTCTTCATGAAGGGGAAAGCCATGTG TACCAGCATGGTTGATAAACCACCAAATCGTGAAACT TTGCTTGCTCCCCAAACCCCCAACACACACACATACA CACACACACACACACATACACACACACACACACAC ACACACACACACACACACAACCTGGGAAATTGGGNAG AAAACCTGGCAAACCTTAAACTAG	SEQ ID NO: 99

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Table 7 The DNA sequence of the microsatellites employed for the association studies across KChIP1 (including Build 33 locations).

NAME	POSITION	SEQUENCE	SEQ ID NO
DG5S1173	169653708 - 169653840	AAGGGAAGGGAGGAAGGAAGAAAGGAAGGAAAG AAGGCAGGAAGGAAGGAAGGAAGGAAGGAAGAA AGGAAGGAAGGAAGGAAGGAAAAATAACTAGGG CCTTTCACTTTTGCCTTCAATAGCAGAGTGGCC	SEQ ID NO: 100
DG5S44	169661202 - 169661574	TATTGGCAGAGGGTGAGTCCAGTGTATAAAAGCAA CTATATTTGTGCAATAAGGCAACCTCTAAACACAA GTTACTACTTCATCTAATGCCACACACACACAC ACACACACACACACACACGAGTCATCTGTTCCA AGGCTGTTGCCTTTACTAAGTGATGCTATGTTGGTC CTTGAGGTGGTGCCTTCCTGAGGGTTTTCAAGCAT AGCTTTGGCCATGCACAGTTTTCTTCTTATACACAC TCTGAGGAGCCCCGCCGTCACGGTAATGCACCTGC CTCACAAGCTGGTGGGCAGCTTAAATGAAATACAC ATTTTGCTCCAGGCCAGCACTAGCTCATCAATGT GAGCTGGTGTAGCCTCACC	SEQ ID NO: 101
DG5S45	169693772 - 169693912	CAGTAGCCAGGAAGCTGAGGAACACACACACACA CACACACACACACACACACACACAAACACACC CCTTCCTGGCTCCAGTTCGCGACCACCCACACCCC CAACACCGGAAGTAGATTTCTCAATAGGCAGGGCT G	SEQ ID NO: 102
DG5S46	169702377 - 169702678	TTTGCCAGAATGTCTCACACCAAATAGTGGACCC CTTCTTTTGCTGATTTATCTGCTATTGTATAGGTGT ATGTGTGTGTGGGTGTGTGTGTGTGTGTGTGTGTA AGGCAGGTGGTAGTATGTGTAGGGTAGGGTTTCCC CAGTCACCTGGAGCCCTGAGTGCCTGCTTCCCTAA ACTAGGCCAGTTTAGCTGACTGGCTTCCTTTGTGTA TTGGTCCATTCTGCATCAAAAGCATCTGAATTTTCA TTCAATCTCTCTTCTGAATTTTCACTTTTAAAAACC TGACCAGTCCCTTGTG	SEQ ID NO: 103
DG5S1178	169745438 - 169745539	GTGCTCAATGGCTGTTGAATAAATAAATGAGAGGA GGAAAGAAGGAACAAGGAAGGAAGGAAGGAAG GAAGGAAGGGAGGGAGAGAGGGAGGGAAGGAGG	SEQ ID NO: 104
DG5S47	169788696 - 169788899	CTCCTCCATGGTAGGGACTGGTTCTCTTAGGCCCT GTATCCTCAGGCCCAGCATGCTTGGGAAAATGTTT GCTAATGCTTTGTGACTCAAAAGGAATCACACACA CACACACACACACACAAACACACACACACAGT TTTTAATATTATCAGTCATATCAGCCCCCTGAGGCA GCTGCTCTGTTCCAGACAAACCTGTT	SEQ ID NO: 105
DG5S1592	169794522 - 169794686	TTGAGCTGTTTGGCCTCAATGGCATTATCTCTCT CTCTCTCTGTGTCTCTCTCTTTCTCTTTTTTTTTT CACATTGAGCCATCTTCTTACAGCTGAGGTTTTTCA ATAAAAAAGCAAGTTGCTGGTTTCTCTTTAAAGT AGGGCAATCTGGCAGTTCT	SEQ ID NO: 106

DG5S119	169843903 - 169844041	GGGTACAGGAGAGTTGTGGTGGGCATTAGTACTAC TCCTGCTGCTGCTGCTGCTGCTGCTGCTGTGTCCAC TGTTAGTGACAGAAGTGGGAAAATATTTAAGTTGA GTTACATTAGTGTTCACAGTTTAGCGTGAGC	SEQ ID NO: 107
DG5S955	169951970 - 169952619	ACTTATGGAACACCTACTCAGTGCCAGGTATTGTT GTAGATGCCAGGAGTACAGCAGGGAATAAAACAA CATCCCTGTCCTCGACACAAACACACAAGTAAATA GAGAAGGTCAGAGATAAATGCTGTGCAGGAAAAC AAAGCAAAGTGAGGGATGGAGAGTGCAGGAAAGGT GGGGCACTTTTGTTCAGATGAGTGTGAGGGAAGC CCCCTTGGAGGAGGCACTGTAAGGGCACAGAATC GAATGAAAAG GAGTATGTGAAGGTGCTTAAATTGTTTCTGTTTGGT TTGGTGTGGTGTGATGTGGTGTGGTGTGGTGTGGT GTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT GTGGTGTGATGTGATGTGGTGTGCGGTGCGGTGCG GTGCGGTGCGGTGCGGTGTGGTGTGGTATGGGTTG AGGCTGGCCTTAGGAGCCTGTTGGCCTTCCAGGCC AGTCCTGAAGCCCAGCCCAGAGCACCAGACTCTGC AGTCAGTCAGTGGAGGGGCCACATCTCAGCCAATG CATGGCTTTGGGTGGTGACTTCATCTCCCTAGTGT TCCTTTCCCCCTCTGCAAAATGGGAATGGGGATGG CTCAGAACTCCCAGCGGGAGTTAGGAGGAATAAT GTATAGGAAGTATGAGCAGAGTGCCTGG	SEQ ID NO: 108
DG5S13	169961410 - 169961530	TGATGTGCTCGTTCCCATAGCCCCGCTGTGTGTGTG TGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTG TGTGTGTTTGGTGGGTGGGAGGGGAGGCAGAAG AGGAAGAGAGGGCA	SEQ ID NO: 109
DG5S123	170015858 - 170015997	TGGTGATCAGCTCAGTGTCCTTGGAAGAGAGCAGA AAGTGGTATCACGAACATATCTTCTCCTTTGCTTCC TTCTCCTCACTCTTCATCATCATCATCATCATC ATCAAATATGGATCTGTGAGGCTACCTCTGGG	SEQ ID NO: 110
DG5S124	170041996 - 170042336	GGAGGAGAGACCAGCATTACATTTCAGTTATTGTT GTTTTAAATCCATTACGCACATACATAGGAGAAAA TTTCAGCAACAGTCACCCCTCTGAACCCAGTTCCTC AGTTCTCTCCAGAGGCAACTAAAAATGCTCAATTAT TAGTGTATCCTTTTGGAAATATTTTATGTATATGAC AGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG TTCCTTTCCAATATTAATAATAATTAACATTGGTA ATAGTGGTACTAAACAACCTTAGGGTGTGTGTGTGT CATTTAATAGTATATTTTATGTATCTTTCCAGGAAA AGATACATGGATGTGCCACA	SEQ ID NO: 111

D5S625	170105556 - 170105787	TCAATAAATGATTCTGGGGATGTGTCTGTCTGTCC ATCTGTCTCTCTCNAGANACANATACACACACACA CACACACACACACACACACACATCCTGTTAGTT CTGTTTACCTGGAGAACCTTGACTAACATACCCAT TAAAACCAAAATATGTCCTTCAGGGTGTTAATGTT TGGTTGAAGAAACACAGAAGTTTAAACAATTGTATC AGGCTGGGCACGGCCTATAATCCCAGCATTTTGGG AGGCCACAATGAGNGGATCACTTGAGCCCAGGAG TTCTAGACCAGCCTATGCAACATAGTGAGACAAAA AAATGAANAAAATTAGGGGTGTGGTGGAGCGCAC CTGTAGTCCTAGCT	SEQ ID NO: 112
DG5S959	170167429 - 170167616	GAGTTCTATGGAACAGCATTATTGAATAATAACA TTTCAGGAAAAAATATAAGCTTTACTGTATATTAA AATACATATATACGTTTATATATTATATTATATT ATATTATATATTATATATATTATATATATTATAATA TTTATATATTATATAGATATAAATCAACTACAAGA TCCAGTTCAA	SEQ ID NO: 113

Table 8: The Build 33 location and size of KChIP1 exons.

EXON	START (NBCI33)	END (B33)	Size (bp)
1a	169716298	169716511	214
UTR 1	169848417	169848523	107
UTR 2	169861083	169861154	72
UTR 3	169864589	169864679	91
UTR 4	169867066	169867173	108
1b	169867120	169867180	61
Ins-r	170075401	170075433	33
2	170081305	170081429	125
3	170082868	170082937	70
4	170084380	170084450	71
5	170085260	170085367	108
6	170095347	170095451	105
7	170096383	170096445	63
8	170098306	170098353	48

Table 9. The Build 33 location of SNPs found across KChIP1 after the first round of sequencing that was limited to the exons and flanking sequences.

START (B33)	MARKER	VARIATION
169716196	KCP_e1a_249924	C/G
169716299	KCP_e1a_250027	C/T
169716321	KCP_e1a_250049	A/C
169740666	KNB_24222	A/G
169740703	KNB_24259	A/G
169741172	KNB_24728	G/T
169746339	KNB_29895	C/T
169747941	KNB_31497	A/G
169751683	KNB_35298	A/T
169751753	KNB_35370	C/G
169751753	KNB_35399	A/G
169848476	KCP_UTR1_382206	C/T
169848542	KCP_UTR1_382272	A/C
169861338	KCP_3UTR2_395068	A/G
169864750	KCP_3UTR3_398480	C/T
169864875	KCP_3UTR3_398605	C/T
169866181	KCP_e1b_399912	G/T
170081291	KCP_1152	C/T
170081464	KCP_1324	G/C
170081473	KCP_1333	A/G
170082788	KCP_2649	C/T
170085097	KCP_4957	C/T
170085115	KCP_4976	C/T
170085151	KCP_5011	A/T
170085191	KCP_5051	C/T
170085217	KCP_5077	A/T
170085342	KCP_5202	A/C
170095344	KCP_15204	C/T

170095540	KCP_15400	C/T
170096291	KCP_16152	A/G
170098209	KCP_18069	C/T

Table 10. The DNA sequence of the SNPs identified across KChIP1.

NAME	SEQUENCE LISTING	SEQ ID NO.
KChIP1	See FIG. 1	SEQ ID NO 1
SG05S872	<p>TGGCTGTCCCCTCTGCCTGGAGCAGGCTTTGCCAGATGTCCCTC  CTGGCTCACTCCCTCACCTCCTTATGTCTTGACTCAGAGGTCAC  CCTTCCAGATTAGACTGCCTGACCCCTTCTGTGCTTTCTGTTTT  CTCCTTATTACAAATGAATCTGCACCATATTTCACTGATTGTGT  TTGCTGCATGCATGAGGGCTCACATAAGGATGTGCTTTTTGTCC  ACTTTGTTTATTGCTGAATCACTAGCACTGACAGCTGTACCTGG  CACAACTGGGTGCTTAAGAAATATTCTTGAATCAAGGAATCAA  TAAATGAATGTTATAGAGAAAGCAGGAGAATAGATGATAATTGA  GAAACTGAAGCCCAGAGATGGGAAGTCACTGGCCCCATGTCAC  ACAGCAGCAAATGCAGAACCGGTCCTGGAACCTCAGCCTCTCAG  CCCCGGCCCTGTCTCTCTGTGCTTCTCACCCTTTATGTAAG  TTTTTTCTTTATTTGTGGAGCTCTCAGCAGGCATTTTCTCTCT  GTGCTCAGTTGGCATTTTTCCCTTGAACCAGCTGTGTCTTCACT  CTCTTCCCCATTTTCTCCAGAATATGTTCTTCTGTTAACTGAA  TGTTCTCTTTTCTGCAGGTCTGGCCCACTGCAATATCCAGAG  ACTTTTCGGGTGCATATGAAAGAAAAGGAGCAGGAAGCCAAGAT  GCCCCACCTGGCTTCTACATCAGGGTGATCTGCATAGTAAGATG  CAAAGACACTGACATATGCCTGGGGGTAACGAGGGCAGTGGGGG  GAGGGAGCTAAGCCAAGATAAGCCTCCTCCCCACCAACATAGG  TGCTACTGAGCAATGATAGGGGGCATGCTGTCTGCTCTGGTACT  TGCGTAGGGAATGCTCTGAGAAACCTCACTAAATCTGCCCTCTA  GAGTAGAGCAACCTGGGAGCTCAGGCTTCCCTTTCCTCTGTGTG  ATGGGTTGGCGGTCCTTAGAGCCAGCCATTTT [A/G] TCCTGCT  CCTTCTCTCTCCCCCTTCTGACCAATAAAGATTGTGTGCTTCT  GCCCAGTCAGCAGGGTGGGCTCTCACTCCATCCTGCCTCTGGTA  TGACAGCACAAATCCCCCTATTCTTTATAATCATTATAAAATAA  AATAACTACCTTTTAGAATACTTATTTGATATGAGGCACCTTGC  AAACCCACAGTCCTGCATATCCCATTGACATATCAGGATGCTG  GGCTTACAGGTTACCCCAGGGGTGGAGTTGGGCTCAATCCTAGG  ATTGTCTGCATCTGATTCTGAAGCTTGTCTTTTCCCCCTATA  CACAATCATTCACTTCACTTCAAGCATTTGATTATGGTGATG  TACTATGTACCAGCACCTGTTCTAAGCATTTGATTATGGTGATG  AATGAGGCAGACAGGGTCTTCCCAAAATACTAATCTATTCT  AAGCAGTGGGAGAAAAGCAATGAATGGGAAATAAATGCACAAA  TCAAGTAATGTTGGATGGGACAACCTGCTGTGGTCCCATTGAAAC  AAGCCCAGAGTGAGCCAGTGTAGGGACTTCTTCACTGACTGGT  TGGGAATTGAGTGACAATCGGTTGCTGCATGCTGATGGGTGCCA  AATACAACCGTAAGGAAACACTCCCCCTGGGAGGGAGGCGGGATC  CAGGTTAGGAAAGAGCCTTGGATTGAGGCAGAGTGTCAGGAAGT  GGGGAGGTACGCAGCTGACCTTGGAGAAAATCCCTGAGTGGTGC</p>	SEQ ID NO. 114

	AGATCTCTTGAATCTCTGAGTGGCTCAGAGTCTTCCTGGAAATG CAGAAATCCCCATGCCACTTAGGGGCATCTTCATTCATCTCCAG CCCTCCTTTATTAAAGTCATGTATACCATCTCCTCTCTTATGCTT AATGTCATGCCACTCTTCAATCCTTGTCCTTCTTTCCCTCTGT GCCTGCTTGTGGTTTACTCCTGCTGACACCAAAGGCTGAGGAGG ATGAAAGAACAATTCCAGCCCTGAC	
SG05S873	GGTAATTCTTAAGCTGGCTGGGCCTAAAACTGCAAACCTGGTATT GGGCATGCCAGAAGGTAACCATAAATGGGCTATTTGGAGATTTT TAGGAAGAAGAATGACATTTTGTTCATTCCATTCCATTTTCATT TCATTCCATTAATACTAAAAATATTAATAAAGCATCATTTCTA CTATATATCCAGAAGAGAACATGGTCTTAGGTCTTTTAATAAAT GAACTTCAGTTGCAAACCTTTCTGCTGTGACGTTATATTTCTCTT TCCACCCTAGACCAGCCCTAATGGGGCCATGAAGTCAGATTTT TGGTTCATGGTGTGTCGGGGCAGCATAGCCAGAATTCCACTT CCTTCCCTGAGGACACATTTATTCTGGTAGATGTGCTGTTTCC ATTTAAATGTCTTTTGGCAATAAAAGAGCTGGCTCCAACAGCAG ACCACGGGGCTGGCTTTGTGCGGCAGACACCACGTGTTTCATGACT GGCAGCTTTGTCTGGAAGAGGGAGCTTTTAAATGCAGTTCTAT GCTGACTCTTTGGAGTCTTCCAGGAAGATAACTGCTATTGCAT TGCATGCTTAATTTAGAGCACCTATTTTTCCCTCTCCTTCAAGG TTTCTGTATATCTTCTCAGTTTCATGAAATTAATTATTTGGGTAC AATAATTGTACAAAGGCACCTTTATCAGACACTTCGTATAAATTA TTTCTCATTTCTCAAGGCAACTTGGAAAGGTCAGTCTAGGGGTCA GCTGCTACTTTTGGTGATCAGGCATCACCCCTCCTTCTCTTA GTACGTTATGACAGTGGCAAGTGAGCATTACCTGTGGACCCCAA AGGAGTTCATTTCTTAGAGCCAGCCATTCTCAGTTAATCTGG TCTGTGACACACTCTGTCCCAGGACACTGAGCCTTGAGCATGTG AAGGTGTGGGCTCTGCTGGGGGCTTGGCAGCCAGCACCTGTCTG TGTATCACCTGGCTCCTGCGAGCGAGAACCTGC [A/G] GTGTGAT TTCTGCAGCCTGGCCCTCTGAGATTCCATGGCTGCTGACCATT TCCACTTTCCAAGACTGTTACATTCCCAGCAATTCTGTGAGGC CCTGGCCTTCAAAGGTGTTCAATACATTCTTTTTTTTTTTTTT TTTTTTTTTTTGAGACAGAGTCTCACTCTGTACCCAGCCTGGAG TGCAGTGGTGCCATTTACAGCTCACCGCAACCTCCACCTCTCGGG TTCAAGCAATTCTTCTGCCTCTGTCTCGCAAGTAGTTGGGATTA CAGGCACACATTGCCACTTACGGCTTTTTTATCATTATTATTAT TATTTATTTTTTAGTAGAGATGCAGTTTTGCCATGTTGGCCAGGC TGGCCTTGAACTCCTGGTCTCAAGTGATTACCCACCTCAGCCT CCCAAGTGCTGGGTTTACAGGCGTGAGCCACTGTGCTGGGCCC CATTTGTTATTTAAGGGAGAGTCCGTTTCTGCTGTTTGTAAC AGGACCTGTCTGATCTCTAGGAATTATTGACCCAGTTTTTCAGA TAAAGAAGTTAAGCTTGAGGTTAGAGCTTTTGAGCAAAAACCTCC TCTCCTAGAGAACTCAAGTATCCAGGAATACTCGGTCAAGGCTG GGCTGGACCAGGTCTGTAATCCTGATATTCAGAAAAGGGATGAT TTCTCCTCTTTGGTTTGGTTTCTCACTGAGGCCTGCACACCAG TTTATTTCTGACTTGTGCATTCAACATGGGCAAATCCAGGTCA ACAAAGACTGGCAGCTTATTCCTGAGTACAGTTCCACCAGGTAT GGCACACAAAGTGATATGAGTTAGAACACAGATGGATATAGATG TTTTACAAATGTAAGTTTGCATAACACACACACACATTGCTA TGTGTTAGAAAAATACAATAAGCTCATCTAATTTATTATTTTCAT GTGTCTTATTGCTCAGAAAGAGGAAAAGATTTTATTGAAGTTGA	SEQ ID NO. 115

	GAAAAGAAATTGAATTAAATAATA	
KCP_rs31 5773	AGAAACTCCGACTGTCTTTCAGCACACAGAAGACACTGTACTGG ACCCGGACATTAGGCAGACACCCACGCCTGACTTTCAGGAGAAA AGAGAACATGACTAACGGATATTCTTAGTAGATGGTTTATTAGA AAAGAGAACATCTTCCAGCATGTGTCTTGGGGTATGGGTGTGG GAAGCACTCAGTCCATAGTCCCTGGTCCCTGGCTTCCCCAAGCCC AGCACCATGAATGTACAGTGGAAAGCAGAGGGTGCAGCGTCTCA GAAAGATGCTTCCACTCACAAGGATTGGAGCTCACAAGTGAGCT CCATAACCTGCAAACCAGAGAAACCTGAGACACTGCCCTTGGC CATTTTATCAACGGAGACTTTATTGTGATTATCCCGGCAGGGGG CCGAGCTCTCCTCTCTGCAACAGGAAATGCTCTTTAGTGAAAAAT GCAGCATTCTCTCAAGGGTAACAAAGCTGAACGCCTGCTTAGCT TATGAACCCCTCAGTTGGCCTAGGTGGTGCAGAGACCCCTGCTGTT ACTGCTTTGATCATCAGTACTGTGGACTGTACAGGAGATCCCT GGGAATGTGCTCTGGGCGGAAGCAGCTTTTATCTTTGGCCCTCA CCCATGCTTTATATGGTGAGGTGGGAAAATGGCACAAGGCTTC TCCTGAACCTCAAATCAACACCCTTGCCCCATTTAGATCCTATC TGGCTGTTTCTTGCTAATATTACTGCATCACTGCACCATCTTTC CTATTTAGCAAAGTGGAGTCATGTGTGGTTTATGGGGTAGATG GACCCCAAACTGATAATATGAATCAAGCTATGGTGTCTTACTCC CTAGGAAATGCACAATTTTCTGGAAACCTACAGAAGCTTCAAA TGCAATTCGCCATGCAAAGCTAAGTCAGCAGAACCAACCGTTTGG CTTTGGAGGCTAGTTCAGTTCCGCGGACAGGGAGAAAGATGAGG CAGACTGTGGTTTTTTCAGTTCTGAGCTTAC [A/G] GAGCTCC AAAGCTCCCTCTCTTCCACCCTGGCTGCACTGTTCTTAATTTT AGATAATACCCTGCCTTCTCGTATTGCTGCTGAGCTCCTAGCAT CCTCAGTTTATCTGTCTGTGAAATGAAAAATCTAATGTTAAATT TTTTACCTATGGCATGAGAGAGATGGCTATGGCTCTTGTGAGCC TCTCTGCAGCCCTCTTTTCTTCAATCACCCCTCTGTCTCTCCT GCCTTCTGCTTATTCTCTCTCTCTCCCTCATCCCCACTTTCCAG TGGGTCTCTGTTCTCTTTTTTTTTTTTTCTTTTAAATCTCTCTA TGCCTCCAGCCGAGAAGATAAAGAGTGATACATCTTCTGGTTAA AAAGTTTGTCTTTGCAGAAACACAGCCAATTTATGATTCTGGCC TTCCAGCTAGGGACAGTGTTCATTTACATTTAGGACCATGAGG AGAGAGGCTTAGCTGTGTGTTTCTGAGGCCGGAGAAAATTACAG TGATATATAACAGTGTGCACTCATAGAGGTGCTGAGCCGGGGT TGGGCTCAGGCGGCCGCTAAGCTCAGAGTGGAAAGTTTCAGAGG GGAGGCAGAAAGGAGAGGTCTATAGCTCCTCCAGATTCTAGGTA TTAATTTACTAAGATATTCCTAAGCCAGAAAAACAGAGACAGAAG ACAAAGAGAAAGAGGGAAGAAGAGCAAGACAGAGAGTTAGAGAG AGACAAAGAGAGAGAGTTAGAGACAAAGAGAGAGTGGAGAGGAG AGAGAGCAAATATTGAAAGGAAAAGGAAAAGAAAGAAACCTGA CAGCTCATGAACCTTTTAAAAAGTTACAAATTAGATTTGAAGAG ATGGGCAGAGGTTTAAAGATTTCTTCATTAGGCTGGGTGTGGTGG CTCATGCCTGTAATTGCAGCACTCTGGGAGGCTGAGGGTGGCAG ATCATCTGAGGTGAGGAGTTCCGACACCAGACAGGCCAACATGGT GAAACCCTGTCTCTACTAAAAATAC	SEQ ID NO. 116
SG05S876	TATATACAACCTGGAAGCTCTTTTTTCCAACCATATCACAGACAA AGAAATTGAGGCTTGTAAGGTGAAGGGGCTGCCTTTCTTTG CTCACAGGAATGTGAGGATGATACAAAAGTGAAGGATATTGGCA TTCTTCAGGCAGGGAGATAACCTGGACAGGGGTGGTGCAGCAGG CATGTGCATAAAAGGAGCAAGAGAAGCCTTCTCTGTCGTGAGCA AGCTTGCAAGCCAGATGGAGAAAAATGAAGTAAAGTACCCCCAA AGCCTGGATTCTCATCTGGAGTGCCTCTTGCCCTCTTGCCCTTCC CAGAACGCTCCAGCTTGGCACTGGGCTGGAATTCCTACTAAGAAT TGAGTTGATTTCTCATCTGAGGCCCTGGGCACAATGACAAGGG	SEQ ID NO. 117



	<p>TGGTTTTCTCGGATCTGCAGTGAGCATTACACCAGAGTGTGGGA  AACAGTGCCTACTCAGGGACCCCACTCTGGGACCCAGGGCAAAC  TTGCCATCGTCTCCAGTCAGCTCATTAGCCGCCAGGACTCTGC  CAGCCCATCCAGGCAGTGATGTAATTACCAAAATGGAGATGAAT  ATTTAAAGGGACTCTTACTTAACCGATATACTTCCTCTCCAAGT  TCCCTCCTTCACCGGCTCTGGATGAATTTCTGGAGGGATTGCTC  TGACATAGGCCCAGAGCTACCTGTGGTTTGACCTCATCATGAGG  CCTTTCTTCACCCCTTCTTGGTGGCTTGCCCTTGAGGGTGTTAGG  AGATGGTCCATTGTCTGACTGTGAACAGCAGGGCAGCTCTTATA  TTCTCCATCAATGGATCTCTGGGGACAAGACCCAGATGGGTGGG  GGGACAGGGGAAGGAAACATAAAAGCCAAAGGGACTGGATACCT  GTAACATAATTACCCCTTACTGTTTCTGTCAACAGACCTTAGTG  CCACAAAGGATTGGGGGTCAATTTGTGACAATGTATGTTGTAAAA  TGTAATATGCAAGTGACCACAAATCTGAAAGC [A/G] GTATAGA  GCTTTGGTTAAATAATGCAGGCTCTCCACTGGCATTATTATTG  TTGTTAGGAGAGTCTGGTGTCTGTTCAAGGGCTTTTCTGTGCT  ATGGATTATCTCTGTTTAGCACAAATATCTTGTGTCCCTGGAA  ACCCCTTAGTCCTGAGAAAACAGGGCAGTTGGTCACCCCTTG  TTCAATGCAGGCATCAGTTCCACTAGGTAGGGGGTCTTAGCTGC  ATTTTAAAGATAAGGAAATAAAGACTTAATGGGTTGGAATAACT  GGGTATGTGCACATAGCTAAAGAAATGGTTACACAAACAACCTC  AAGTCAAATATTAGACCTGCGTATTCCTAAAATCCCTATGGCTG  TTTGCAATAACTTGAGGCCAGCCTCCCTCTCCTCTTTTCTAAGC  CCTCTTTACCTTTCTGTGTCTCTGATGGCTGTTGTTTATCAAG  GCAACCATCGTGATTACATCCTCAAAGCAGCTTTGAAATTCTAC  TCCTATAGGCTCCAAAACCTTATTATCCAGGTTTCAATGCT  CTAACTAGGTGAGGTCTGAACAGACCCAGATTTCAAGCATAT  TCAGGTGGATTTGTTTAAACAGAGTGTGGCTACTGGAACATCTGG  AGCCCAAAGTACACAGGAGGCAGGAGAGAGCCTACTTTCCTGAA  GAGAGGGACGGGCCAACTGTCCGACAAAGAGGAGGTGGGCATT  TTTCCTTTGTAAAACAAAAGTATCTGAGACAGGGGTCAAGTCAA  TTCAGAAGCTTATTTTGCCAACTTATGGACCATAACCCATGAC  ACAGCCTCAAGAGGTCTGTGAGAACATGTGCCCGAGGTGGCTGGG  TTACATCTTGGTTTTTACATGTTTGAGGGAGACTGAAGACATCAG  TCAATACATGTGAGGCATACATTGGTTGGGTCCAGAAAGGCGGG  ACAACCTCAGAGGTGGGGAGTGGCTTTTAGGTCTAGGGTGGATT  CAAAGATTTTCTGGTTGGCAATTGG</p>	
KCP_rs95 2767	<p>AAAAGTAGCATCGAGAATCAATTTGCATCTCAGAATTGGGATCC  CTGCCCTAATCTCTCTACTTTATGCGGCCGTGTCTGCTTTTCA  TGACTCTAGAAAGCAGAGGAGAAAGTGGATGTAAGATATAAATT  AGTCTGTCTTGTAGGGCTTTCTCTTGGTCCCATTCTGGGACCAG  CCAGTGTCCATACCTGTGGCCTTTGGTATCCAATTTAAGGCAGT  TCTTCTCTTTCCATGATCACACAGTAAAGGAGCCCCCGTATACA  GTGCTCCAGGACTGAGTCCAGTTTGTAGTGTAGCGTGCAACAAG  AGCAGAAAAGGCAGAGTTGGGAAGGACATGTCAACGGGCAGCAA  TGAGGTGGTATAAAGACCCTGGGCATTGGAGGCAACAGAGGGA  GAAAGGTCTGCTTCAAGGACCAACTTGGTCTCTTCCTATCTCTG  CCCTGGCAGCACCAGCAGCTGCACATTGGCCCTTCTTACCCTT  CCATGGCAAAACCAAG [G/T] TTTCTCTACCTCGCCTAGCCGGC  CCCTGCAGACTTGCTGACACAGCTGAGTGCGGAGTGCATCTAGA  CCCCAATGAGGCGCCCTTCTCTCAAACAAATGAGCCTTCGA  AACTCCAGCAAACAGTGCTAATGAATTGCCCTCGGCTTCTTAGG  CATCATTTTCTCGTAATTATAATGGGAAGAAGACATGGAGTCCC  ACTGAGAACGTGGAGCTAGCCTGCCCTAGAGCAAGGCAAAATC  CCTCTCTGAGGACCACACTCAAGCAGAACTGATTTTCTAAGAC  TTAGAGAAGAAACAAATCTGATTTAATCTTAGGAAATTGCTT  TTTTTAACCCACCTGTGTAAGCCTGTATTTAAATGCTAATATAT</p>	SEQ ID NO. 118

	TTGGCCTGCCGGGATGCCACATTTATTTTCTTCCTTAGCAGCAA CAAAAATCATTATTTATGAGAATTCCTAGCTCCTACCTGCTCTC CTGAGTTCCTCATCTTCATTTCCATCTACCAGCTGGA	
KNB_2422 2	GAGGGGTTTTTAAGATTGTGTGTTCTGAATGGCCTGTCTCTGAC TGGAACCCAACTCCGTCCCCAGACCCACTTCCATCTTTTTCTGT GAGGGGGACACACTCTTCAACTTTTTCCAAAATGGCATCTACCA TGGCTTTTCTGATTAAAAGCAAACGAAACACACCCTTCCTATAA TCAAAAATTTAGAAAAGCAGCAAAAATAAAAAGGGGATAAGGAA GAAAACAGAAATTAACCACCATCCC [A/G] CCGCTAAAATTTTG ATGAGTTCTCATGTGTTTCTTNCAGCTGATTGTTGTTTGGCAT ACATTTATTAA	SEQ ID NO. 119
KNB_2425 9	CACTTCCATCTTTTTCTGTGAGGGGGACACACTCTTTCAACTTT TCCAAAATGGCATCTACCATGGCTTTTCTGATTAAAAGCAAACG AAACACACCCTTCCTATAATCAAAAATTTAGAAAAGCAGCAAAA ATAAAAAGGGGATAAGGAAGAAAACAGAAATTAACCACCATCCC NCCGCTAAAATTTTGATGAGTTCTCATGTGTTTCTT [A/G] CA GCTGATTGTTGTTTGGCATAACATTTATTAATATTGGAATTAATA ATATATATGGCACTTTATATCCTAGAAAATAGTAATACTGTAAA TGTGTTCTAGAAATGGGAGCTGCTGTTGCTCTTATTAGAGAATT CAACAAGAAAGGGAGGCTCGCTGGGGACAGCTTCTGGGGGAGG ATGGGTACCGCTTTGAGACA	SEQ ID NO. 120
KNB_2472 8	AGGTATGAGTCAGTTGAGTGGGGACAGGTAATAGAGAGCTAGAA CTGGCTGGCCTTATGGCCTCCAAGGCATTGGGGAGCCACTGTAC ATTCTTGAGCAGGCAATGACTTCACAAAAGGATTTCTCAAAGGT TAGTCCTGCAACAGAAGACAGCGTGGATTGGACTGGAAGAGTGG GAGGGCAGGTGGAGAAGGCATTG [G/T] CTGCAAGTGGGGAGCA GCCCCTGGGGGCCCAGCCAGTCCCCTGTGCCCTGACAAGTGGTAT GGCATGGATGGATGGCTCTACTTCTGGGCCGCCAGGATGGACAG GTACTGGTTGCTCTTCACCATGGCGATAATGAGGAGGCCACCGG TCAGCAGGAAGGTGGGCCAGAAGAGGGAGAAGAGGAGGGCCTGG GGCCCGTAGAGGCGCTGGAAT	SEQ ID NO. 121
KNB_2989 5	CCCCATCCCTCCAGTTCAGTACCTGCTGGTTCTGGTCCCGAGTG TCCTCCGTGTGGTACAGCACAGCCCACCTGCCGGCAGCTGACAC GTTGACCCACAGGCATGGGTACTGGGGCACCTTCTTGCCCTTCA GCT [C/T] CTCCTGGTCCCTGATGTTGGTCTCAATCAGGTGGCA CTTGGAATTCCTGGGTCCACAGCTGAGGAGACCACACACATGCA CACATACACATCTCAGAAGTGGGTGACACACAGAACACCCATT GAACCCATTATCCCTGGGAGCCTCTAGAGGGATCCAGGACTGG GCTCCTCATCTTGTCTTCAGCATCCAGCAATAAAGGCACAT	SEQ ID NO. 122
KNB_3149 7	TTCCCTGCACTTGAACCCTAGAACCTAAGAATGAGCATCGTCTT GACCTTGCTGCCTTGAATGAGGGTCAAGGAGAGGGGTGAGTAGA AGGCCAGGGTTCCTTACAGATGCCAGACCCTTAGGAGAGGGTTG GGGGTGGGCAGGCCNGGAGAGCTCAGTACCTTTTCTGGTAGAG GGGCAGCACAGTCGTGACCAGGATGTAGTAGGTGATGACGGCAC ACACCACCATGGTTACACCCAG [A/G] CAAAGGGCTCGTGTCTC TCCCCGCTTCTGGGCCATCACCAGCTTCTTACCATATTCAGTG GGGGCAGTGATCATTTCTAGGTCCACAGAAGCAAACAGAAGTGA GATCAGCCCAGTTCACAGGTGATCCACAGAAAGAGAGGACAGGT GAGAGGGGAAGTACTCAACTATTAATATCACTCTTGTATTATAT TTGGAGCTTTGCAACTTCCAGAAGTCTTGCTTTTGGACCCCAT GTA	SEQ ID NO. 123
KNB_3529 8	AGAGGAAGGGAGTCCCTGCCTGCCTCCCTCCCTGCCCCGTGG CAGGCTGCTTTCCCC [A/T] GTCTCCCTCCAGCCCGGTCTTCAG AGAAATCACTTCCCAAGTGCTTTTCAGGCCCGGTACTCACAGTCT TCCCCGCGTCTGTGGGTCTTGAGCAGCAGACAGTTTCTTCTG CCTGGACCC	SEQ ID NO. 124
KNB_3537	AGCCCCGTCTTCAGAGAAATCACTTCCCAAGTGCTTTTCAGGCC	SEQ ID

0	GGTACTCACAGTCTTCC [C/G] GGCGTCCTGTGGGTCTTGAGCA GCAGACAGTTTCTTTCTGCCTGGACCCCCGCCCCACCCCAAAA GAGGCCACAGAGCTTCA	NO. 125
KNB_3539 9	AGCCCGGTCTTCAGAGAAATCACTTCCCAAGTGCTTTTCAGGCCC GGTACTCACAGTCTTCCCGGCGTCTGTGGGTCTTGAGCAGCAG AC [A/G] GTTTCTTTCTGCCTGGACCCCCGCCCCACCCCAAAA GAGGCCACAGAGCTTCA	SEQ ID NO. 126
KCP_rs31 4129	CTTATCTCCACCCCTTCACTTGACCCAAGAATCAAAGAACCTGAA ACTGAGACTTGGAGGCTTGAAGTCACTGGTGCAACCCCTAGGGGC CAGAACTAGATTGGAAGCTGGCCCTTCCAGATGGCACAGCTTGG TCTGTCTCTGATGACCCTGGGGCTGCTCTGAGACATTAAAAATC ACCTCGATCATACAGTAAGCTGCCACCTGAGGCTCTGGAGGTCA CCCTGAGTTTCCCCAGCCCCCAGGGAGGTGGGTGCAGCCTGGCC TTCCCTGCTGAGCGAGCTCACCACCTTCCCTCCCTCCTGCCTCCA GCAGGCGCGAAATGAAGGCAGCCACTCAGGCCTCCCTGACACAC TCTCAGGCGGTGAGTGCCCTTCTCCACCCCTTTCTTAATTGAAT CTTATTAACAGGAGACTACAGTGTCTGTTAATGGGCACCATAG CACCAGAGGGTCTAAGACCAGCTTCAAGCCTTGACAGGCAGATTG ACAGAGGGATGTAGGA [C/T] CTGGAATTCAATCTCAGAAGAGC AATTTTCCAAGGATGATCCTCTGTCCACTCAGAAGCAGGAAAG TCCTCCTGGGGCTAATCCAGAAATGCCAGGCCCCCTCCTGCTT CCCTGGGGGAGAGATACACAGTGCAACAGGCTGCCATTTATGAG TATAACCGAAGGGCTCCTTGCTCGTGATACTCTGAATAAGTTAT TAAGGGCTACATATTATTTGGAAATCATAAACAACCTTTAGCAT TCTTCCCAAGGGAAGGTGGGAACAAACAGGGAAGGGGGGCCGTG GGGTCTTCTGCTCCCCCTAAATGAGCCACAACCAAAAGGCATTG ACAAGCCCTGTCTCGAGGGTTTGTGGGTGAAAACCCAGGTCCT TTGCTGGCTGCGGGGTTGTGTGTGACAGATGGCTACAGGTGGAG GGCAAGAAAATAACAATGTGTGCAACAATAAATATTGACGGTTTG CATTAGTACGGGTGTGACAGATCACAATAATATCTTC	SEQ ID NO. 127
KCP_rs18 3398	TACTTTTCAGCCTGAGGTCTCCTCCTCACCCTAACACCCCTTCC CTCCAATCAAACCTGATCCATTGTACCTACAAAAGCCCGTCCCA CCTCCTAGCCTTTGTTTCACTGGGTTCTCTGCTGGATCACCAT CCCTCCACATTTCCAGGTGTCCCTCAAGACTACTCAGCAGCAGC TATCCATACAAGTTCTCAACCCTGGCTTTCTTGCCCTCAAGTA ACCAAGTTCACTCCTCCCAGTCATATAGCCCTCTATTTACATTC TTTTCTGGAAGCTATCATTTTTACGTGCCATTGTAGTGAGTGT CCTCGCTAAGACGATATTTTCTTTGAGGGCAGTAACCTTTCTTA TATGTCCTGTATCCCATGAACTTAGCAAAAAACAAGGGACAGA ACAGGTGCAAAGTCTACGTGGTTAGTGAATTTAACAGATCTTCC TAACGTGTAAACGTCTGTTGTCCAGGTGAATGGAAGAAGTGAGCT GAGATAGAGGGGACAGACAGAGTCAGTGTCCAGTGCTGACCTCT GAAATGGAAAAACATGGCCAGTCCTTAGGAGGCTGCAGAGGCCA AGACCCAGTGAGGTTTGGGGGTTCCACAGCAGAGGAGGAGCTG TGGACCACAGCAGGACCCCGATGCCATCAGCAGGGGAGGAAGTA ATCAGAGAGGTGGAGGAAGGAAGCCAAGGGAAGTCAAGTAAACA CCAAATATTCCCTCCCGGTCCAATGCTGTGACCTGCATAAGCCA CCACTCCCCAGTCTAGACTCTACCCATGGAAGAAGGAAGA TAGAACTCTGGATTTGAATATAATTCTAAATAACCAAAATTTAT CTGAAAATGACTAGGCTGAGTTTTCTGCTTCAACCAGAAATGGA GCTTGGAGTCAGAAATTATGTGAAATTATAGAAGAGAAAAGTCAC CATCTTCCATCTCTGAGTCGTATGATCATTTTAGACATAAAAT GTGCACTTACGATGTACCAAGTGCTTAATATA [C/T] GTGATCT CATTTCAACCGGGAAGTGTATAATTCAATTGCTTTAAGTACAA AATTCTGCAACTGAAGAAGGTGCTGTTAATAATTGCATTGGGAC GCAGGCCTGAGCAGGCCATGATTTGTGGCTGTCTACATCTGAC CCTCACAGTATCCATGGGAGAAGGCAGCATGTTTATGCCCCCTG	SEQ ID NO. 128

	ACAGCTGGGGAAACCAACACTTAAAGTGATTAAGTCACAAGTCC AAAATAAATGACAGAGCTGCAGTTCAAGCCCAGGTGGTCATTTA CCAAAGGCCATGCTCTTTTCACTTTGCATGGGACTGTGACCGCT GGCTCTACCCAGCTTCCCAGTGGGACCCCTTCCCCGCCCACTGTT TCTCTTCTCTGGCCAACGGAAACACAATGAGACCACATATGTAA CATTACATTTTTTTCATAGCCACATTGAAAAAGAAAGGAACCAG GTAAATCCATTTTAATATGATATTTTATTTAACCCAATACAGT TGAGGCTTGAACAACACAGGTTTGAAGTGTGTGGGTCCGCTTAC ACATGGCTTTTGTTCAGTCTCTGCCACCCCTGAGACAGCAGGGC CAGCCCTCCTCTTCCGCCTCCTCCTCAGCCCACTTACATGAA AACAAAGAGGATGATGATCTTTTTGATGATCCACTTTCACTTAA TAAATAGCAAATATATGTTCTCTTCTTTATGATTTCTCGTAATA ACATTTTCTTTTCTCTAGCCTCATTTACTGTAAGAATACAGCAT ATTCCCAGCTACTCAGGAAGCTGAGGCAGGAGAATCACTTGAAC CTGGGAGGCCGAGTTTGCAGTGAGCCAAAATCGCACCATTGCAC TCCAGCCTGGGCAACAAGAGCGAAACTCCAACCAAAAAAAAAA AAAATAAAAAGAATACAGCGTATAATGCATGTAACATATAAAAT ATGTGTTAATCAACTGTCTATGTTATGGGTAAGTCTTCCAGTCA ACAGCAGGCTATTAGGAGTTAAGTT	
rs103285 6	CGCTCAGCAGCCATTAAAAGGATATCATCCAGTCACTTAGTTTC TCAATTTAACTTTAAAGGAAAGTTGCCTTATTAGAGAAGTGGCC TCTATTTCAATGTAATGGTCTTTGTACATCTTCCAATGTGCTG GCTTAGTGCTGAAGGATGGGGAAAGGCAGTTTTTCACATATTGCA GCCACCATAACCACAAAGAAAACAGGTGCACCTCCAGGCATCAT TTAGCGGGGTACCA [C/G] ATTCCTGGTTCCAGTTTCCTTTTTTA GAAAATCTGAAAGTAACCTTTGGGGCATATCTTTTAAGGAGTACT CCAACACGACTAGTGGACAGACCCCTAAATTAATTGCCAATCAGC TCTGCCTTCTGGTATTTACACCTTTATGTAATAACCTCCACTTG AAGGTAGATGAGATCTGTGACTTGCTTCTAACCAGTGGAATATG GCGGAGGTGGTGGGACGTTACTCCTGTGATTACATTACATCATG TGGCTCCTTTTATGATGGAAGATTCTAGCTAGAGATTCTCCTTGC TGACTTGACAAAGTATGTAACCATGATGAAGACTTCCACGTGGC AAGGAGCTGTGGGAAGCCCAGGTGCTGAGACTGGCATCCAGCAA ACCCCAGCAAGAAACAGACGTCCTTGGTTCTACACATACAGGA AATGAATTCTGCCAACATCCTGAGTAAGGCTGGAACCTAGATTCT CCCCAAGTTGAGCCTGACAAGTAAATACAGACCAGCCAACACC TTGATTGCAGTCTTGTGAGACCTGGGGAAAAGGACACAGCTGAA CCGTGTCCATTCTTCTGACCCACAGAACTGTACATCATAAAG GTATGTTAGTTGTTACACAGTTTAGAAAATATTACAGCTGCTC AAGAAGGTTAGCTAGCTCCAGATTTCAATCCATTACAGGAAAG CAAGCTTTATTCCTAGAAGAATAATTCATGCTTTGCAAAAAGAG GAAAACGTCCTGCAGTTTGTAGAAGGTCTTTCTTTCTCAACACA CCCAAATTTCTTTAAATCCTCAAGAAGTGCAATTTGTTTTCATG GTTGACTCGAAGAAGTGAGTATAATTAACCTACAAAAGGTGGGA GGAAGGGACAAATTAAATTTTGGT	SEQ ID NO. 129
KCP_rs88 8934	CACTCAAAGGGCTGGGGACCCTTGTCCTCCCATGTGCATCCAT CTCTCCTATCTCTGAGTCCCCAGTGAAGTCTGCCTCCCTAGAG AAACAGTGCTAGAAGTCAGTGGCAAGAGCAGCAGGAGGACTTGG AGCTACATGCAGAGTGTGAGCTCCGGAGTCAGACCAGCTGAGTT CAAGGCCAGCTCCACCATCTATTCACTGTGACTTCAGGAAGGTT GCTTAACCTCTCTGTGCCTTAGCTGCCTCATCTATAAAACAGGA AACAATGAGAGTCTTTCCTTATGGGGCTATTGAAATGATTAAGT GAGATCAGGCATGTGATGGCACACAGTAAGAAGTCCATAAACAG AGGTCAACCACTGCTAATGCAATTATTCTATCACCTCAGGAGACT AAAGCAGGGGAGGAAACACCATTGACTCCTGGACATTTACCCAA GGAGATTATGGATCCATGTTTTGCACACACTTTAGAAAGACAAG	SEQ ID NO. 130

	GAATTCTAACCACAGC [A/G] TCTGTCTCCACTGCCCCGTCAT TTCAGTCTCACCCTGCCACCCTCAACCTCACCCTGTGGCCCGG AAATGCGGTTGCCAGGGCCACTCTCACCACCTCAGCCCTGC TCTGCTCAAGTCTCACTTCCACTCCTTCCAGCTCCCATCCCTTT CTACCCAGCTCCACCCTGATTTCTCCACCATGACCTTTACCCTC CTAGTCTGATCTAGACCCCTGATCTTGCCGAGTATCTAGGACTT TGGTGCCCTTTGACCCTCAGCAGCAGAGGTAGAGAGGGATCTCGG TGAAGTCTGGGATGTTATAGTGACTTGTTTATCTAAGTGCCCTG AGACTGTGAGTTCCCTAATGCAGGGAGCATCAACCTCTGCAGAG AGCCCCAGAGCCCTGCTCAGGTGTGATGAACAGGAGGCACAC TTGATGCCCTCACAAAGTTGTGAGTGAATGAATGAATGAGTGAA TGAATGATTGAATGAAGATTAGTGATTATGTTAATGA	
rs905823	GGTGGGGGGGAGAGGGGAGGGGAGGAGAGGGGAGGGGAGTGGG GGAGAAGGGGAGAAAAGCGCAGCTGGCTTCCCTCACTCTCCTTTT CTTCCTCACCATCCTTACCCTGGGCCAGGGCAGGAGGAGGATTG GCAGAGTAGAGGCAGGGTCTTCTGTCTTAGCTGGGCCGTGTGGT GACTTTCTGTTGGCCAACATGGGCTGACTGGAATGTTCTCCAGC ATGGCACATGGTCATCCAGATGCAGGCTCTTCCCTGGGGCATA TAGCAGAGAGGGCTCTCTTCCAGTCTATTGCAGATGGATGCCCT CGTGAGCTGAGTTTGTATGAACATCCCATGTCCCCAGCCACCCC ATTGAGAGCCTCTTTCTACTCTGGTCTCTGGTCCCAGCAGCAG CCCTCTGGGTACTGAGGGGAGGGCATCTCACCAGCCCTTAA ACCTGCTCACCTTCTTCCAGAGCCACGTGGCCGAGGAAAGTCA CAAACCTTGTGCTCCCACAGGGCACACGTGTGCACACGTGTGC AGCTACCTTCTCTCTAGTTGGTACCTGAGGCTGCCTCCTGGATT TTCCAGTCTCTGTGTCCAGACA [A/C] CCCCAGCCCAAGA ATACAAGAGCTCTGTTCACCAAGCATCGGGCTGTGGCTGCACTA CACGTCTGCAGCTCAGGACCCCTGGCTGCGGCGTAAGCTACCAG CATCCCCCTTCTCATGGGCACCCCTCATCTCCGGCTCCCCATCGCT GGGCTGTGACCTGCGGGGGCGCCCCCTCTATGGAAGGGAAGGAGA AAAATTCACAGTGCTATCTACTCCTCTGAATGCACTCCACCAA TTTCCTTGGAAATTTCTAGCTTTCACTGACATATCTGGGATGGG GCGGTGGTCAAAAATCA	SEQ ID NO. 131
rs883849	CTGGCTGGGGGACCATGGGCTCAGGGCTGCCACCCCTGGCTCTG TGCCCTTACCTGTGTAAACGAATGGGGCACTCACAGCCCTCTCA AGTGGTCCCTGGGGATGAAGTGAGAAGGTGACATATACAAGTGAG TTATACACGTTCTGTCTGTCACTCACCAGTGCTCACTGGGTG GGTCACTGAACCTCCCTCAGCGTTTCTTCTCCATCTGTAAACC ACCAGTGCAAACCTTTCCAGATAGTGCTGACCCGAAGCAGGAA CCAGTGCCCCCTCTGCCCTCAGTAAGTCTGCCAGCAG [A/G] GGA AGCCCATAGAGGGTCTTGGGAAATGAAGCCAACAGAGTCAAGAG GGTCAGATGATGAGGGACTTCAAGTGCCACCTTCATCCCATTCT TTCTGCAAATATTACACACACCTACGTGACCTCAGGCTCTGT GTCAGGTCTTGGGGATGTAATGGTGTCCATGAAGAAACAAGGTC CCTGCCCTCATAGAGTGGCCTGACATATGCCCCGAGGCAGTCAGC AGCCGAGTGCGGGAGACTCTTGAGCAGAGATTGAGTGTGTTGAT ATCTGTAGGCATCAGCCTGGCTTTGCTGAGTGAGCTATATCAGA GTGGAGGAAGCCAGAGGCAAGTCCAGACTCCACTGATCCTGGA TTGAGGGGAGAAGGGGCTTGGCGGAAGAGCAGCCTGAGCACCTG CATCTCACTCCAACCTGGTGCTGATTGTTCCCAT	SEQ ID NO. 132
rs213504 6	TCCACAGGTTTGTATTATAAATGTGTGATTGAATTGGAATTTCT GTTGAAATTTGTATCCCTTCTAGACAAAGAGGTAAATGAA ACATGTCAATGGATATCTAAATATCATTACTCACTGGCTTTATT TGCAAATGGCTTTCCATTGACAACAGTTACATTTTGTTCAAAGC AACAAATGATTGGCGCTGACAATCCACAGGAACATGGTGCAGTC ATTAATGAATGTGCTCATTATTCCTCCCTGCCGGGAGGCATCGA CTCCCGTTCTCCAGCCTGTTTTAAGCAGACAGACCTACATCTGC	SEQ ID NO. 133

	ACCTGTCAGCTTGGAAACCCTAGTAGGGGAGGGGGATGCTGATGT GATGGAGAATGAAGAATGGGCCCTGCAGGCTGACATTTTGGGAG AGTAGGTTCTGAAATTTATCCCAAAGGACATGGAATCCTGGAAG CAGGGTTCAAGATCCTCCCAAATTTGATCTCCAGGATGCTTGG AATGATTGTTT [C/T] GAGGGTTTTGTAAATGCCAGGGGAAAA CCAGGAAGCTTCTCTCCAGTTGTCTTGCCTCCTTCTCTCCAGT CTCCATGGAGCTGACTTTGAGAATTAACCTCCTGAGGGACAGAGA CCCTGGGATGGAGAGCCAGCCCTGCTGGATTCCACAAGGTGCTG CTTAAAGCACAAACACCTCTTCCCAATGACAGGTTCTGAAAGAAG GCCTTGTAGCTAGATGCACAGAGGGTTTTGTGTTTTTTTTTTT TTTTAACCTTTTCAGCATCTGTCTAAAATTGCTCTGGGCTGGGTA CAGTGGCTCCACCTGTAATCCCAACACTTTGAGAGCTGAGGCA GGAGGATCGCTTGAAGCCAGGCGTTCTAGACCAGCCTGGGCAAT ATAGTGAGATCTCTATGTCTAG	
rs50057	GGATCTGTGCCTGAAGCTGAGCTGCTGCAATGAACTGACATTT CTGCCTTGCAGCCTGGCCATGGGCTTAGCTGGACTAAAATGCTG CTGCAGTGGTGAGGGCAGTGAGAGTCCCTAATGTACATGGCCT TGCTCCTTGTCTGACACATCTTTTAGGGCTGCTGCTTTCTCTA GTGCTGGAATCTAGATAATTCTTTCCAGCCGTTTGTCTTCTTC AATCTTGGAAAATATCTGGATGAATGTAACACTGTACACAC [A /G] AACAGAATTATGACTTACGTCACATTCTATGTCGTGATTTT GTGGACTTTTAATAATTGCATTACATTTGTGACCATTAATTTCC ACCATCGCCCTGCTCCTGAGAATCTGTAAGGGACATTTGACACT CCTCTCCCCACCCACCTCAACATTTGTGCTGACCTGAAGGTCAC ATTAAAAA	SEQ ID NO. 134
KCP_4976	GCAACTTTCCCTGGCCTGCAGGAACCTCAGGGACTCAGGGGACTA ATAACAACAGTGATGAGCTTCCGGGCACACTGCTTCCAGTG CAGCCCCGTACTTAGGGCTTTGTATGTATTAATTCATTTACTC CAATTTCCACAATAACCCTATAGGGTAGGGTTTTATTATTGATT ACCTTTTTACAGAAGAGGAGAGTAAGGCAAAGAGAGATAGAGTA GTTTTCCCAAGGTCAAAGAGCACATAAATGATAAAGGATGGATT TGAATGTAGGCAGAATGACCCTCAATACAGACTGTTCCCTACAGT CCACGTCCTCAGCCACTAGACCATACGGCCACTGGGATGATAGA CAGACCACTGCAGCCATGGATAAGGCAAAACAGGGCTGGCTGT GTTGATCTGTGTCTCTCAGAGCTCCATTCTTCTCAAGGGGGCA CCTTGCAAAAAAAACAAAAAATGGGGCAGGGTAGGGAACTGA AGGCAGGAGCTCTTCA [C/T] AGAGCATAGCCACATCCTCCAGG CAGACAAGAGGACGCAGGAGGCACCATTCTGTGAGAGTATCACA GTCTGACCCAAAGACACAGCTTCACACTGTCTGATGGCTTGATG GTTAATGTCACTCTGCCTTTTCCCCCTTCTCAGGACTTTGTAACC GCTCTGTGCGATTTTATTGAGAGGAACTGTCCACGAGAACTAAG GTGGACATTTAATTTGTATGACATCAACAAGGACGGATACATAA ACAAAGAGGTAAGTGAGCTGGGGCCAGGGGTGTGAGAGGGCTCC AGTGAAGGTAACCTAACCAACAGAAAAACAGCCCCAGGCATGAGG ATAGCACTGTCTGAATGAGGCAGGCTCTGCTTTGGGGCTAACAG AGCTGGTCCCTGGCAAAATAAAGAAGGCCTCCCTCATTGCCCTA CCCTGCCCTGTTCCCAAGCGCCAGAAAGGATTAAACAGATTCA TTCTCACTGGGTACCTAGATTTCAGTAGATATTACAC	SEQ ID NO. 135
KCP_5077	TAGGGCTTTGTATGTATTAATTCATTTACTCCAATTCCCACAAT AACCCTATAGGGTAGGGTTTTATTATTGATTACCTTTTACAGA AGAGGAGAGTAAGGCAAAGAGAGATAGAGTAGTTTTCCCAAGGT CAAAGAGCACATAAATGATAAAGGATGGATTGAATGTAGGCAG AATGACCCCTCAATACAGACTGTTCTACAGTCCACGTCCTCAGC CACTAGACCATAACGGCCACTGGGATGATAGACAGACCCTGCAG CCATGGATAAGGCAAAACAGGGCTGGCTGTGTTGATCTGTGTC TCTCAGAGCTCCATTCTTCTCAAGGGGGCACCTTGCAAAAAAA AACAAAAAATGGGGCAGGGTAGGGAAGTGAAGGCAGGAGCTCT	SEQ ID NO. 136

	TCACAGAGCATAGCCACATCCTCCAGGCAGACAAGAGGACGCAG GAGGCACCATTCTGTGAGAGTATCACAGTCTGACCCAAAGACAC AGCTTCACACTGTCTG [A/T] TGGCTTGATGGTTAATGTCACTC TGCCTTTTCCCCTTCTCAGGACTTTGTAACCGCTCTGTGATT TATTGAGAGGAAGTGTCCACGAGAACTAAGGTGGACATTTAAT TTGTATGACATCAACAAGGACGGATACATAAAACAAAGAGGTAAG TGAGCTGGGGCCAGGGGTGTGAGAGGGCTCCAGTGAAGGTAAGT AACCAACAGAAAACAGCCCCAGGCATGAGGATAGCACTGTCTG AATGAGGCAGGCTCTGCTTTGGGGCTAACAGAGCTGGTCCCCTGG CAAAATAAAGAAGGCCTCCCTCATTGCCCTACCCTGCCCTGTTT CCAAGCGCCCAGAAAGGATTAAACAGATTCACTCTCACTGGGTC ACCTAGATTCACTAGATATTACACAGTGGATAAAAATGACTTGT TTCAGTGTGAAGAGTTACTCTTCCCTAGGGAACCTGCATTTGGG AAGGTTAGGAGCCACAAGCTCAAAGCTAAAAGTTGAAA	
KCP_2410 99	TTGAAAGAGAGCGCTTTGGGGGGTTTTCTTACTGTATGTCTCTA TTGCATGTTCTGTATTTTACATTTTCTATTATTTCTTCTCTGA GGTATAGTATTGAATGTAGAAAAATCCTCAAATGTTCCGGTATTA AGCAATACACTTCTAATTCATGGTTTCAGAGAAGAAAATATCTCG AATAAAAAATAAAAAATAAAAAATGACTTATCAAAATTTGTAGGAT CTAAAGCAGTATTCCAGGAATGCAAGGTTGGTTTAAACATTCAAT AATTGGTCAGTGAATTAATCACATTAATAGAATAAAAAGAGAA AAAATATAATCATTTTCAGTGGATGTAATTGTTTCAGAGCTTCTTA AAAGAAGCAACTCACTATTTTACTAGATGATTTGTTTCTTCTGA ATTCTCTTTAAGGCTACAGGTGGTGCTTCTTACTTTGAACTGA TCACTTTCTAGGTCCCCACCCTTACTTCTTGTTTTTCATACCCT TGTAGAGTTTCTCCA [C/T] ATAGGAAACCCATGCTTGACATT TGCTCACCAGAGTTACAGAGCTCTCAGGGAGGAGACTCAGAGTT CTAACCTCTTGCCCTCCTTTTTTCCCAGGACGACAACATCATG AGGTCTCTCCAGCTGTTTCAAATGTCATGTAAGTGGTGACACT CAGCCATTCACTCTCAGAGACATTGTACTAAACAACCACCTTA ACACCCTGATCTGCCCTTGTCTGATTTTACACACCAACTCTTG GGACAGAAACACCTTTTACACTTTGGAAGAATTCTCTGCTGAAG ACTTTCTATGGAACCCAGCATCATGTGGCTCAGTCTCTGATTGC CAACTCTTCTCTTTCTTCTTCTTCTGAGAGAGACAAGATGAAAT TGAGTTTGTGTTTGGGAAGCATGCTCATCTCCTCACACTGCTGCCC TATGGAAGGTCCCTCTGCTTAAGCTTAAACAGTAGTGCAAAAA TATGCTGCTTACGTGCCCCCAGCCCACTGCCTCCAAG	SEQ ID NO. 137
rs189530 1	TTTTTTTTTCCCCAATCATGCTGTATTCTTAGCGTAATTTTAAAA TACTTAAACAAGATCATGAGAAAATAAATGCCAGATTCTAGC ACCAAAATTGAGAGGGGGGGCTATGAGAATGAGGGGGCGGGGAG AAGCCTTCCTGAGAGTTTCTAAGAGGCATGGAGGCAGTGGGGAT AGTGATTAGCTCTGGGGGAAGAAGAGGCTACTGGCTGGAAAAGG GCATGAGGTAGGGTTGGTAATCACCTA [C/T] TGTGTTTATCTGA GTGCTGGTCACACAGATGTGTTCACTTTAGGAAAATGTATTGAG ATTACACTTGTGATTTCTGCATTTTACATACGCACATTAACCTc agtcatatgctgataaatgtttaacaatgggtttgctggagaaa aaaggggtcccccgatttgtaatgtctgcccatttccgtgggtgt aaataactcccttcacaactgatttcaagcttcccatgcactgta actgaagacagagttgggaagatacgtgcagtagcacacaatta aatcatatttccaccatatacacacaatataggtgtaataaacacc cagagcatagaaaa	SEQ ID NO. 138
rs142275 2	GGTTGGCAGCTTTTAATACTTAGAAATGGCTGGGGGTGGGGGG GAGGAAGTACTGAATCATTTACTCATTGAGCAATAAACCAGGGA ATACCTACTCTACACTGGTCACTGATGGAGATA [C/T] AGACTT GGGCAAAGCCGCGTCATCTGGTTGTGTTCAAGCTGAACATTCC CTTGACCCAGTCACTGATGGAGATATAGACAGGCAAAAGCCACG TCATCTGGCTGTGTTCAAGCTGAACAGTCCCTTGACCCAGGGCC	SEQ ID NO. 139

	CATGACAGGGCAGAGGGCAtattattatccccattttacaaagg aaagagctgtcagacacagTGTACACAGGAAGGTAGACGATAA TGTCAATATCCCTCATCTTAGTATAAAGTTGTCTTAAAACTC TCCATTATTTATTAATTTATTGACTCACTTATTCATGTTTTCTG CACAGTGATACTTATCCTGCACGAGACTCTCACACCAGTGCTTT GGGTGTAAGAACACCCCAAGGATTGTGTTCCCTTTTCTCGAAGA GTCTGTGGTCTAAGGGGATTCAATGGGGTCCACTTTCCAAACCA AGACAGCAAAGGAACACTAGGAGAGAAGTATTCTGTGCAGAGAT TCAGTTAT	
rs142275 4	GGATTAacaggcatgcaccaccgcacctgggctaattttgtatt tttagtagagatgggtgtttcaccatgttggccag [A/G] atggt catgatctcttgaccttgggttctaccacctcagcctcccaaa gtgctgagattacaggtgtgagccgctgcaccgGCAACTGGT TTCCTTTTACTGCCACTTTCACTAACCGTGGTATTTCTCCATGG GCAGCATTCTTGGCATTGTTGGGTGTGTAGGACTGTCCCTCACATA GTGACCTCTTACTCATGAATTGCCAGTGTACATTGAGATTCTT ATGGCAACCAGAAGCTCCCTGCTCCCAGCATTTCTGGACTCAG CCTGGGCTGGGGAGGTTAGCTCAGACCAAATATCTCCTTTCTGC CAGTTGCTCTGCTAGGCCCAGGTCATGCTGAGCAGAGCAAGATG TAGCTGAAAACCAAATAAGTCACGTGTTCCAGCTTGCTGGGGTT TTGTGAAGAAAGCAGCCACCCCTCCAGTCATATAGTTTGCAGGT TGGGATTGTCATT	SEQ ID NO. 140
rs205560 6	tggctattgtcttaagctactattaccttcttgcctgtcaagtt gcgcatcttacttttcaaggcttgctacgtgcctggaatttctag attttcctttatttccatgcttggggagaggagtgcctggcagg ctcctaagaggggtctgtgctccatctcGCCCCCTATCTTGAAC TATCGGTTGGGTGCTCTAGAATCTGTATGGGGTGGAAGTGTTCA TTCATTTTCTGTACAAAAGCAATCAATGCTTATTGTGGAAAACC CAAATAAGAGAGTTGCTCTAAACAACACCCTCCCCAGTCCCAAT ACCTTGCTCCAGAAGAAACCACTGTTTGGTGAGTATATTAGT [C/ T] AATGCTCTGCAGACCAGATCGGATGACCAAGTTTTCCATAAAT GGATGGCCATCCACTTCCCTTCAAGGGCGAGGGTAGTTTGTCT GATCCATCTCCCTGTTTACAGCTCAGGGAGGGAGGAAGACCCA GGAAGGAGAGCTGCCACAGTTACTAGTGCCCGAGCTGGGATTTA AAGTCCGCCGTGACTGAAGCTTGGCTCCACATGCCAGTCTGCAA GGCCCTGAGTGCCCTCAGCAGTAATTCCAAGCAAAGCAGGGAAG CAGCGGGCCAGGTGCTGAAGTGAAGTCTGCTCAGGGCTCCTG	SEQ ID NO. 141
rs933656	CTGCATATGTTCCCCAGGTATTTGCCCCCGAAGCACAGTCATC TCACTGCTTGCATAGTGGAATGCTAATCAGCAGAAGACCCTTC TATGGGAGGCAGCTTGGAACCTGGAGGAAGCCCTGGCTGAGGA GGCTAGTGGTCAGGGAGCCTATCCTGGCCAGGTCATTTTCCCC ACTGGGGCCTCGGTTTCTTCTTTGTAAAGGGAGAACTTACATT AGGCATTTCTCAGGTTCCATTTGGTTCTCAAATCTAATATTT TTATGGTTGATGCTCTCACCAGAGCTGCTGCTATGATCTCAGAG ACGTGAGGCTCAGATCTAATTAGAAGCAACCGGAAGAGAGCAGT TGGGATTTTTTCAactcaggaatcagtcctccctgctgggttcaaa ttcaggctctgccacttacagctgtatgacTAAGCCTTGTTTTTC CTCAACTATAAAACAG [A/G] GATAGTAGTAGTTACCATCTTAA AATAGCTGTTGTGTTGTGTTGGATTTCAAGGATCATGCAAGTCAA GCATTTAGCACAGTCTCTGCTACATAAGTGGTCAGCAAATTTGA GGTACTATTC	SEQ ID NO. 142
rs233909 1	AGACCCTTCTATGGGAGGCAGCTTGGAACCTGGAGGAAGCCCT GGCTGAGGAGGCTAGTGGTCAGGGAGCCTATCCTGGCCAGGTCA CTTTTCCCCACTGGGGCCTCGGTTTCTTCTTTGTAAAGGGAGAA ACTTACATTAGGCATTTCTCAGGTTCCATTTGGTTCTCAAATT CTAATATTTTTATGGTTGATGCTCTCACCAGAGCTGCTGCTATG	SEQ ID NO. 143



	<p>ATCTCAGAGACGTGAGGCTCAGATCTAATTAGAAGCAACCGGAA  GAGAGCAGTTGGGATTTTCAactcaggaatcagtcctccctgct  gggttcaaattcaggctctgccacttactagctgtatgactAAG  CCTTGTTTTCTCAACTATAAAACAGAGATAGTAGTTACCA  TCTTAAAATAGCTGTTGTGTGTGGATTTCAGGATCATGCA  AGTCAAGCATTTAGCACAGTCTCTGCTACATAAGTGGTCAGCAA  ATTT [G/T] AGGTACTATTCAATTTATGGCTCTATTGTTTGGGG  CTTCCAAATGTCCAGAGTAAGGCCATTTTCGAAGTAGGCAGTAC  ATCTGAGAGCCTTAACAGCTCATTCTGGAAACCTTATCCAGCC  CTATCCAGATAACTAGGACCAAAAACCCAGCACACAGATGCTC  GTCCCTTGCTTCAACCCTCACTGACCTCTACTCTGTGGCTGTGTC  CTGAAAACATCAAAGCCTGCTCAATTAAAATCCTGAATGCCTTG  ATAATACAATTTAGAAACATACATAGTTTTTAAATAGGGCAAAA  ACTCTGCATGATTAGTGCTGCAAGAAGATATCCAGCCCAACCTG  GGTGTTTCAAGGAGCGCTCTCTAAAGGCAACAGAAATCTAAAGTA  ATTTAAGAGCCATGCCACTGAATAAAAATATTAGGTTTCATTTT  CTGTCCTTCTCTCTGTTTGGGATCTTTGTGTCTTTAATTAAA  AGTAGGAGAGCCCTGCTTTT</p>	
rs186233 1	<p>ACTACTTCTAAAGCCTCTTAGACCCTGGTAATCTTCCTCCTAAC  ACCATCGGGTGACTGCAAAGCACTGCAGGCCAGACTTCAGTTCT  GCTGTGTAATTTGCAAGCTGGGTGACCTTCCTTATCTATAGAAT  GGGCTCT [C/T] CTGCATGGCTGGCATGAGGAATAAACAAAATG  GTTGTGTCCAGTGCTGGGGCATAGCACAGCTCAAAAAACCTTAG  TTCATCCTCCTGAGGGATCAAGAAGATACTTGGAAAACAAATGTC  CAAGGGCGTAATCTTGAAGGGGCTTGTGCCAGGCATATATGGAG  AGAAGGGTTTTGTGGGATGTCAGACTTAATAGTGCCCTTTACTC  CCCACCCCGTCTCTCTGTTTCATAGACAGGAAATCTGTGGCCTA  TTCTGGGACCTCAAAGTGCCACAGGGTTAAAGATACCAAGTCAG  AAATCTAAGGTTCTAAATGGACTTTAGACCATTTTTCATTTGGG  AAGGAAGAATCTTTAAGGGGTTGTGCTGGCGCTGTCTCTGTAT  GCATGTGCAGAATGTGCTTCCAGATGGGGTAATGGTCTGAGTTT  GAGGACAGAAGTCCACTCCACTGCATTCT</p>	SEQ ID NO. 144
rs233913 9	<p>GGGTGTGGCCTTTGGACAGCACCTTAGCAGGAATGTGGTGGAGA  GCAGCCCCATTCACTCCAGAGGAGAGCCTCAAACCTCTCAGGCA  GATCTAGCCTAGGTAGAATCTTGGCCTGGCCCCCTCCGGGATGAC  AGGTGCCATTGCCCAAGAATGGGGAAAAGGCTGAAGTGCTCCAG  CCAAAGACCCCAATTTATCTTCAGGACAATTTTCACTGGAAACC  TTGCCTCACTGCCCCACTTTTTTCAAGTAATTAGAATGCTA  ATCTATAAGAAAGATGACTattataaaataaattaataaGATA  ATACATTTTGGCTTACAATTTTGAATAATATAGCCATCCCATCT  TAAAGTAAAAATTCATATATTTTAAATAAGCCTGAGACATGTTT  TCCAATGAACCACAGATGGTTTCAATTTTATTATCTATAAAGAG  ACATTATGGGCAAGTGTTTTTTAAATGGTAAAACAGAACCTTA  GAGCAGCTCTCTTTTG [A/G] AGATCTCTAAGCACTTTCTAAGC  ATCAGGACCCCTTCTGTCTATCAGAGACTGAAATGAGGAGAT  GGTCTCTGTCAACCCCTCACTCACCAGTGAGCCCCAGACCTTCA  TCCCTGATCAGATGGAAGCAGTGTGGCATGATTACAGTTCATAT  TTCAACTCTGCCACTCAATGACTAATAGCCAAGCACTAATAATG  CAGAAAATGTAAATTTAAAAAATAATCTTCTGAGATTGGTTAT  GAAATGCACTCAACACAGCACCATCCACAGAGAGGTTCTTTTAA  ATTGCTCTTTTCTTCTCTCGACACCCAGAATCAAAAGCATG  CCTGAAAGCGTCACACATATATGTCTGTGACCATAACATGGCAT  TGCACATGCAAGGAAATAAATAGGTGTTACCCATGTGACAAAG  GTCCATGAGCTCTGTCCGCAAAAAGCTGTTGAGTTTAAAGAACA  AATAATTCTGAAAAATCTTCCAG</p>	SEQ ID NO. 145
rs872435	<p>CTGCCATTCTGATCACTGCAAGACCCCAACCCCAATACTCCCA  ATTGTACCACCCCACTCACCAGTGTCTCAGAAATGCCTC</p>	SEQ ID NO. 146

	CTCCAGAAGGAAGGCATCCTGTCTAACCCTGCTTCTAGCCAA GCTGTCTTTCTTCAGAAGGTAGAAAAA [G/T] ATTGTTAGTCAT TGTTTAATCTTTATTGAGTATATACCGCCACACCAATTGCACTG CCATTCAATTATCTCATTAAATCTGACAAGAGCCTTGTAAGTA GGGATTATTTCCACCATTTCAGATGTTGAAACTGAAATTGAT AAACACGACATGTTGCCATGGCTACATGAAGATCTCCAAGCCGG AGGATCTCCACCCTCACCTGCCTAGCTTCCCAGACCTCTCTGCA GAAAAGGGACTGACCCCAAGACAGCCCTGGCCTCTGGGCTCCA CCCCCTCCACATCCATCCCAGGGCCGCTGAGGACTGAAGAGTTC TCCACGTTTGCCCTTTAAAGTGAAGTAAATAATCTTTATGAA TTTCTTCATATACAAAATTTGTACTTACTCATTGCAGCAAAATTT AGAAAATACACATAAGCAAAAAGAACGTAACAGCCATCCATAA CCCTAACTCTCAGAGATCACCCTATTAAATGTTTATTATCTA AGAGAGAGATGATATAGACAAAGATGAGACAGATTGACACAGAC AAGATGGGTACATGATAGATATTTTCTGTGTTATAACCCCTTGCT TTTTCTTGCACTTCTAGAATTTTCTGAGAACTAATCTGAAAT CTGCACAGGGTCCCCACGTTTGGATCCTCTATCCCATTGCCTTC CA	
rs329468	AGCTGAGCCCCAGGGCTCCCCATGAGTGGGGAGGAAACTCATG AGTGCCTTCTATATGCCAGCGCTCTATCTGCAGGGGTTCTTTTG ATAGCAGCAGACTGAGAGATGATGTTACTGTCCCCTTTTCTCTG TTGTTGGCAACTGAGACTCAGAGGATGGAAGTGAAGTGTCTCAGG TCCACCACCTCTTCAGCTGTGGAGCTGCGACAGGAGCCTTTGTT TGACTTCAAAGCTCACCATCACTCCTCTCTCACTGATGCTCAAG TGGGCTATCACCTCGCCTTTCCTGAGCCTTCTTCGCTATCCTA AAACAGCGCCTCCCGaaatcaccactaaagaacttattcatgta accaaaccaccagcgggtcccctaaaaaacctatggaaataaaAAT TAAAAATAAAAAACAGTgcctcccatgacccatgtctctccagtc ccataactctgctctatttccattcacagctccatccccacott tatgtcttttgttcaactgctttatccccagtgcttagaagagtg cttggcaccttagtagacactcagtaagtatttgcgaatgagtt aatAAGGTTGTGAAAAGAACGTTAGATTACTGGAAGGATTTCATC TGAGTTTAATTCTGCTATGCTGGGAATCCAGTGTGCGGCCTTGG ATGA [A/G] GCCAGTTCCCTCCCTGGGCCCCAGTAGCCACATCT GTACATTTAGAGGGCAGGAGAAAAGCCACACGCTCTGTGACTTA TACAACCTGTTGCCAGAGTGGAGGCTGCTTTGATGCTCAGAAA AAAGAAACAAACATGGAAATGCTAAATGGGTGGCAGAGAGCTTG AGGGAGGAAGGAGATGGGGAGGGTACTCTTGAAACTGTTTGGTG TCTTCCCTCCTGCCCCCTCAGTACCAA	SEQ ID NO. 147
rs50364	GCCTGACAGATTTTACTGAAGGGTGACATTGGAATAAAAAAT GTGTTACCTATCTGGTTGAGTCTTCAGCTTCAGAAAGGTAATAG AGCAAAGGCAGATAAATCCAAACAGGGACTGAGCTGTTTTCATG CAGGCTGCCTTGGTAGCTCTCCAAAGCCTTCAAAATGATGAGA TTTTTTTTTAAATCCTTTTATCC [A/G] GTTGTCTCAAGGGA TTCCACCCCTGCATAGGAGAGCTCACCATTCTGGGATCTTCAG CTTCTATGCCTTTGCATATGCTCTTCCCTTGTTCCctcattctt caacactcaactgaattatcacctcccttgaagccttctctgac atcccTTCTAGTCCCATGCCACCCAGGAGGCACTAAGAGCTTCC TCCCTCAGCTCCCAGTTCTTAAACATGTCAACACTGTTTTGAA ATGATTTGCCAATGAAAAATCTAGACCAGCAACCAACAacatc cttcccaaagggtgtgttatatatggtacatgctctatgtgctaa acaccaaattcattgataacagctaagaaccaggaaacaaacca tcgttaattatggcatctcttgaaaaatctaagatctggactc actgggcttaaatgactgcatgataacaactggttgagtaacaa ctgtttccctttcatggagcagttactctccagttctcagttcc taccactctctatagttgtacactcatcatctgtcctcatctga attacctgccaatgactactggcatttgagtttctaatacatgG	SEQ ID NO. 148

	TCTATGTGTATGCCTCCTCACCAGTGTGAGAACTCATGTAAACA GGTATTATGTCTTTTCATCTCTCTCCTAA	
rs155158 3	ATAATGGTCACGTTGGAGCAATTGCCATTTCAAATCATTAGGAA CACTCAGGTCACCTTTGGCATGGAGCTATTTTGTAAAAGACGTAG AAGCCATTTATAAACTTTGGTTTGCTTTTAAAAAATTTATTTCA TTC TGAGGCTTATCCGTGTAAAATTACCAAATGATTGTGGTTA GACTCTACATTGTACAGTATTTAAATGTGCACAATATTCCACT TAGAAATAATGTCAGTACTAAAAGTAGTAGAGGGCTTTGATAGC AATATTAATACATCGTTAAGCCCTTCTCATTAAACAGTGTAAATA GTCTTGTTGAAGTTTGTTAGGCATTTTAACCACACTAATTAAA AATAGACCTACTGACTAGTCTGTTTTACTGTGCTTTATTTGTGTC TTGGATGTTTCATTAGATACTTTTGCTGTTGAGAAATCAAATCG TCTCTTATGGTTTTAATTACAAAATACATATTAGAGGGATACAG TTC TTAGGGCTGTGATTTTTAATTTGTGTAACCTTTTTTTTATTT TGGAAAGGAAATTTTCAATTTTTCTAGTAATTTTTTCATTTGTG AGTGTGTTTTCTAGATACAGAAAATGTACCTAGATAGATGATC ACATTTT TAGGATATTTTGCTTACGTGTTATTTTATATTTATATA CTATAATACCATTGTATAGTTTCAAGAACAGAAAATATCTTGATA AATCATCTGCTACTGTGAGGCAGTTAAAAAATTTGAGGCTCAC TGAAAATGTGTGACTTGCCCACTGTCTCATATTGCTAGTATTGG AGAGAAAAC TAGAATCTAGGCCTTTATTTTCCTGATGTAATGAT TTTAGCTAATTATTATTTATTTTCTTAAATCATTGCATTAATT [C/G] ATTTTTCACAAGTAGAGCCTATATCAGTGTTTGCaataat taaattttaagtatatatttctataattgtaataaaaatCCTGACA TTTGTACAGGATGGGGTTTTCTTTTCATCattttttataataa aaattaaGCAGTTATAAAAATAAATAGCCTAGTTTTTCAATTGG TATAAGCTGGCTTTATTTTATACTGCTAATAAAGGCACATTATG TTCAAGCA	SEQ ID NO. 149
rs145769 2	CttatatattcattaattaataatttatattCACACAATGATTG TAGAAATGTGAGTGTCTTCTTAGATTACCAAACATCTGTGAAATC GTGAAGGAGTATTGAAATTTAGTAATTTGGTTTGGATCTTTGAA GATATTCGTAGAAATTGTTTTCCAAAAGTTACAACCTGGTTTACA ATTTTTTTCTTAATTGCCATTAAACAAGTTTGGACCCTGAGATGA GAAATTATTACAAATTTCAATTAAATACTGGAATGCTTCATAT TTTCTGTACTTTAGGAcagggatccccaacccccagggcacagg ttggtactggtttgtgacctggttaggacctggactacatggcag gaggtgagcgggtgcgtgagaa [A/G] cattactgcctgagctcc acctcctgtcagcgacagcattagattctcataggaggacggac cttattgggaacacacacaagagatctaggttgaggactcctca tgagactctaattgcctatgatctgaggtgggacagttttatcct gaagctccccactatccgtccagngaaaaatttggtccctgtg gccaaaaacactggggacacctctgCTT	SEQ ID NO. 150
KCP_1035 5	AGGGCTGGGCGTCCCCGCCCCCACCCTGCAGCCCTCGCCCCG CCCCGCCCCCTCCGTAGTTGCCCCGCCCCGCCCCCTCCGCCGCC CCCTCCGCCGCTCCGACTCTCGCCCCGAGCGCTGGCAGCAGGCA GCAGGCAGCAGGCGGGCGCGCTGTGGCTCCGCGCCGCGCGGTCC GGGCTCTGTTCATTATGATTGGTACTCGGCCCTCCGAGACCCA GCCCCGAGCGCAGGGAGGGGAGCCGAGTGTGCGGCAGGAGGGGCG GGCGGACGGCGGCTCCCGCACCGCACGCGGCGCTGGCTCGGCAG CCTCGGCCGGGCGGCGCTCTGGCCCCGTGTCCAGTGCCAGGCA GGCTTCAGGGCACCGTCTCGGCCCTGGGCGAGGGAAACCGCG GCCGGGTCTCGCGCGGGGAAGCGGTTCCGAAGGCTCGCGGGGA GCGGCTAGCCCTGAGTCCCTGCATGTGCGGGGCTGAAGAAGGAA GCCAGAAGCCTCCTAGCCTCGCCTCCACGCTTGCTGAATACCAA GCTGCAGGCGAGCTGCCGGGCGCTTTTCTCTCTCCAATTCAGA GTAGACAAACCAGGGGATTCTTTCCAGGGTAGGGGAGGGGCC GGGCCCCGGGTCCCAACTCGCACTCAAGTCTTCGCTGCCATGGG	SEQ ID NO. 151

	<p>GGCCGTCATGGGCACCTTCTCATCTCTGCAAACCAAACAAAGGC  GACCCCTCGAAAGGTAAGCCACCTTCTTCTTTTGTTCCTGTC  TGGGCTTGGGGGTGCTAGGCGCCGAGGTGGGCTGTGCCACCTGC  CTCCCTTAGTCCGGACTCTCCTCTCCACGAGGAGCCCGACAGG  TGCTTGTATCCAAAGGAGAGAGAAATCGGCGGGAGGGCTGGTGT  GAACACCCAGAGGAGGGAGCCGGAGTGGACGTCTGCCCCAGCGG  CAACTGGACCCCTCTGSGGGCACCAGGTGTGSGGACTCTCCTCCT  GGGGAATCTCTGAGAGCCGAAGGAAGCGGCA [A/T] GTTCACA  GGTGGGGGTGACCGATTCTCTGGTGGAAGTGTGGTGAAGCTCT  TCCCATTCCCATGACAGCTGGCGTTTGAGCACTCAGTGAGGGTG  CTGCCACACTCCCACACTCCTCCTAGGCGGCTATGCCAGGTGCA  GACCTGCGAGTCCCTTCATCAGGAAGAGTGTCTGTCTGCACCC  CCAAAACCTCTGCAAGCCAAAAGGAATCAGCTGCTGCCAGGGGT  AAAACCTCCAGGCCTCATGTCTGGTGGCTCCGGGAGTCAGGAG  GAGCAACCGTGAAGGGCTGGCTGCGAGCTGAGCTTACATCAAGG  ATTAAAAAGCATAATATCGTGGAGTCTCTTCTGCCTGGACGCTG  TTCCTTCACCACCTGTCCCCAGCCGAGGCATGGCTGATCTCACC  ATCCGTGGGAGAGTCTCAAATGGGTCCAGGTGAAGTTGGAACC  AGTGTGTTGGGCCCTGGAGGACAATGCAGGTCTCCTTACCAGCA  GTTCAAAAGTTAGTGGTTGGAATAAAGAGACTGGAAGCAGTTAG  GAAACGGGAAATGATGGGTTTTGTTTTGTTTAAATGTTCAAATGT  CACTACGAGTGGTAAGATTTTAAGCAGCTTGACACTTAAACATT  CAAATTCTACCATCAGAGCCCCCATCCTGGATACAGGTGGGAGT  TAAGCTCCTACCCTACAGGCCTGATAGTGAGTAGAAGTGTAATG  GGTAAGGGACCCCAAGTGAACAATAAGTCTCCTCTTAGAACTT  GGTTGGTCTCACCTGTTTAGAACCACAGAGATCTCCATAAGTA  AGCTGTCCTTGAAACCCCTGGAAGAAGGGGTCCCAGCTTCTGG  CCCAGCTCCCAGGGGCATCAGGCTGGCTGAGCCCCGAGGAAAGA  GATCTCTGGGTGCAGATCTTAGGTGCTGAAGCTGGGTGGCATT  TACATCCTAGAACATAGGAAGAGGCTTTGGCCCATTTGTCCAGC  TGAGTTACATGTCTCTGCTGGCAAGG</p>	
KCP_1044 6	<p>TGGGGGTGCTAGGCGCCGAGGTGGGCTGTGCCACCTGCCTCCCT  TAGTCCGGAATCTCCTCTCCACGAGGAGCCCGACAGGTGCTTG  TATCCAAAGGAGAGAGAAATCGGCGGGAGGGCTGGTGTGAACAC  CCAGAGGAGGGAGCCGGAGTGGACGTCTGCCCGAGCGGCAACTG  GACCCCTCTGGGGCACCAGGTGTGCGGACTCTCCTCCTGGGGAA  ATCTCTGAGAGCCGAAGGAAGCGGCATGTTACAGGTGGGGGTG  ACCGGATTCTCTGGTGGAAGTGTGGTGAAGCTCTTCCATTCCC  ATGACAGCTGGCGTTTGAGCACTCAGTGA [C/G] GGTGCTGCCA  CACTCCCACACTCCTCCTAGGCGGCTATGCCAGGTGCAGACCTG  CGAGTCCCTTCATCAGGAAGAGTGTCTGTCTGCACCCCCAAAA  CCTCTGCAAGCCAAAAGGAATCAGCTGCTGCCAGGGGTAAACT  CCCAGGCCTCATGTCTGGTGGCTCCGGGAGTCAGGAGGAGCAA  CCGTGAAGGGCTGGCTGCGAGCTGAGCTTACATCAAGGATTAAA  AAGCATAATATCGTGGAGTCTCTTCTGCCTGGACGCTGTTCCCT  CACCACCTGTCCCCAGCCGAGGCATGGCTGATCTCACCATCCGT  GGGAGAGTCTCAAATGGGTCCAGGTGAAGTTGGAACCACTGT</p>	SEQ ID NO. 152
KCP_3858 9	<p>TCAAACCTTTTCATTGCTCAAAGCCTACAGCAAACTCAGTCCAC  ACACTTGGCTATACAAGAAAGGTTGCTTTCTTTGTTGTTCTATA  ACTGACTTTAATTTCAACTTCAAGTCCCCATTCTTGCCAAGGGG  TAGAAATGGAATCTTGGTCAACTTAGGTTCCCTCCCTACTCTC  TGGGGTTGCATTTCCAGGCCAGGCAGTTTCTGCTGGTGCTTTTG  TTCCTTGGTCTCTCAGTCTTCTTTCTGTGTTGACATCCATTGACA  TGTCTCTGACTCCCTCATCTCAGATCACAGGCCCATGCTGACT  CCAGGAGTATTCTTGTATTCTCTTCATCTGAACCTCAACACTTT  TTGAGACCACGCATGCATGTGCTCTCTCTTTCTCTCTCTCTA  ACACTTCTGGAACACTCTTGGACATGAGGAGATATTGGTCTTTT</p>	SEQ ID NO. 153

	<p>             TAGGATGGGGTCAACTGGCCCTGCCTCAGATCCATTGGCCTGTA              CATATCTTGTAGCCATTGTGGTGCCATGGATCACAGGTCACGAT              GCTGTGTGGCTGCCTCTGCTCTTAGACCTGCCCCCATGCCACC              AGAGGGAGTGTCTGCCTCCCCCTGCCCTGGACACTCAGCTGGAG              GGGAGGGTCACAGTCCCTCACAGTCCCTTCTCCAGTGACAAGCA              ACAAACCTCCAGTCTTCCTTTCTTTCTGATCCTCCTCCTCTT              CCTCCTTCTCCTCTTCTCCTCCTCCTCCAGTCCAAGGAAGTTTAT              GCAAAGGCCAGAGGAGGAATAATGAGGTGGAGGTCTCTCTGAC              CAAGCATGTAGCCTTCCGGATCTGTTGTGCTTTCCAGGAGTCCT              TCAAAGCTCTAAGCTTTTGGAATTCTGCAAGCTCAGGAAATTGA              AAACCTTTTCTCTCACAACTGCAGGTCTTTGTCTGCAGTTGTAA              AAGTCTGTTTAGAAACTCAGGAGACAAGCAGCATCTTCTTTGTT              CCTGCTTTCTGGAGGCAGTCAGCGTGGAACA [A/C] CCTGCCT              GCAGTCTGACTCAGGGAAAGGGTCACTGAGTGTGTGTGTGTGTG              TTGAGGGGTGGATAATAAGCAAGGAGAACACTCAGACAGAGAGC              TCACAGAGGGGCACCCAGCACCTCCCTCACCTCTATATTTCCCC              GCCTGGGCATAGTGGAGGGAGGGTTAATGCCAGCCAAGTTTAAC              AGGCATTTCTGATTTCGGGCATTGTTGTTGCGCTATCCTGCAAT              CCTACGCTGCGGGTACTGTTTTTATCCTGATCCTTCAGCTCTGG              AAACCTAATATAGAGAGCTGAGTAACTTGCTTGAGGCCATGATGC              CAGGATCCACGGTGCCCCCAGGCTGAAGAGCCTTAACCACTGGG              CTGTACCACCTCACAGGAGGGCAGGTGGCACAGTGCCTGGAAC              TGGGAGGGTCCAGCACGTGGAACATGCTCTGTCAATTTACTTAC              TGTGTGTCACTGGATCAGTCACTCAACACCGCTAAGCCTCATTT              TCCACCTCTTCAAAGGGATCTAATAAACCTGTTAGCAGAAGGC              TGCTGTGAACACTAAATGAGGTGGCTTAGGTGAGAGCTCTGGTC              TGAAGATGCTCACACTTTGAATCTCAAGACTTGTGTGAACCAAT              ATCAGATTTCTCCTATTAGATTGCAATTCTCAGGGAGTCACATT              CCGTCTCCAAATGCCATCTCCTGATCCACAAAATGAGCACAAC              ATCTCTGATAAACGGTAAGTAGATGGTTCCAGTGGGCAGCGGGA              GTGGGAGGGCGGTTGACTGGGCCAGAACCTCAAATGTATTCCTG              TGTAAGTTTCTCATGCATTCAATCAGTTTGGCACCAGAAGGTGCC              CAGACTCACTTTGCAGCCAGTCTGTCCCCATAGAGGTGATAAAG              GAAAAACATATGCACATTTAACTTTTAAAAAGTTTATTTGAACA              TTCAGCGATTACAAAACGGTATAGCACAGACAGCAAGCAACTAG              CACTCCTCTAGGAGGGGCCAAACAG           </p>	
KCP_6519 9	<p>             ACAGAAATCCTTAAGAGCATCAGCCGTGACACAGAAATCTAATA              CAATAAAACAAAGTGCTTATAAAACCCAGAGTTGTTTAAACCC              AGAAATTGCCAATTGACATATGGGACTATATCTTCTTAGCCCC              AGTAACTGAGTGGCTTCAAACAAGTCCCTATCACCTCCCAGGG              CCTCAGTTTCTTACCTGTGAAATAAGAGGATCAAAAAAGATA              ATGTTCTCTCTGTTCTCTTCCAACCGAGGCAGGCATCTCAAGTA              TTTCTTAGTCAGTTCTACTCTAGGCTACACAGTATCTGTATCTG              GCAGCTGTATGAACTACTGTTGAAAATCCTCTTCCCAATCCCAG              TTTCAACATCACTCCTCAAGGCAGCATCCACCTTCACTCTAGAC              TGAATTAATTCCTCTGTCTTACCACCTAAACTCCTCTAGAAAAC              TTGATAGAGGTAAAGATAAATGCATTTTTTCAAATAATCTACTT              TTCTAGTCCCAAGGCATTGTGTATATCATTCTTATGTAAGTTAT              CACAATAAACCATAATTAGTTACTTCCATTTATGTCAAATCGC              CTACAAAGCAGAAACATGTATTATTCATTTTGGCTTCCCTCCCC              AGTATCTAGCATACGAACTGTTTGCAAACATGCCAGTTCTTCA              AACTTTGTAACCTTCATGCCTTTTCTATCTACTACTTGGGATGGG              CCCACCTCCCTTTGTCTCTAAGCACACTCCTATTTCATCCTTC              AAAGTCCAGCACAAAATCCCCCTCCTCTGTTAACTTCAACTGC              TCCAGGCTGAGTCTTATGTTTGGGTCTTCATACGTACCCCTCT              TCTATTGTTTGGGGTATTGTGTGCTGTGGGATCTGTTTACTCTC              AGTTCTCCCTCTAGGCTGGGTTCCTTGAAAAACACCTCTGGA           </p>	SEQ ID NO. 154

	<p> CATTTCACCTCTACATCCTCTGCATTCTTGGCCAGGCTCTGAGA  GGGCATTGGTAAATGTTAACTGCCTGGCAATG [A/G] TGATGCT  GTTAACCTGATGTGTCAGGGGTCTGAATAAAGCTGCCTCAAGGT  AGGCAGATGCCCCACAACCAAGCAAGAACTCAAAGCTGCAGGCTC  CTCAGCCTGAACCTTAGACAGCGTCTTGGTCACCATTTCAACAC  CTTGACCACATTTCTCACTCTCCCAAATTTCTCCTGCTTATTC  CTCATCCACATACATAAGGCTGTGTCTCCAGGGGAAATTCAAC  TACTTGGTAATTATCCTGCTTCTTAAGTTTGGGGCTAGGGGATT  CATAGATGATGTTTCAGTATTATGCTGTGCAATGTAGATGCTTCC  TAAACCTTCTCAGGAGCTACCACTGAGTGGCACCTGGGGACCTC  TCAGGAAGAGCCAGTTTTCTGGGCAGTGTGGGGCAGGACAGAGC  TCATTAAACCAGCCTACCACCTGTCTTCCAGCTCCTCCTCTCAG  CCTCTGGGCTTCCAGCAGAAAGCACACGAGAGCATTCTTGTGG  TTTTCTTATGACTTGAGCCAGCGAGACGTACATGCCCAGCACCT  GTTACCTGGGCTGGCTCTTGGCTGAGAGCATAATGCATTGGGT  CAGGTTTCAGATCTGCTGGAGGAACACAGCCAGAATGTCTTGAC  AGGCAGCCCTGGCAAAGCCCCAGAAATATAAGATCTGAGTCTT  ATGATGGACTCTGTGACCTTGAGCCTCTCACCTCGTGACCTTGG  GCATCTCATGTTCTCTCCACAGGTCTCGGTTCTGGACTCCTTCA  TGGGAGCTGTATGCCCCTGTACACAGCAGTGTGTGCCCCCG  GGGATCAGGGACCAGGATGGTCTTTCTTGGTGGTGAAGGGGGC  ATTTTGCATATTCCAGAGATTCAAGTTTCCAGACCTATCTAGAA  AGAAACATTTGAGTTTACAGGTTGGCGCTTCTCAGCCTCTGTCT  CTCTTCTCTCTGTTTCTATCTCCCTCTGTCCCCTCTATGTATGTT  TGGTCTCTTTCTGTCTCTCTGCG </p>	
KCP_8246 8	<p> CTCACTGCCTGCAGTTTATTACAGGCATTGGATGAGACAGCTTCT  TCCTGCTCCATGTGGAGTCAGCTGGGTACTTGAAGTGGGACATG  GATGATCTACTTTCAAGATGGCTTATTCTCAGGGCTGCCAAATG  GATACCGGCTATCAGTTGAAAGCTATAAGCAGGGGCACTCTGCA  TAAGCATGGCTCATCTCTACAAAAGCTCCTCCCCAGTCTCCTTG  TTTGGGCCTCACAGTGTATGGTAACCTCAGGGCAGTCAGAAATGT  GACAACTAAAGACTTCAGGAGTAAGTATTCCAGGAAGCAAGATA  TAAGCTATGTGGCCTTCTAAGACCTAGCCTCAGAGGTCACATAG  TGTAACCTCTATCACACCCTATTGGTAGATATTGTAACAGAAGC  CCACCCAGTTTCACAGATGGGGACATAGACTCCATTTCTTAATA  GGTAACTGGCCAGAGTTGTAAAGAGCATGTGGGATGGAAGATA  TTGTTGCAAGCATCTTTAGCAAATACAAGTGGACATACCCAATG  CAAGCACAGGATTGATCCTCCACTCTGCCCCATACCCCATGAT  TTATTAGCCACTCGGACAAGTGACTTCAACTCTCCAAGCCTCTG  TCTCCTCCACTAAAGTGGGGACAAATGAGTATTACAAATGAGAC  CATTAATAAGATAATACATTTTAAAAATTAACCTGGTACCTGT  CACAAAGTACATGCCTAACAAATGTTTGCTTCTGTCTCACTTCC  TCAATTTTCATCTCAGTCAACCTGGACTGACTCAAAATGGCATTCT  TTCTTGGCTGCCCCCTTTGAAGTATTTCTGCTGAGAAAATAGTT  TCTGTGTATTTGTAAATTTACAGGTTGAACATAGATCATTATTC  AAGCATTGCTGGTCGATTCGTCTTTTCAAAGGCGGGAGCTGCTG  GCTGTGGGAAGGGACCCAGCAGGGGTCTCTTGCAACCCTGCTCT  ATGGGTGGGGGAAATCTGGACCTCCCTCTGGT [A/G] GGGTTGA  TTGAAGTGAAGGGTCACCATATGTCTTTCCCAAGAGGGTGACTG  ACTTCCTGCTTTGGTCCCAGTTTCCCTGAGATTTTCTGAAAGC  CCTTCCGGCTAGCCAGTTGGGAGTGTTAGTACATCAGATCCCA  TGCTTTGGTGAAAAATGTAAACACAGACCTGATTTTTTCATTTTA  AATGAAGCCAAGCATATTGCTCCAGCAGATGCCGAGTGACTCA  ATCTGTCTCTCGGTTCTGAAGGGAAGTGAAGAACAACATGGTA  AAATAAAGCAAACAGCACATTTATTGGTTGATAAAATGCTGTTT  TAGTCTACCCTGGCATTATATGGTGTATGCTATGTGGCGAACAT  CTGTTATTAAATCCAGACTTCTGTTGCTGGATACATTGAGTCA </p>	SEQ ID NO. 155

	AAAGCTGGAGCGGATGAGAAATCCATTTATGCGTCTGTTGCGTG TGAATGTCAGAGCTCATATGATGCCTTTGTCTTCATTCTAACTG AATCTTTTAATATGGACCGTCTCACTTGTTAATTCAGACTCAGG GGCAATAATGTTTTTCATTTGATTAATAAGGTTAAAGAAACAAA GAAACAGTGTTTTCTCAGGTGCTCTAAGTAATTCGTTAATGAA TTTTCGGAGACAGCGTGTGAATTTGAAAAGAGTAGGACTTTTTA AAGAGTTCATACTATGAACCAATAATTCAGATCCTAGGGCCCTT ATCCTAAGGACATAATAGAAATGAGCACATTTATAAGAACAAAG ATGTTCAATGAAGTGTTACTTACAACAGCAAAAAAACTTGAAAG TCACCTAAATGTTTGTAAGTCAAGAGCTTCATTGATATTGACTG CAAAGTCCATGTTATTCCATGTGACGAATTTTTTAATCAATCAC CTCTTGATGGATTTTAAATTTTTTACAATTTTTTGCTATCCTAA AAAAAATGTGTCAATGAACAACCTTTGAACTACCCCTGACTACCAC TTTAGGATAGATTGCTAGACGTGGA	
KCP_8579 3	ATCACCCCAAATAGTTATGATGAAGGTGATCTATGTACGACACT TAGAGAATCAGTGATGGAAAATTCACCAAGAACAGCCACAGGCA GGCCAGAAGAAATGGCCCTGCCCTCTACTTTTAGGATTAAGCAG AAGCTGGCCCTAGATCTCACCAGTTACCAGTGATCTTGCGCAT TTTAGCATCATGTGCATTGCTTCACTGTGATACCATCTTGCTGG CACAGCCATGGAAAGCCATGAGTTAATGCATCTCCCATGTAAC AAACCTCCCCCTAGGACTCTGGTCCACACCTATCTCTGCTAGATT CTCTGGCATTGCAAGAAATTTCTCAGACTGCCCAAGAGATTCTG TTCCAATCTAGGGGCTCCTTATCCCCAGCTCAGAGCTGGATTTG GCTCTTGCTTGAGGCGGGAAGCCCTGCTGGGCCAGGGCTTAGA GGGGCTCACAGAAATCAAAGCAAGCATTCTCCGCTCTCTCCT ACAGCCCTGCATGCATCTTCTCTGATCCCTTGCTGAGTGCGGG GTGGCATTCAAAAGCTCATTACTGGCTTACATACTTTGCCCTTA AATCAGCTCTTAAATGCCCTGGGATGAACAGCCCTAAATAGGAA AGAAAAAAAAAAAAACAAGTTTCTTGCAAGTTCACAGATATGCTT GGTGCTTTCTGTGTCAGGCTAGGGTGTAGCCTTCTCTGTCTAAAT TTGATTTTCTGAGTCTTTAAGGAAAAATGGCTACTGGTCCCCCTG GACGCTGATTGCTTCAGCATCTGAATCTGCTCCATCACTTCTAC CTCCACCCACTGGTCCACGTCCAGTGGGTAGAGGTAAAGGGGAT GGAGATATCATTTATCTTCAAAGGATAAACTGCTCTGAGAGAT CTTTGCTTTCTTAGAAACACTGCTGGAAAGTTGTTTCTTTAGAC TACATTAACAGAAGTACCATCTCTAGGAAGACAAGGTGGTAATA ACTAACATCAAATGAGCAGTTCCTATGTACCC [C/T] GTACATG TCTTAGCCAACTTCATCCTTGTAACAAACCTGGAAGGCAGGCAC TGTTATCACTCTTATTTCCAGGTGAACCAGTTGAGGTTCCAAGA AGTCTTTTGTCAGGTTCATGCAGAGTTGAGGCCCCCAAGTCGG TAGACTTCAGGAGCCAGACCCTCAACCCCTCACTGCCTCCCCG CTCATGCTGCACTGAGCAGACCATAACCCGGATGGTCATGTTTCA GTTGGCTATCAATGCAGACCACGCTGGGCATATTCAGGGGACGG ATACTCAGAACTATATAACATAAGGAATAGAGGAAGGACTGGAG GATGTATTAACATGAAGAAAAGGTAGACTCATGGCAGGAGATGA GCAGGGTAAAGAGGTGCAAGACATAAAAAAGCCAATTTTCATATAC ATGAAGATTTATCAAGAGCCAGAAGGCCCTCTATGGGTCCAAGA GTTACAAGGCCATAATGAGGTGAATTAATGCCAGCATATAAGGAA AAGCTTTTGAATACTCAGAAGTGTCCAAAAAGGGTCAAGGCTGC CTTGGAAGTAGTAAGCTCTCCATCAGAGGCTTGGCAACTTCTT ATTAGGGATGGTATGAGTATCTCAAGTACAGATACAGATGACCC AAATAACCACTGAGGCACCTTCTGACCCCAAGTATAAGAGATTCT ATTGTAACGCACAGGAGTCCATCTCAAGCAGCACACTGAGCCAT CTCCTTGATAAACCTAAAGGTAGGTATTATCTCCCTCCAGATGCT GTCTTCTTAGCCTGGGATGCAAAAGCCATAGGATCACTTCACGT CCAACCCCATCAGGTGATCTGTCTATGAATCACAAGTTATTGGA GCCAGATGGAACCTACAGAGCTAAAAGATACATGAAGACACCCGAG	SEQ ID NO. 156

	GCCTGCAGACAGGGACTAAGTTTCCAAGGTCACAGAGCTAACAA GTGTCAGAGTCAGGCTAGACCCAGGACTCACAAGTTGAGCTCAC AATTAGTTCCACTTCCTACACCACC	
KCP_9354 5	CCTGAGCCTCTGCCTCCTTCTGAGAAAGACCCTTGTGATTACAT CAGGTTACCTGGATAATTCAGGATAATCTCTTCATCTCAAAAT CCTTAAGTTGATCACATCTGCAAAATCTCTTACCATGTAAGG TAACATATTCACAGCTTCTGGGGATTAGGACATGCATCCCTAGG GAACCATGATTCAACCTAGCATGGGGGAACCCACTACAGGCAGG TGTTGTCCTTGCCATCGCCAGCTCAGTGCTTGGCACAGTAGAGG CCATGGATATTCATTAGAGAGAGCATGCCTGAGGCAAGCCTG ACCTCAAGATCAAGACAGGAAATTGGCTTTCATGGGTAAAGGAC CTGTTACTTTGCTCATCAATGTATCCTTAATCATCAGAGGTCAG ATCTGCTGGAGAGTGCAATCTTTCAG [G/T] TTCCAAAAGTAAG ACTGGATGCCTTAGAACTTAAAGTCAGGGAGGTACCCAAGAAAG CAATCATAGACTGAGTCCCCATGCAGTGCACTTTCCTCGGATGGA CAATTTCTCTGTTCTGACAGTCACTGTTGACTCCATTTCTCAGA TGAGGGACCGAGGCACAGAGAGGTGCAGTCAGTCACCTGAGGCC ACACAGTCAGGAAGTGGAAATCCATGGAAACTCATCATCAGCTG CCTCGCATCAGGGCCAGTGCTCTTTATCTCCACCCACACATTA TAAAGCCACTCAGCTTTACACTCAAGGGAACCTCCTATTTCCCT ACTGGATTATATGTATAATTTGTAGTATTGCAAGATTGAACAG AAGCGAGCAGCAGCTTGTAGTTGTGTGTCTCACTCACTCCTGCC TGTGGGGATGCCACGTGATTGTTTAAAGGGTTGGAATCAGGAGA AAGGCAGGCTCAGAGCAGGACCAAGAGAGAGCCACCCCTCGCC TCCC	SEQ ID NO. 157
KCP_9784 4	ATTATAAGTATATACCACACTTTGTTTATCCATTCACTTGTGCGA TGGAATTTGGGTTGCATCCACCTTTTTTTTGCTATTGTGCATAA TGCTGCTATACACATGGCTGTGCAAAATATCTAATATTAGTCCCT GCTTTCAGTTCTTTTGGATATGTATCCAGAAGCAGAATTCTTGG ATCATATGGTAATCCTATTTTTTAATTCTTTTAGGAACAGCCATA TTGTTTCCACAGCAGCTGCAGCATTTTACATTCTACCAGCAG TGCACAAGAGTTCCAATTTCTCCATATCCTCACCAACACTTGT ATTTTCTGTTGCTGCTGTTTGTGTTTTTTTATTAATAGTCATCCTA ATGGGTGTGAAGTTGTTTCTCATTTGTGGTTTGGCTTTCAGGTTT TGATTTGTAGATTTTCTGATGATTAGTGATGGGTGCATCTTTT CATGTTCTTACTGACCTTTTATATATCTTTCTTGGAGAAATGTC TGTTAACTCTACTCATACTTTTGTAAATAGTATCCCAATCCTT CTAACTCCCCAATGAGGTGGATATTAGTATGTTTCGTGTTACAGT AAAGCCAACTAAACCTTAGAAAGACTAGGTT [A/T] ATTATCCA AGGTCACACAGCTAGAAAATGACACAGCTTGTATTGAAACATCA GTTTTTCTCTTTCCAAACCTAACGCACATTTATGAAACCTACA TTATTGCACCATAACATCATGTTGATTTACTTATCTGCTCTCCT GCCTGTCCCATCTACTACATAAATTGAGTGTGGTTTGAATCAG AGACTACTTCTCATCTTTGGGCACAGTGGCAGCCATGGATCAGAA TCTCTTACATGCTGGATAAGTGGATGCAAGCTCAAGGCCACACC TAAAGTCCCCAGGTGACTTGATCACTTGAGTTAGCTGCTGGAAA CCTGGGCTTCCTCTTCTGCAAAATGGGGAGAGAAAATAAATTCT CAGTGGATTGTTTGAAGATTTGAGCAAAGACCTCTGCAAAGTG CTAAGCATGTGGCTAGCATGTGGCAGGTGCTGCCTAAATAGTAG AAATTAACACTGCCATGCTTATAAGCTCCGGACAAACACAAGAA GCCCCGAAACATAATCTGTGCCCTTCTGCTTGCACTTCTCCTAGTT GGGGATGTAAAATAGCCCAGCTACAATCAAAGAAGAAAATCAAA GTCAGCACAGACTATGGATATGCTTCTATATGTGTAGATTATTT CCAGACTCATTCGGAAGAATCTGGACATACTGGTTGCCTCAGAG GTCAAGAAAATTGGCTCATTACTTCTGTAACCTTAATTTGACT CTCTATGCTTTTACATAGTTGGAATTTGCCATGCACATATACTA CATTTAAAAGAGCGTGTACGCG	SEQ ID NO. 158



KCP_1028 82	<p>CACAATTATGCTGTAGGTGAGTTTACCTTGGGAAACCAAGGCA  CAGAATTTAAGTAACATATTGAAGCTCATGCAGCTGCTAACAGG  GAAGGCCAGGGTCTGAACCCAGCTGATCCGGCTCCAGCATCCGA  GCTCTGAACCACTGGTCTATCCTGCCTCTGTTAGGACTTGGTCC  AATGTCATCATCCTAGAAAGGAACATTTAGGCCCGCACGGTGGGT  GGCTGGTTCAATCCAGTTTAAAGGCCAGGAGCAGGACAGTGACT  TGCAGCTGCAGCAATCCTATGACTCAAACCAAGCAGCTGTGAC  AAATAAAGGGACTGACTCTCATTCTCCCGTGCTAGGGAAGGATG  AGCTATCAGGCCCTTGTGTCAGGCTGAGTCAGTCATCCCACAAAC  CACCTAAGTGAAACCTCTTCACTGAGCCTTATTTCTGAGCGCT  CTCCCTTTATCTGTGCTTGCAAAGAGG [C/T] GTCTCCCTCCAT  GCCAGCCAACCCACCCACCCCGCACACACATACCCTCTGGC  TGGAAC TGACGACCATGGGTTTTAGAAATGAGATAAATCTGGGA  GATGAATGTATTTCATGAGCCCATAAAGGGGTTCATGAATCACTGG  CCCCAATTACTGCCCTTCAATCCTGACAGGATGAATTCCTCAAG  CAGATTCTCCTTGTGTCAGACAACACGGGAGGCAGTGCTAGGCTG  ATCTAGAGCCACAGATAACATCATTATTCCATAACCAGGCTGGTT  TCGGTTTCCCAAGCCACCTCCACTTGATTACAGCTCACTTCTG  ATGCTGGAGAGAGAGATAAATATATATATATATATATATATA  TATATATATATATATATATATGAAAGAAAGAAAGAAAAGAGAGA  GAGAGAAAGACACAAAGGGGAAGCTTTCATGCC</p>	SEQ ID NO. 159
KCP_1073 80	<p>ATCCCAATAGGACACATGTTGTATTAAAAAGCCATGCGAGACGG  AAGAAGGAAATTGAATGAAATTTGAGGGCAGGTAGGAGCAGAGA  CAATAAATAATTTCAGCAGTGAAGGAAGCAGAAAAAAGATTGCAC  TCATTTTCGCCCTTCAACAATTATACATAACACCTGTCTGGGCC  ACAGAAGGGCCAGATCCCATTCCTGTGCTCAGGAAGCCACAGG  CCGGCAGGGAGAGGCTGGTTGGAATGTGTGCTTTGCACTGTAAC  GGAGGCATCGAGCATGGTAAGGGACTGGCGGTGGCTGCTGCCTG  CGGACGTGAGCAGGGGCCCTTTGAAGAGGCAGGACCTGTCTGGA  GTCTTACCTGGGCCTTGGCCCTGGCAATGGGGAATGGAGCAGGC  AGCAGGGGACAGATGCTGCCAGA [A/G] ACCGAGATGGTGCCGG  AGGACTGGGCTGAGTCTGGGTCAAATGACACCGCCCAAGGCTCT  CTGCCCTCTGGGGTGAGGCAGGAGGCTGCCTCTGTGTGTGATT  AGAGACCCTAGAATCCCAGTGGCCATCACCCACAGCACATGCC  AACCTTTCTGTGATAACTTCTCTTGTGGAAGTGTGAAAGTGTA  AGACCAGCTCCTGTATAGTGCATGGCCATCCTTTGCTTTGGGGA  CAGTAAGTCAGTCAACACATACTTATAAATGGGGTCTGGGCCG  TGGCACTGATCTGGTCTCCACCTTGCCCTCACACTGCCCTTCC  CACTACCACTTCCCTCCTCTGCATCTTAGCCGCAAGGGACTTT  CAGACCAAGCAGACCTGGAATCAAATCCCACCGCTGGGCCTCAA  TGCCAGTGGAGACAGGAACAGCTGATCCCTGGAGCCCTCAGGAG  GAAGAGGACGGGATGCCTGGC</p>	SEQ ID NO. 160
KCP_1087 03	<p>CCCACTCACCCTTCCCTCCTCTGCATCTTAGCCGCAAGGGACT  TTCAGACCAAGCAGACCTGGAATCAAATCCCACCGCTGGGCCTC  AATGCCAGTGGAGACAGGAACAGCTGATCCCTGGAGCCCTCAGG  AGGAAGAGGACGGGATGCCTGGCTTGGCTGCTGGTCTGGGGCAG  GTGCCCAGTTACAGCAGTTGGAATAATCCTCAGTGTGGAAGGA  AATTTGGAAGTGAGCATCTACCTGCCTGCCGTGCAGTTTGTGAC  TTTAAAGATGGTTGACAGAACATTCCCAAAGGACCACAGCGGTG  ACCACTGTTCTCGTTTCCCTTTGGTGGCTCACTCACTCAGTGCT  GGACACAGTGGTCTTGACAAGACAGTGCTGTGGCTTCCATGAAC  CTAGGACAGGGATAGACTCAAGGACTAAGAACAAACCAGGAAGA  AGCATCACACAGGCTCCTTGCCAGTCACCTCATCTACCCCTCC  TGGCCCTGGCGGATGGGTCTCCATATTTACAGGGGCCAGATGAA  AAAACCAGAGGAGCCAGGAAAAGGAGCTTCCCTTCCCAAGGGC  GCAAGGTGAGGTGCCAGTCATGAGATGCAAGCCCTGAGCTTTCT  GATTCCACTGCATGTGGTCCCAAGGTTCCGGCGCCGCATCACACA</p>	SEQ ID NO. 161

	<p>GTTAGTGAGCACACTCTCCTCCCCTGGCCCCGAGTGAGCCAGCT  GGATGGCAGATCAGAAAGAGAAGTCCCGGGTGCCCCAACATGG  CTAGCTCCTTCCAGGACCAGGGGCTAGGCCCCAGCTAAGGCTGG  TGCACACAGCAGGGCAGGGGGCGAAGGAGTGGGATCCCACCCAG  GGATCCCACCCACCCCAAACCTGCTTTTCGGACATCTTTCCAATG  CATAATGTGCAGATGAGGCCCTTTGATAAGGACCAAATCCCTTT  CCGTTGCTTGGCAACCTGGCTCACAAGTCATAGCAGGGAAGTAA  TTTACAGGAATTCAAAGTGTGCTGGAGGTTTC [G/T] GCTGAGC  TGAATTGCTGCAAAGAGGAACCTCAATGGTCCAAATCACACCTC  TGGCGGGGAGGAGGGGCTGAAGGAAAAGCTTCCACTTCCGTCAC  TTGAGAGTACAGAGCCCTGAGCTCAGACTCAGCGATCGTTTTCC  ATTAACGGATTACTGGTTCCATGTTGAGCTCCTGCTGTGTGGC  AGGCCCTGTGCTGGGAGCCAGGGACACAGTGACAAACGAGACAG  ATGCCAACCCCGGATGCACAGAGCTCAAAGAGACAGAGGAGTAA  ACAGGGCTACACATGTGACAAGATAGGCTGTGCACAGGGGCTG  AGCAGGACCCTTGGGGCAGGAGGAGGCAGTGGAGGGATGGGAGG  GTAGGGACGCAGTGGTGACCAGCTAGCCAGATAGAGAACAGAGG  GTGTCCCAGCACAGGGCCACACAAGCAAAGGCAGAGGTGGGGAG  AGAAGAGCCTGCCACACTCTCAGATCACCATGTGGTTGGGCCAG  GGCCCCAGCTGAGGCTGAGGACACATGGAGCCCAGATCCGGCAG  GGCCTTGAATGCCAAGTCAGAAAGCATCTGAAATTTAGTCTACA  GATGATGTGGGTTATTGACAGCCAGGACAGGGAATGACATTTGT  GTTTCAGGAAAACCACTGTCTTCACTGTTAGGGGGTAGATTTCAG  GGAGAAACAGGAGGTGGAGGGGAAGAACTGTGAGTAAAGGAGT  CTCTGGGGTACAGGTGAAGTTTCTGTGAACTGGAGAAAGAAAC  TGTTGAGGCAAGAGTTGACAAAACCTTGAAGTAGGATGGAGAGGA  AGGGACAAGTTCCCTTGGCATGGTGACGGCCCGGTGGTGGGAAC  CAGGGAAGAGGAGGGGCTTTGCAGGTGTCTGACTTGCCCAACAG  GTGGCGCCATTTACCAAGATGGGAAGGGCCGGGGAGAAGGGAGG  GTTCCATTCTAGGGAAATCTCAGGTCTCGCTATTAGGATTCTT  TCGGTTGCCAGTGACTGAAACCCAG</p>	
KCP_1248 77	<p>ACTGTCTAGATCTGGGGACCCTCCCAAGCTCTCAGAGCTTTGGA  AGGAAGGTCCCTGCAGGGAACCTGTGTGTTTCTTCAACAGTG  TATCCTCAGTGCCTAGCACATGGTAAGTGTTCATAAACAGCTG  TTGAAGAGACGGATGGATAACTGAATGAATGGATGCTTCCATGG  GCAATGACACACTAATCTGAAAAGCCCTGTATCAATGAAAGAAT  CACTTAATAGTTTAACTTTTCCCTCATCCTTCAGAACACAGATG  GCATGCCATCTTCCCTTCAAATCTCTTCCAGTGCCCCACACAG  AAGAGGCACACTTGGACACTGGTGTCTGATGGACCCAAGTTCAC  AGCCTGTCTCTGGTCATCAGGTATCATGACCTTGGGCAAGAAGC  TTAACTCTCTGAGCCTCAGTTTCCCTTCTGTCCCCCAGGGAAA  ATGAGTCTTGGCCCTCCTAAGGGAGGTATGAGATGTAAGACCCC  GAAGGACACAAAGGTT [C/T] GCCAGGAGCCTTCAGGTAGGAGG  CAGGTAAGGAGGTCTGCTAGATTGGAATGAGTTTCTGGAAGGCC  CCAAGGAGCTCAAATCAGACCTGGGGTGAAGGTGTCTTGACCA  AAATGAGACCCATCAAAGAAGCCTGGATGAAGGTGCCACAGCA  TCCATCAGTGCCAAAAACAGAAACACTTTAGCCCAGGATACAAG  GAACATTTTAAAGCAACAGAGATAAGAGATAGTTAGAACTCAGG  CCTCCTGGCTCTTGCTGTTCTTGGCCCATAATTAGTTGTTATGG  GACCTTAATAAACTTCTTGCTTCTTGGTACCTTTGCCAAACAA  TCTGATGAGGAGAATATTGAGTCATGGTGCCAGGGAAAATTAGC  ATATTCTGCAAATTCCTGGCACTGTTAACTGGAATCTGTCCA  CCTTTAGAAATCCTCAGATCACTATGTCAGCATCCCCAATCAC  AGCTCTCCAACCTTCAAGGAGGGTTGAGGGGTCTGAAG</p>	SEQ ID NO. 162
KCP_1260 86	<p>AAGAATATCAGTTCCACTTCCCTTGTCCCTAGAGAGCCTTGATG  TGGATGTTGATGTGTCTTCCAACACATGCACCAACCTTTCCCTG  TCCTGTAGCAGTTGAGATGGAATCATCCCACTCCCAGCTCCAGG</p>	SEQ ID NO. 163

	AATAGGCTCTGATGGGCTTGAACCCAGCAGCTTAATTCCATTGG TTCTCTAGGCCCTTCATCATTAGTACAGGAAAGGCACCTTGACCTA AATTAGTTTCGATAAGATTTAAGCTCAGAAAATCTGGTTTGTTGGA TGGAGAAAGAGATGCTTTCTTTCTCTCTGGAAGGAGTTTATTGC AAAAGTAAGGGCTGGGGCTGCTACAGCCATTGTGCTACCATGAG GGAAGTAGCCATGATAACAAAACCTGCCTGGGGAGGGGCTACGC ATCACAGAAAATGATGCAAGTCCTGCTCAAACCTGTGCCTGAT GCCTGCCTGATCTATGGACTTCTTAGTTCCATGTAATGGATTCT CTCTATTTTAAAGCC [A/G] TATCAGGTTGAATTTTGGAGAA ATAAAACAAAAGCATCTTGACTAATTTAAAAAATCTTCTTTGG GTATTCAACCCCTCCTAAACTCACCCCAAATCCACTGGGAGCAT GTCAAGATTTTTGTGAGCCGATTTAGGAGATGCAAAATTCATTG CCTTAATTTGGATCTCCAGGAAATGACTTCTGCCCCCTCTTAAAT CATTTAAAGCTCAAAGAGGCATGAGGGCCCTCCCCAAGGATGCA GGTATCCTCTTGACTGACAGCCTGTATGCTCTGCTTCCAGGATC CTTCCATCTCCTCCCTTTACTGAGGGAGTCTGCTATGTGTTAGA GGTGTCCATCACTGGTCACACTGGGAAGCTGTGGCAGGGAAGCT GGAGAAAAAGCAAGATAGGCCCCAGAAAGAACACCAACTCCAGA CTCAGGGAGACTCAGGCCAGAATCCTAGCTCAACTTCTTCCAAG CTCCCAAAGTCACACTCTTTTCTCTGAGCCTCGATT	
KCP_1262 08	ATCCCACTCCCAGCTCCAGGAATAGGCTCTGATGGGCTTGAACC CAGCAGCTTAATTCATTGGTTCTCTAGGCCCTTCATCATTAGTA CAGGAAAGGCACCTTGACCTAAATTAGTTTCGATAAGATTTAAGCT CAGAAATCTGGTTTGTGGATGGAGAAAGAGATGCTTTCTTTCT CTCTGGAAGGAGTTTATTGCAAAAGTAAGGGCTGGGGCTGTCTAC AGCCATTGTGCTACCATGAGGGAACTAGCCATGATAACAAAACCT TGCTGAGGGAGGGGCTACGCATCACAGAAAATGATGCCAAAGTC CTGCTCAAACCTGTGCCTGATGCCTGCCTGATCTATGGACTTCTT AGTTCCATGTAATGGATTCTCTCTATTTTAAAGCCGTATCAGG TTGAATTTTGGAGAAATAAAACAAAAGCATCTTGACTAATTT AAAAAATCTTCTTTGGGTATTCAACCCCTCCTAAACTCACCCCA AATCCACTGGGAGCATGTCAAGATTT [T/C] TGTGAGCCGATTT AGGAGATGCAAAATTCATTTGCCTTAATTGGATCTCCAGGAAATG ACTTCTGCCCCCTCTTAAATCATTTAAAGCTCAAAGAGGCATGA GGGCCCTCCCCAAGGATGCAGGTATCCTCTTGACTGACAGCCTG TATGCTCTGCTTCCAGGATCCTTCCATCTCCTCCCTTTACTGAG GGAGTCTGCTATGTGTTAGAGGTGTCCATCACTGGTCACACTGG GAAGCTGTGGCAGGGAAGCTGGAGAAAAAGCAAGATAGGCCCA GAAAGAACACCAACTCCAGACTCAGGGAGACTCAGGCCAGAATC CTAGCTCAACTTCTTCCAAGCTCCCAAAGTCACACTCTTTTCTC TGAGCCTCGATTTTCCCATCTGCAAAATGGGGATACTAAGGGTC ACCTAGCTGGGCTGCCCTGGAGATTCCAAGACATTA	SEQ ID NO. 164
KCP_1290 93	GGGTCCCTAACAGGCCACAGACCCATCCGTGGCCAGGGGATTGG CGACCCCTGTCTTTTTTTTTTTCTTTTTTTTGAGATGGAGTTTC GCTCTTGTTGCCAGGCTGGAGTGCAATGGCACGATCTCGACTC TTCAACCTCCGCCTCCTGGGTTCAAGCCATTCTCCTCCCTCAGC CTCCCAAGTAGCTGGGATTACAGGCACCCGCCACCATACCTGGC TAATTTTTGTATTTTGTAGTAGAGATGGGGTTTCTCCATGTTGGT CAGGCTGGTCTTGAACCTCCGACCTCAAGTGATCCGCCACCTC AGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACACGACC TGCCCGGGGACCCCTGTCTTAAACCACCCAGCCTGTGATACTT TGTTATGGTGACCCTAAGAGGCAAATACACCCTCCTTTCCCCAA CCTCTCCCTCAGACGAAACCGATGCGAAAAGTGCTTCATGAAG TTTCAGGTAAAGAAGT [C/G] TGGGACGAAAAGGGATAGTGAGG ATGGCGGGAGGGGCTGAACTCCAAATGGGCTTATCAAGGCTCTG CAAAATGGCGTGACGGCGCTGCCCCCTTCTGGTGGCCTGAAGAC TAACGCACATGATGTCAAGTGCGGGGCCCAAGTACTCAGGAAAA	SEQ ID NO. 165

	GGTTCTCATTGACACTGGGAGGTCTTACATTGGGGGCCCTGA GCCTCCAGCCCTTCCAAATCTATTCTCAGCAGGAGCTCAGCCAC ACCTGTGTCCAGAACTGAGGCCAGGCCAGCCTTCACTCCACG CCCAGCCAGCCCCAAGGAACCGACTCCCTGAGGCTCTATGCTCC CTGCCTCCAGTGGCCCCGTGTCTGGGAAATAGTGGCCCTGGCCCT GATGCCCTGACCTGGGCAATCCATCCCCTGGTCTCTCAGCTCC CGGGCCAGGTTTTCTGGGCTACTTTAACCAGGGCAAACCTCATT CCTCGAGTACAAAATAAAAGATTGGAACAGCATAATC	
KCP_1291 27	GGTTAGTGGGATGCAGCGCAGGCTAAGGAGTGTCTGGGGCCAC CAGAAGCCAGGGAAGCCTAGGAAGGGTTTTCTAGAGCCTTTGG AGGGAGCACAGCCCTGCTGACACCCTGACTTCAGACTCCCAGCC TCCAGAGCTGGGAAGGGATAAGTAGCTGTTGCTTTAAACAGTG GTCCCCAACCCTTTTGGCACCAGAAACCGGTTTTGGTTCACTGG AAGACAATTTTTCCACGGACAGGGTGTGTGGGGTGGGAGATGGT TTCAGGATGAACTGTTCCGCCTCTGATCATCAGGCATTAGCAT TAGTTAGATTCTCATAAGGAGTGAGCAACCTAGATCCTTCGCAT GCGCAGTTCGCAATAGGGTTTCATGCTCCTATGAGAACCTAATGC GGCGGCTGATCTGACAGGAGCGGAGCTCAGGCGGTAATGCTTGC TCGCCAGCTCACCTGCTGTGCAGCCGGGGTCTAACAGGCCACA GACCCATCCGTGGCCAGGGGATTGGCGACCCCTGTCTTTTTTT TTTTCTTTTTTTGAGATGGAGTTTCGCTCTTGTGGCCAGGCT GGAGTGCAATGGCACGATCTCGACTCTTCAACCTCCGCCTCCTG GGTTCAAGCCATTCTCCTCCCTCAGCCTCCCAAGTAGCTGGGAT TACAGGCACCCGCCACCATACTGGCTAATTTTTGTATTTTTAG TAGAGATGGGGTTTCTCCATGTTGGTCAGGCTGGTCTGAACCTC CCGACCTCAAGTGATCCGCCACCTCAGCCTCCCAAAGTGCTGG GATTACAGGCGTGAGCCACCACGACCTGCCCCGGGGACCCCTGTC TTAAACCACCCAGCCTGTGATACTTTGTTATGGTGACCCTAAG AGGCAAATACACCCTCCTTTCCCAACCTCTCCCCTCAGACGAA ACCGATGCGAAAAGTGCTTCATGAAGTTTCAGGTAAAGAAGTCT GGGACGAAAAGGGATAGTGAGGATGGCGGGAG [A/G] GGCTGAA CTCCAAATGGGCTTATCAAGGCTCTGCAAAATGGCGTGACGGCG CTGCCCCCTTCTGGTGGCCTGAAGACTAACGCACATGATGTCAA GTGCGGGGGCCCAAGTACTCAGGAAAAGGTTCTCATTGTGACACT GGGAGGTCTTACATTGGGGGCCCTGAGCCTCCAGCCCTTCCAAA TCTATTCTCAGCAGGAGCTCAGCCACACCTGTGTCCAGAAGTG AGGCCAGGCCAGCCTTCACTCCACGCCAGCCAGCCCCAAGGA ACCGACTCCCTGAGGCTCTATGCTCCCTGCCTCCAGTGGCCCCG TGTCTGGGAAATAGTGGCCCTGGCCTGATGCCCTGACCTGGGCA ATCCATCCCCTGGTCTCTCAGCTCCCGGGCCAGGTTTTCTGG GCTACTTTAACCAGGGCAAACCTCATTCTCGAGTACAAAATAAA AGATTGGAACAGCATAATCAAATAGGTCATACCCATAAATCAAC ACATTTGAGCACCTATTTTGTGTTCTTTCACTAATCCAAACCA TATTTATTGAGCATCTACTATGTGCCATTCTCCAGTAGCCATTC TAGGTGCAGGGGATACAGCAGAGACCTTGAAAAAAGGAACAGTC TCTGATCTTGCTGAGCTTAGAGTCAAGTGGAGGTGAGGAGGAAG GAAATGAATTAACAACTAAGTGAAGCAGAAGGTAACCAATTGAT TGACTGACGAAGGGGTACAAACAACAAACACCTTCCTTTCTCCA AACTCTATCTTTAACTGTATTCTCTCGTTTTCTTCTCTCCAT TTTACAATCATTTTACAACATCTCTGGCTATTCTCTATATTTTC TGATCACTTCGGTTCTCATCAATAATAATTTCAAGTTTTTCAAG CATTGGAAAGTCCCATCCAATTTAAATGTCAATCTCACACGCAG TTTAAACGTTTCGCCTGCCCGTGAGCTCAGACCTGTCTTGGTGC CTCAGTTCTGTGTGGAGGGGAGGA	SEQ ID NO. 166
KCP_1296 90	TGGTGGCCTGAAGACTAACGCACATGATGTCAAGTGCGGGGCCC AAGTACTCAGGAAAAGGTTCTCATTGAGCACTGGGAGGTCTTA CATTGGGGGCCCTGAGCCTCCAGCCCTTCCAAATCTATTCTCAG	SEQ ID NO. 167

	<p> CAGGAGCTCAGCCACACCTGTGTCCAGAACTGAGGCCAGGCCC  AGCCTTCACTCCACGCCCAGCCAGCCCCAAGGAACCGACTCCCT  GAGGCTCTATGCTCCCTGCCTCCAGTGGCCCCGTGTCTGGGAAA  TAGTGGCCCTGGCCTGATGCCCTGACCTGGGCAATCCATCCCCCT  GGTCCTCTCAGCTCCCGGGCCAGGTTTTCTGGGCTACTTTAAC  CAGGGCAAACTCATTCTCGAGTACAAAATAAAAGATTGGAACA  GCATAATCAAATAGGTCATACCCATAAATCAACACATTGTAGCA  CCTATTTTGTGTCTTTTCACTAATCCAAACCATATTTATTGAG  CATCTACTATGTGCCA [G/T] TCTCCAGTAGCCATTCTAGGTGC  AGGGGATACAGCAGAGACCTTGAAAAAGGAACAGTCTCTGATC  TTGCTGAGCTTAGAGTCAAGTGGAGGTGAGGAGGAAGGAAATGA  ATTAACAACCTAAGTGAAGCAGAAGGTAACCAATTGATTGACTGA  CGAAGGGGTACAAACAACAACACCTTCCTTTCTCCAAACTCTA  TCTTTAACTGTATTCTCTCGTTTTCTTCTCTCCATTTTACAA  TCATTTTACAACATCTCTGGCTATTCTCCTATATTTCTGATCAC  TTCGGTTCTCATCAATAATAATTTTCAGTTTCAAGCATTTGGA  AAGTCCCATCCAATTAAAAATGTCAATCTCACACGCAGTTTAAAC  GTTTCGCCTGCCCGTGAGCTCAGACCTGTCTTGGTGCCTCAGTT  CTTGTGTGGAGGGGAGGAGAGGAGAGGGGAGGGGAGGAGAGGAA  AGGAGACCGGGGAGGTGGGGGGGGAGAGGGGAGGGGA </p>	
KCP_1303 09	<p> CTATCTTTAACTGTATTCTCTCGTTTTCTTCTCTCCATTTTA  CAATCATTTTACAACATCTCTGGCTATTCTCCTATATTTCTGAT  CACTTCGGTTCTCATCACAATAATAATTTTCAGTTTCAAGCATT  GGAAAGTCCCATCCAATTAAAAATGTCAATCTCACACGCAGTTTA  AACGTTTTCGCCTGCCCGTGAGCTCAGACCTGTCTTGGTGCCCTCA  GTTCTTGTGTGGAGGGGAGGAGAGGAGAGGGGAGGGGAGGAGAG  GAAAGGAGACCGGGGAGGTGGGGGGGGAGAGGGGAGGGGAGGAG  AGGGGAGGGGAGTGGGGGAGAAGGGGAGAAAAGCGCAGCTGGCT  TCCTCACTCTCCTTTCTTCTCCTEACCATCCTTACCCTGGCCCAG  GGCAGGAGGAGGATTGGCAGAGTAGA [A/G] GCAGGGTCTTCTG  TCTTAGCTGGGCCCTGTGGTGACTTTCTGTTGGCCAACATGGGC  TGACTGGAATGTTCTCCAGCATGGCACATGGTCATCCAGATGCA  GGCTCTTCCCTGGGGCACTATAGCAGAGAGGGCTCTCTTCCAGT  CTATTGCAGATGGATGCCCTCGTGAGCTGAGTTTGTGATGAACAT  CCCATGTCCCCAGCCACCCCATTCAGAGCCTCTTTCTACTCTGG  TCCTCTGGTCCCAGCAGCAGCCCTCTGGGTAAGAGGGGAGGGC  ATCTCACCCAAGCCCCTTAAACCTGCTCACCTTCTTCAGAGCCC  ACGTGGCCCGCAGGAAAGTCACAAACCTTGTGCTCCACAGGGC  ACACGTGTGCACACGTGTGCAGCTACCTTCTCTCTAGTTGGTAC  CTGAGGCTGCCTCCTGGATTTTCCAGTCTCTGTGTTCACAGACA  ACCCAAGCCCCAAGAATACAA </p>	SEQ ID NO. 168
KCP_1305 57	<p> AGTTTAAACGTTTTCGCCTGCCCGTGAGCTCAGACCTGTCTTGGT  GCCCTCAGTTCTTGTGTGGAGGGGAGGAGAGGAGAGGGGAGGGGA  GGAGAGGAAAGGAGACCGGGGAGGTGGGGGGGGAGAGGGGAGGG  GAGGAGAGGGGAGGGGAGTGGGGGAGAAGGGGAGAAAAGCGCAG  CTGGCTTCTCACTCTCCTTTCTTCTCCTCACCATCCTTACCCTG  GCCCAGGGCAGGAGGAGGATTGGCAGAGTAGAGGCAGGGTCTTC  TGTCTTAGCTGGGCCCTGTGGTGACTTTCTGTTGGCCAACATGG  GCTGACTGGAATGTTCTCCAGCATGGCACATGGTCATCCAGATG  CAGGCTCTTCCCTGGGGCACTATAGCAGAGAGGGCTCTCTTCCA  GTCTATTGCAGATGGATGCCCTCGTGAGCTGAGTTTGTGATGAAC  ATCCCATGTCCCCAGCCACCCCATTCAGAGCCTCTTTCTACTCT  GGTCCTCTGGTCCCAG [C/G] AGCAGCCCTCTGGGTAAGAGGG  GAGGGCATCTCACCCAAGCCCCTTAAACCTGCTCACCTTCTTCA  GAGCCACGTGGCCCGCAGGAAAGTCACAAACCTTGTGCTCCCA  CAGGGCACACGTGTGCACACGTGTGCAGCTACCTTCTCTCTAGT  TGGTACCTGAGGCTGCCTCCTGGATTTTCCAGTCTCTGTGTTC </p>	SEQ ID NO. 169

	CAGACAACCCCAAGCCCCAAGAATACAAGAGCTCTGTACCAAG CATCGGGCCTGTGGCTGCACTACACGTCTGCAGCTCAGGACCCC TGGCTGCGGCGTAAGCTACCAGCATCCCCTTCTCATGGGCACCC TCATCTCCGGCTCCCCATCGCTGGGCTGTGACCTGCGGGGCGC CCCTCTATGGAAGGGAAGGAGAAAAATTACAGTGTCTACT CCTCTGAATGCACTCCCAACCAATTTCTTGGAAATTTCTAGCTT TCACTGACATATCTGGGATGGGGCGGTGGTCACAAAA	
KCP_1312 44	GTCTCTGTGTTCCAGACAACCCCAAGCCCCAAGAATACAAGAG CTCTGTACCAAGCATCGGGCCTGTGGCTGCACTACACGTCTGC AGCTCAGGACCCCTGGCTGCGGCGTAAGCTACCAGCATCCCCTT CTCATGGGCACCCCTCATCTCCGGCTCCCCATCGCTGGGCTGTGA CCTGCGGGGGCGCCCCCTCTATGGAAGGGAAGGAGAAAAATTCAC AGTGCTATCTACTCCTCTGAATGCACTCCCAACCAATTTCTTGG AAATTTCTAGCTTTCAGTGACATATCTGGGATGGGGCGGTGGTC ACAAAATCAATCCCACTTTCCTCGGCTAGTCTTACAAGCACCC AACAGCTCTATTGAGAATACAGGGCTGCCAGCTACTTCCCAT CATTATCCCCAGGTTGCAAGCTTTAGTCAAAACCCAGAGGCAGC AGGGTGCTGGTTCCACCTGCTGTTAGGATGATTTAGGAGTGC AAAGTGTTAGAAACGC [A/G] GTAAAACATGATGCTTAGAGATT AAGTGGGATGGGGACTGGGCAGATGATGCTGCTTTGGACCCAGC GAGTGAGGTGAGACTGCGACAAGACAGAGCCACTGAGCAGTGAC CTGGGGGATGGGCATTGCAGGCAAGGCAGAACCCCAAGTGGGAA CAACCTCACTGGGCTTAGCAAACTAAAGAGGCCCAAGTATAC TGAGCGATGAGGTGAGTGGCGTGGGATAAGGTTGGAGAGGAGGC TGGAACCAGACCCCTGCAGGGCCTTGCAGGTGATGGGAAGGAGTT TGGAAGGTGCTGGAAGGTTTGAAGCAGAGGAGGGATATGATCAT GCCTGTAGCTGCTATGTAGAACAACCTGTATGCATGCCAGGCCTG TGCCACGCATGCTCTAATCATTACTGGCTTTAACCCTTGCACTA ACGTTGTATGCAGGTAGGAGCATCTGCACCCAGCAAATGGAAA CTGAAGCTCAGGAATATTAGTCACTTGTCCAAGGCT	SEQ ID NO. 170
KCP_1318 54	ACCTGGGGGATGGGCATTGCAGGCAAGGCAGAACCCCAAGTGGG AACAACTCACTGGGCTTAGCAAACTAAAGAGGCCCAAGTAT ACTGAGCGATGAGGTGAGTGGCGTGGGATAAGGTTGGAGAGGAG GCTGGAACCAGACCCCTGCAGGGCCTTGCAGGTGATGGGAAGGAG TTTGGAAAGGTGCTGGAAGGTTTGAAGCAGAGGAGGGATATGATC ATGCCTGTAGCTGCTATGTAGAACAACCTGTATGCATGCCAGGCC TGTGCCACGCATGCTCTAATCATTACTGGCTTTAACCCTTGAC TAACGTTGTATGCAGGTAGGAGCATCTGCACCCAGCAAATGGA AACTGAAGCTCAGGAATATTAGTCACTTGTCCAAGGCTCCCCA GCTGTTAGGTGCTAAGGCTGGATTCAATCCAGGACTTGCAGACT CCAGTATCTTGGCTTTTCTAACGAGAGTGTGCTAGCTTTCTAAT GGGGGTGGGGAAGGCA [G/T] TCTGCCCCCTCCCATGGCACCG TGAGCAGGTGTCACTGCTCCAGCCAGTACGCCCTGGACACCGACT AGGAAGGAGTATGTGCTACTAGGAGGGATGGTCTGGGCTGACTC TTTGAAGTTGACAAGGAGTTGCATAATCCCAGCTAATAATTATG CTGGACCAGGGGCAGAGACATTACTCCAAGGTTGACCAGGTGTG GAGAAGAGGCTGCTGACTCCGGGGCCCCAGGACCTGGCCCCCAG GTCTCATTGCCCCAGTGCTGCCCCAGAAGGAGTAGAAGCTGGAG CTGTCCGGGCCACAGCCGAGGCTGGGTGAATGCTGCAGTGAGGC TGCCGCACAAGTTGCGTGTGTGACATTTGTCTTCTGGAGGGGA TTGGGATGGGCTACTTCAGCATTTAAAAACCCCTACTAGGTCTG AGAAATCCCCTCAGCTTATGAGCCTGGGTGGGCAGCAGGCCTTC TCAAGAAGGCCAGAAAGGCCAGATGCTCACTTCCAGG	SEQ ID NO. 171
KCP_1326 77	CAGTGAGGCTGCCGCACAAGTTGCGTGTGTGACATTTGTCTTC TGGAGGGGATTGGGATGGGCTACTTCAGCATTTAAAAACCCCTA CTAGGTCTGAGAAATCCCCTCAGCTTATGAGCCTGGGTGGGCAG CAGGCCTTCTCAAGAAGCCCAGAAGGCCAGATGCTCACTTCCCA	SEQ ID NO. 172

	GGCTCTCTTGCGGCTGAGCTGAGAGCAGGCACCTGAGGCCTGGC AAGTGTGACAGCTGGTGACACAGACAGACAGGGACAGGGAGATG GGACTGTGCCTGCAGCGGTAGCCCTGGCCGGTGTTCAGTGGGGC CAGCATCCGTGTCTTTCTGCGGGCCAGTGGGGGCCGTGGCTCT GACGATGCATCCCTCCCCACGTTTTTCTCTTCTTGTCTTGGA CTTTGCAGGGAGCACTCTGCTTTTGGGAACAGGAGCTGGGTCTC TGGCCATTCTCCGCAGCCCCCTACCATTCACTCAGTGGCTCTCA AAAAATAGAACCTGGG [A/G] CAAAGCTGTTCTTGGCCCCAAAC AACATGAGGAAAAATAAATAAATAATGTACCTGGTAACCTGAGAG AGTTCCCTCTGCATCTTGGGCTCTTTCAATGAGATGTCTCTGTC CTGCAGCAAGCCCCAAGGGCTTCCCTCACCAGGACCAGCACCCCT GGTTTGCCTGACCCACACCTGCCAATGCCGGGGCAAGAATGTC CCAGGCTGCCCTGGTTCCCAGAGCTGATGCTTCCCACAGTGCCC AGCTGTGCTGGCATGGAGCTAAGGACAGGGCCAGTCCCAAGAAA ACAACAAGGCTCCAGGGCCACCGGCCACTGCTCAGGACCCCTGGC TGACCCACAGATGCGGAGTGCCTGAGATGGCTCATGGGTGACC CCCAGGCATCTGGCAAAGGTCACAATGGCTGTTTGGCTTGAAGA CAGCCCTTGCAAGATCTGTTTTGAGCCAACCTGTGGCATTTAGC CCTCCCTGGGTGACAAATAAAAAGGCTGAGGCTTGTA	
KCP_1340 45	ATTGGAAGATAAGAATGCAGCCAAAGAGGTCTTCAGGGTAGCGT GTGGCCTGGGCGCTGAGACTATTGGGCCTAGCAACTTCTCAAGC AGTCTATTAACACAGCCGGTAGCCAGCTTTTCCCCGCCCTTCT CCCAGGCACACACAGCCACCTCCATCACCAAAGGTGAGGCGAAC CACCTCCCATGGCTACCCCCAGCCTGACTTGCTTTATAGAAATC ATGGCATCTCATCTCACAAACAGCCCACTCAGAGTGAATCTT GGCCATTATGACAACTGGGGACACTGAGGCTCGGAGTGGTGGA ATTCTCAGAAATCACATAACAATAAGTGTTAAAGTCAGAAATTTCA ACTTCATCTCTTAACCTCAAAGGGCGTGTGTGTGTGTGCGT TTCTGGCCATAATCATATTGTGCCCTACAAGCCCCAGTGAGGAA TCTGCTAGGAACACTGGTTTGGGGAAAAAATGTAATAAAATATG TGATCCAGAAGGCGGC [C/T] TTGGTACCTGTCATAAACCGCAG CATGGGGTACTCACTATGCCTGGGGTCTGGGCTCTGAAGGCATG ATTGAATGATCTCACTGCAGGCCTGGTTGTCTGCGAAGACACC CGTCAATACATGAATATTGACACACAACGCTGCAGTGACGCGC TTCTGGCAGGGGAGCTGCTGCACTCGAGGGCAGCTCAAGGTTAA TTTGCAGGGTTTCATGTTTGGAGTTTCTGAGCAAGTGTGTCAGCT TTGGCCCCCAGCCCCCTGAGGGGAGCTCTGCCCCGTGCATGAGGG TCAGACAGAAAAATCTCCTTTCTCCATCCAGGCCTGCAGTCTGC AGCACTGAGGTGAGCGCTGGCCACAAGCCCCACCTGTGCCTCGT CAGCCCCACTGAGCCTCTCCATCTATCATGCCACAGGCTGACCC TGAAATGCAAAATCATTCTGTCTCCCGCCCTCCACTCCACCT CGCACATCTATGGATTGTGCTGTTGAGAAAACATCTGT	SEQ ID NO. 173
KCP_1355 18	AGTTAGATTGAGCTGGGTCCCCTCTTGGGCCTTTGCTGGTCCCT CCCTAGAAAGTCTGCCCCCTCCCCCTGCAGGGTGGCATCAGCAT TCAGGCCTGGCCCTGACGCCCTCCTCTCTGGGCCACCTTCACCT CCACAACCCCGGCACCAGCACCCATCCCCACCACATCCCCAGCA CGCAGCATCTAGTAAGGGCACCAAATGCATGCCAGACATATGA GTGAAATGAATTAACCCTGAACCTGAAAAAGGGCAACCACCACA CAAGATTCTCTAGAAACAATGTGAATTGTGCAGAAGGAAATTAA CCCTACTCCATCCAGCCCCTCCTAAGGCAGGGACTTGACCTGT TCCTCTTGATGGGGCTGGGGCTGAGGCGGGCAAGGCAGGCAAGT GCTGAACAGTTGGCAACATTGCCCATCCCGTCTCCCTGCACCAG GCTGGGCCCTGGGGTGAAGGGGTGGGGGCCGGGGTAGCTGGGCTC CTCCAGCAAAGAGCAG [G/T] ACTGAGTCCCTGGTGAATATTAG GTAAAAGGTCCCTGACAATTTTGAAGGGGCCAGATGCCAACTCGA GGGATACAGAGAAGATCTAGGCACAGTCTTTCCCCACCATGTCA GACAAAAGGTTAGATACAGGACCTGATATGTTATAAAACTCAA	SEQ ID NO. 174

	TCAATATTTACTTAGTGAATAAATGGACGGATGGATGGATGGAT GCATTAGGCAGCCAAGTGGGCAGCACCGATGACTTAATGTACTG AGTGCTCCGACTCCAGCAACATGCATTTCATTGTTCTACTGTGT GCCAGTGAACAAGAGCAATGAACTCAATGACTTCTGCCCAGGGT GGGCCAGGGAACCAGGGAAGACTCTCCAAAAGGCAGCATTG GCTGGGACGTACAGATGAGTAGGGGGTCGAGTGTGTCTGTTATGT CGCTGGAGCCCAGAGGCGTCCATCAGGACTTGGGGGAGGGCAGA TGAAAGGGCCTTACTGCCTAACTTGGAGCCACTGTAT	
KCP_1360 36	CCCATCTTGGGCCTTGTCTGGTCCCTCCCTAGAAAGTCTGCCCC CTCCCCCTGCAGGGTGGCATCAGCAATTCAGGCCTGGCCCTGACG CCCTCCTCTCTGGGCCACCTTCACCTCCACAACCCCGGCACCAG CACCCATCCCCACCACATCCCCAGCACGCAGCATCTAGTAAGGG CACCAAATGCATGCCAGACATATGAGTGAAATGAATTAACCCT GAACCTGAAAAGGGCAACCACCACACAAGATTCTCTAGAAACA ATGTGAATTGTGCAGAAGGAAATTAACCCCTACTCCATCCAGCCC ATCCTAAGGCAGGGACTTGGACCTGTTCTCTTGATGGGGCTGG GGCTGAGGCGGGCAAGGCAGGCAAGTGCTGAACAGTTGGCAACA TTGCCCATCCCGTCTCCCTGCACCAAGGCTGGGCCTGGGGTGAGG GGGTGGGGGCCGGGGTAGCTGGGCTCCTCCAGCAAAGAGCAGGA CTGAGTCCCTGGTGACTATTAGGTAAAAGGTCCCTGACAATTTT GAGGGGCCAGATGCCAACTCGAGGGATACAGAGAAGATCTAGGC ACAGTCTTTCCCCACCATGTGAGACAAAAGGTTAGATACAGGA CCTGATATGTTATAAACTCAATCAATATTTACTTAGTGAATAA ATGGACGGATGGATGGATGGATGCATTAGGCAGCCAAGTGGGCA GCACCGATGACTTAATGTACTGAGTGCTCCGACTCCAGCAACAT GCATTTCATTGTTCTTACTGTGTGCCAGTGAACAAGAGCAATGAA CTCAATGACTTCTGCCCAGGGTGGGCCAGGGAACCAGGGAAGAC TCTCCAAAAGGCAGCATTTGGGCTGGGACGTACAGATGAGTAG GGGGTCGAGTGTGTCTGTTATGTCTGCTGGAGCCCAGAGGCGTCCA TCAGGACTTGGGGGAGGGCAGATGAAAGGGCCTTACTGCCTAAC TTGGAGCCACTGTATGTTTCAAACAAAGGAG [A/C] GAGAGGA TCCTGGGAAAGAGAAAGGGTACTCTAGGCAGAGGATGTGAATGG GCACAGCACAGGTGAGAACATCAAGACCAGGGGTCAGGGAATCT ACTGGTAAACAATTGTACCCCAAGGGAGCAATCACAGCCTCTCC ATCCACAGGGAAATGCCTGGTGGGGAGGAATGGGAGGAAAGAAA CAGATTGCATGACTGTGTCTTGAAGGTCTAATTCCAGAGTACAG CATCACCCCTATCTTCCAGGTCCAGAACTGAGGCTCAGAGGGA GACTTTCTGATGAGTGCAGCGTGCAGATAAGAGCATCTCCAAAG CTACCTCCTTCCCCAGTCAACCAGGGCATAAGCAACTGATAAC AGCTGTTCAGCACGGGACAGTGGAGGGAACTAGGTTAGGAATA AGGGTACGAGGCTTGAGTACAGATTGTCAATGACTCAGTGTGTG AACTTGCTCAGGTGACTCCAACCAGATGACTTCTTCTCTGAGC TTCTGTTCCCTCCTCTATGAATGGGGACAATCACTCAGCTTCAC AAAACAATGGCTGCGAAATTGCCTGGTACAAGAGAGAGAACTTC CAGTGTGTAGGGGCTGTTGTCTTAAGTCCCAGCCCCCTAGATA GGTAGTTATGTCATCTGTGAAATGGGTGTTAGAATTCCTACCTC CCAGGACAGCTGTGGGCAGAAAACCAAGAATGTGTGTGAGAGC CCAAGCACCATGCCTGGCACATAGTAGGTGCTCAGGAAAGGCTG AGGGTGACGCTGCTGTCCACACACATGGTACCACTGCCCCAGGA AGGGGCTTCAGGAACCAAGAGCAATTCTGAGCACTGGTGACTGG ACTCTGCCATTCTCCATTTCAAACGCTTTTTGAAAGCAGCTCCA GACCAAGCAGGAGAGCAGGAGGCAAAAGAAACGCAGGGGCTTT CCCGAATGGAATTTTAGAAACACACAGAATTGTCTCCTGCACAG AAGGGAAGCTGTCTCCACAGCACA	SEQ ID NO. 175
KCP_1376 60	CACTGGAGCTGAGACTCCCAGGTCCCCTAGGGCTTCTCTCCAG GGGCCTCTGGGCTCCCCAAGGCCACGTGCTGCCCCACTAGAGA CCTGGGCCAGTCCTGACCAGGGGAAAGAGTAGCGCCGACAACAG	SEQ ID NO. 176



	<p>CCCCAGATGGTATGTGCACTGGCACATACTGGCAGCTGCCTTCA  TGACAGCAAGCCATAGGTCCAAATCCCGCCCTTCACAGGGACA  TCCCCAAGTGGTCAGGGGTGGACCTCCCTTCCCGCTGTCTTT  GGTGTCCAGGACGATTTGCCACAGACAGGGGGAGCTAAAGGGGC  CCACGCTTGAGGCCGCTCAGCTCTGAGTCCTCGCCGGCCACAGA  GGACCTTCGTGCCTGTCTCTGTCTCTGCCCAGTCCCCAGGC  CAGGCTCAGCTGGAGTTGGGGAGCAGAAAAACACGCATCTGAAT  CAAGGCTCTCGGAGCCTTTGCTTCTGCCTCCAAGAGGCGAGGGA  AAATGAATAACCCAGGC [A/G] AGCGAGCAAGAGAGACCCCTCAGA  AAACCCAGATGCCCCTGGAATCAAGCCCTGTCCACCAACGCC  ACGTGGATTGACAGGCTATTAGTCTTCTGTAAATTAGGATTCTC  GCCTCAAATCTTGTATCTTTTTCCCCAGAAGATTCTCCTCCAG  CCTTCACCACTGCCCCCTGGCGCTTCTTGCAAGGCTTTTGAAG  AATCCTTTGCAGAGAAGCAGCCTCCTTTGGCAGGGGGCTGCAGAG  CACTCTGCCTCCCTAGGCCAGGGCGAACCAACAGAGGCGGGAGA  TGAGGAGGAGCAGCGCGCTCTGCTGCGTGGCCCTGGGCAAGCA  CCACAACCTCTCTGGGCGCTTTGCACATTCTTACCGCCAGGGAT  GTGGGCGGTAAATGAAAGAGACCAGCACAAACAGTGTACGCTC  CCTTCCTCGATTCTTAAATGTGATGCCAAAGATGGGCCAGCC  TCCTGCTGTGCCTTCTCTGGGGGGACATTAAATAAGT</p>	
KCP_1436 12	<p>TGGCCGCCTCTTCCAGATAACAACCTCTCCTCTCCTTCCCTGCCC  TCCTGCTCCTCCTGTTTCGCGCTACATAACAGACTCTGTGGGGCC  TTGGTTTATGTATTTCTTCTCTCCCCTACTGAAATACATGTGA  GCGATGCTGGGGCAGGCCGACTAGAAGAAGCAGACTATCTGCTT  CTTCTCCACCTTAGAATGGTGCTGGGCCAGAAAGAGGCATGCA  GTCGATATTTGCTGAATAAATGAATGTGAGATAAAGTGGTGTGG  GGACTCCAGGGGAAAGATTTGTCACTTCTCCACCCTCCCAGTTCA  GCTTAAAGCAGAGAAGTGAGAGGTGCCAAAAAGGGGTGTGTCT  GGGGGGTGGGGGTGGGGATGTTCCAAGATCTCCAAGGCCTGGA  TTTTAAGCAAGGTTTGAGATGCCAGCAAGAGGGCCTGGCATTGC  CAGATTGATAGTCTGCATTTCCAGAGAAGGACAACCCACCTCTG  ACCTTAGCCC [A/G] AGCCTCAACAGCCTGCTCAAGGAGATCCA  CCCTTAGTAGGAGGAGGCAGCCAGGCCAGGTTCCAGTCCCTGCC  ACCGCTTGCCAGGTGTGTCTTGGGCAGCAGTTGCCTTTGCTCGG  TGGTCTTCAGCTTTGCCCCCTGCCAGGCAGTGCTGGCCTCCTG  CCTGCATCGTAGCTCATGGAGTCTCTCAGTCACCTCTGTATGC  CCTGCAGCATCCCCAGTTCTCAGTGAGAAGAGTGTGCTCTGAAA  GTAAAGTAACTTACCCAAGGTCACACAAGGTCTGAGTCTCAAAT  GCATACAATTTGACCCCATAGTCTAAGGTCTTGACCGCAATGGA  ATAAGAAATTATTTTACCATTCTGAGTGGCAGTCTCTGAAGACT  ACAGCAATAATTGATGCCTCTCAGGGGATAGGTGTGTCACTTA  CAGGTGATAGTGAGGTTGTCTCAGCCTCCCTGCTCTTCGTTAG  ACCTCCCTCCTCTCTTACCCGGGCCAAGCGT</p>	SEQ ID NO. 177
KCP_1449 60	<p>GCGGAACACCTCTGCCGCACCTGCAGCAGCCTTGCTCTATTTCT  TCACAAGCTTCCCCATGACACTGACCCAAGGCTGTCTGGCCACT  ACAGCTGCTGATGATGATTAGCAATAATAATAATAAACGAA  ATGCCTTCTGCTTAGATCATCTTTAATTTCCCCTCCAGAATGAC  ATTCGACTCTGCTTAGAGTTACAGGCAGCCCAGCAATTACTGAG  CGCAAATACCGTGTTCAACCGCCTCACCTCATCCAGCCCCCAC  AACACCCAGCCCTGAGACTGGCTCCACGATCACCTCCACTTTAT  AAAATAAGATATCAAACCTCTGAACAGAACGGACGTCTCAAAAA  TGGGCATATTACATTTAAACCCCTCAATCTGTTGGGTATTTGAGT  GAAATGGACATACCTCCAGGGAGTCGGTGGCGAGGGCCGGCTCT  GAGGACTTCTGGGTGGGATCCTGGCTCTGCAGGACTGCGTGA  CCTTGGTGAGTTACTT [C/T] ATCCCTCCAAACGCGCTGTTCTC  CTTCATAGAATGGAGATGACCACAGGGCCAGATTCATAAGGTTG  TTCCTTGTAATACAGGTGAATATCCATACCCAGCAACTGCTGGA</p>	SEQ ID NO. 178

	CCACCTGTGGTTTTCAAGGATAATTTCCCTCCCACGTCCCCGTGG CCCTTGGAACCTTCCTCTCCTCCTGTCTCCCCCTGCCCCCATCA CTTTGTAATTGAAAAGTCATGATTGCTCTCCCAGGTGTAGCACT GCTCACAGGTCAGATTGCCTGCTCTGACGTAGTGACTCAGTTGG ATGCGGTTTCAGCTGTGTATGATCAACTCCCTCCCCCTGACAAAA ACATTATTTTGCATCACAGAGAAGTTGATTCTTTTACACATAA AAGAAGGCAAAAAGTGGTGCCTAAAGGGCTGGTACAGCAGCTTC AAGAAATCAGGAAGAACCTGGGCTCCTTCTGCCTTCTTGTTCTG CCAATATCACCCCATGGCTGCCACTTCATGGCCCAAG	
KCP_1467 46	TTGTGAGTAGGGCACGCAGGGAAGAAACCTGTTCAACCCAGCCC CGTGCTAGAAAGACATCAGCAGGGCCTGCAAAAGCCCTGATTAA ATCTCACAAGTTTGCACCTGGAGCCGCCATCTTGAATTGCAGGT GAATATCAGCCTTTGGTTTGGGCTGTGTGCCCCAGATGATGGTG GTCCCAAATTACATAGGCCAATATCCAGAGCTGGGTTAAAATGA AGCATTTCGAGGAAAAAATGCAATGAAATTTGTTTAAACCGGTA CTTCAGGCCTTTTGAGCACAGAACAGCGTCCATCCCTCCAAACAC ACACTGAGGATATACACTTAGCCAGGAGGGAACATAAGGAGGGG TGGACAAGCCATGTTTACTAAAATCTCTCAGTGTGTGCCAGGCA TGTTTCATGTATATTAGGAAGAAGTGTGAGTATTTAAGATCCTC GGCCCTTGCCCGAGTCCCAACACGCCTTCTTGTCTGGAGAAGT GTAAATCTTGGAACATCTTGCAAGGGGGGACACCTCACAGAAG GCAGGCTTGGCATGGGATAAACAGAATCGACTCCTCTGCTTCCT TCTGATGCACAGTGAATGGGCAGGTGGAAGCATCGTTGCTTAAA GAGGAACCAAACTCCACCCAGAGCTGCTAATTCCTTTTGGCT TGCAGTTATGCAGAGGGCTAAAAAATCCAACGAATCAAAATCC CCTGGTTGCTAAGTAGAAAGAATATGTTTTGGCTGCTGCTGTTT CCTTCCCAAGGAAAAGATTCAAGCAGAGGGGTCCTCCACCTCT CAACACAGAAAGCAACATCTCTGATTGCCTCTAGACACACCTTC ATGCTCGTGGCACCTTTGGGACCCTCTGCCCCGCTGGCTTATGGG ATGGCTTCCCCATCACTCTGGGTCTTGGGAAGAGCCTCTTTCC CAGACCCACCTCTGTGCCTCATCACATTTCTCCAGGCTATTG ACTTGTTCAAGGTTAAGGTATGAAGAGAGTCA [C/T] GCAGCAG CCCTACCTGGCTCTGCTCTGCTGGGGGAAGCCTTTTCAGAGCCT GCCTCTTCTCAGCATGAGGGGCTGCTCGGGCCAGTCCCAGAG GCCATGCTGGTCCCAGGGGAAGGTGGCCGTCATCCCCATCTGTG TTTTCTCTTGCAGGTAAGTCATGCTCCAGCAGTCGGGAGGGTTG TGTGATGACACACTTGGCAGTTTGGGAGCAAAAGCCGCCACAGT AAGACACAATTGATTCAATTGCCTCTCAACCTCTGCTGGGGTGG ACTTTCATGCGTGGACTTCTGTCCCCAAGAGGCTTCTCTGGGT CTGGAAAGGGCCCTAGCCTTGGTTGGGGGAGGCAAAGGGGTGGC GGCTTCCAGGTACCATCTGGCCAGGAACCGGCTCCATTGTCTGT GCATGTAGCTTGCACCTGGGCTGCCTGCTCCAAGGAGGCATCTC CCCACGATCTACGACATTGGCTTCAAAGAGCTGCTCCTGGCAGC TTCGAATGGCTGAGACCTACTGGCATGGGATGGAGGAGTGCAGG GAGCTTCCCGGGACCTCGCTAGTCTGCTGCTGGATGCTCAGAAGG CCCTCGTCTCGGTGGCATGCAGCCTCGGCCATTTCCAAACTCA CGGCATCTCACCCAGCCATGTCAACCCACCCCGGCTCTGTGCCC CTTCCCATCACCTTTCTCCCACCCATCACCTCACATCAAGGTTT CAGCCAGCGGGAACCAGGTTTAGACTCCAATTACCTGTGCGTGT GGGAGGTTGGATTGTGACATCTTTGGAGGGCCGGGCTTCTGAAG CGACATTTGATTTCTGGTACTGAAATGTCAAAGGGTCTTGAGGC ACCCGCTAGGGCAGCACGCGGAGCATCCACCTGCGTGCAGCATCC TGGGCTCTCTGCGGCCACTTGGTGTGCTGGGGACATGCCGGGAGC TGGTGGTCAGCCCTCCTCCTGCCTCCTCAGTGTGCTGCTCTCAC CTTCTGCAGCTGCCTACCAGAAGCA	SEQ ID NO. 179
KCP_1492 16	ACACCTTGACTTTAGCCAGTGCAACTGACTCCACATTTCTGGC TCCAGAAGTGAAGAGAATACATTTGTGTTTTGTTAAGCTAGCA	SEQ ID NO. 180

	AATTTGCAGTAATTTATGACAGCGCTATGAGAAACCAAAACACC AGGATTATGCCCCAAGGATCCTGATGCCCTCCCTCCTCTGCT CTGCAGTGTGCTGGAGCTCACAGGGCTCTGCTGCTGGGAGTTAG TATCTAGTCCAACACTTTACCCACTCACCCCCAAGCTAAGGGA CTCCTGAAATCAGGGACCAGATGCATAATAGGTGCCCAGGAAGT GAGACTCGCCTTCCCCAGATTAGAATAAAGAAGACAACTATC CACGGCTGCTGTGAGCCTCTCATCAGACCTCAGCTTCTAGGGCA GGGTCCCTGCCTGTCTCCAGTATGTGGCCTCTGTGTCTTCTTCG CCCTCCATCCCCACAGTGGGACGAGAAGTCATCAGGAAGGCAGG GGATCTGCAGGCAGCC [A/G] TCAGGGCTCTAATTGCAGCTGGC TGGGGGACCATGGGTGAGGGCTGCCACCCCTGGCTCTGTGCCT TCACCTGTGTAACGAATGGGGCACTCACAGCCCCCTCTCAAGTGG TCCTGGGGATGAAGTGAGAAGGTGACATATACAAGTGAGTTATA CACGTTCTGTCTGTCACTCACCAGTGCTCACTGGGTGGGTCA CTGAACTCCCTCAGCGTTTCTTCTCCATCTGTAAACCACCAG TGCAAACCTTTCCAGATAGTGCTGACCCGAAGCAGGAACCAGT GCCCCCTCTGCCCTCAGTAAGTCTGCCAGCAGAGGAAGCCCATAG AGGGTCTTGGGAAATGAAGCCAACAGAGTCAAGAGGGTCAGATG ATGAGGGACTTCAAGTGCCACCTTCATCCCATTCTTTCTGCAA TATTCACCACACACCTACGTGACCTCAGGCTCTGTGTGTCAGGTCC TGGGGATGTAATGGTGTCCATGAAGAAACAAGGTCCC	
KCP_1495 35	TCCCCAGATTAGAATAAAGAAGACAACTATCCACGGCTGCTG TGAGCCTCTCATCAGACCTCAGCTTCTAGGGCAGGGTCCCTGCC TGTCTCCAGTATGTGGCCTCTGTGTCTTCTTCGCCCTCCATCCC CACAGTGGGACGAGAAGTCATCAGGAAGGCAGGGGATCTGCAGG CAGCCATCAGGGCTCTAATTGCAGCTGGCTGGGGGACCATGGGT CAGGGCTGCCACCCCTGGCTCTGTGCCTTCACCTGTGTAACGA ATGGGGCACTCACAGCCCCCTCTCAAGTGGTCTGGGGATGAAGT GAGAAGGTGACATATACAAGTGAGTTATACAGTTCTCTGTCTG TCACTCACCAGTGCTCACTGGGTGGGTCACTGAACTCCCTCAG CGTTCTCTTCTCCATCTGTAAACCACCAGTGCAAACCTTTCCCA GATAGTGCTGACCCGAAGCAGGAACCAGTGCCCTCTGCCCTCA GTAAGTCTGCCAGCAG [A/G] GGAAGCCCATAGAGGTCTTGGG AAATGAAGCCAACAGAGTCAAGAGGGTCAGATGATGAGGGACTT CAAGTGCCACCTTCATCCCATTCTTTCTGCAAATATTCACCACA CACCTACGTGACCTCAGGCTCTGTGTGTCAGGTCTGGGGATGTAA TGGTGTCCATGAAGAAACAAGGTCCCTGCCCTCATAGAGTGGCC TGACATATGCCCAGGCAGTCAGCAGCCGAGTGCGGGAGACTCT TGAGCAGAGATTGAGTGTGTTGATATCTGTAGGCATCAGCCTGG CTTTGCTGAGTGAGCTATATCAGAGTGGAGGAGCCAGAGGCAA AGTCCAGACTCCACTGGATCCTGGATTGAGGGGAGAAGGGGCTG GGCGGAGGAGCAGCCTGAGCACCTGCATCTCACTCCAAGTGGGT GCTGATTTGTCCCCATGGCCCCAGCACCCAGGCAGGTACCAAG TAAGCTCAAGACAAAATGATGAGTGACTCAACAGTG	SEQ ID NO. 181
KCP_1567 32	ATAAATTGGATTTTCATCAAAAATTTAACTTCTGCTCCAAAAGA CACTCTTAACAAAGGGGAAAAGCAAGCCACAATATGAGAGGAAA TATTTGCAAAGCATCTGATAAAACATGTGGATCTAAAATATGCA AGGAGAATAACAACCTTATTTTCCACTAAGGAATGAATGACTGT ACAAGGACCACATTCTAATTAGGAGCTTCTGAACCCAAAGGAAT TTCAGATAAGGGGAAATTTAGGCCCAAAGCCAGGAGAAGGGGTG AGTAGGGCTTGATCTCTGCCTCTGAAGGGCAGAGGGCGTGGACT ATTCTTGGCTCTTAGGGGACAGCTAGAGAAATGTGGGTCTCATG GCGACAACCTCTGGACTCCATTGGAAGAACCTTCTAACAGTCAGG GCTCCCAGAGATAAAC TAGACAAGTCACCAAGAGAGGCAGTGGG TACCCCTCACAGGAGGGGTGCAAATCAAAGCCAAGGCTTGGAGT GGACCATATTAAATCC [A/T] TTTCTTATCCTGTGATTCTTAGA GTCCTATCTGTATCAGGGGAAGGCAGGTGGGTCTAGAACTTTC	SEQ ID NO. 182

	TAAATGTGTCCCTGTGGGTTTTCTTCTCCAGCTACACACAAA CTTGGGCCTAATAAGAAGTCTATGGCATTAAACCAGCAGGAATG CTTAATGCTTATATCTGACCTCAAACCAAGACTGTCTCCACAGT GAACAACCCCGTCTGTCCCCTGGGCGTCTCCTTAGCAAATGCC ATCAGTCAATGGTGCAGCCATCTTGGAGCCCTTGCCATCTATAA TCTTCTACCGCCACCCCCCAGCTGATTGTTTTCTTTGTATGTC TCCTTCCTGGACATTACTTATTCTTTACTTTTAAATATTTGCTT CCGTAAAAAACAATGAATGCCTCGGACAGATTTATAAAGAAC ATTCTGGAGAGGCGGGTGGATTAATTATTACGCATCCCTCTCCC TTTGTAACATTTTATTGTCTCATATGCATTTATATGG	
KCP_1586 17	TTGCCCAAGTGATGTTCCATGTCAGGCTCTAGGGTCCCTGCAGG GACAGAGAGGGACTAACATTTACTTACATGCCTATAGTATGTCA GGCATATACTTGTGCCTTTATATATATCAGCTCTGTTTTTGTCA TTAAAACATCCCTGTAGAAAGATAGGCACTGCTGTCCCATTTTA CAGATGGGGAAACCCAAGCTCTGAGTGGTTCAGCAAACCTGGG TGCATACCCCCACCTTGCCCCCTGCAAAACCAAAAAAACGAA GGCCCTGCCTTCCTGGAGCTGACATTTAGGTTGATTCTGAAAGT CAGTAGGCCCAGATTTTCACTCTTCATTTTCTTGTTTGGAATG AGAGAGCACACAGCTGGGTCTGGGGGAAGGAGCGAGGGTCTAGGC CTGCATCCACTCACCCCAAAGGAAAGGAGTAGGGGACCAGTCTG CTGGACATGCAGACAGCGATTGGAGAAAAGTCAGCCCAGCTATG AACCCCATTCCTTTCAGTA [C/T] GAGCCAAGAGGGATGGCATC TGTCAGAGTTGCTGGATTGTTGGGATTTTGATCTTGCCAAGTGTC CATGAGGAATTGGGGAAACTCTCCCCCTGGCTGGACTGAGGCTT CAGCAAGCATTGTTGCTGCCCAGTGGTGATCAGCTCAGTGTCTT TGGAAAAGAGCAGAAAGTGGTATCACGAACATATCTTCTCCTTT GCTTCCTTCTCCTCACTCTTCATCATCATCATCATCATCAT CAAATATGGATCTGTGAGGCTACCTCTGGGGTTGAAACTTGGTT TTGGGCAAAATTTGTGATGTTCTCTCTGCCCAATCCAGCCTCAG GCTACAAATGAATGTAAAAATCTCTAATTTAGTGCCAAGTAACA GAAAACAGCTCTACTTATCTTAAGCCAAAAGAGGGACTTCTCA GAGGCATACTAATGGAGGATGGCAAGAGGGCCTCACGTGGAA	SEQ ID NO. 183
KCP_1601 45	GCTCTTCTGCTGTGGAGGATCCATGCCATTGACCTAGGCACCCG TTTTCCACATATTGAGCATTGCTGAGCACCTATTCTGTGCCAGG CACTGTGCTTCAGGGCCATGGGGGATGCTCCAAGCGGTAAATG CAACCAAAGCCCCGAAGGAGCTCACATTCTAGTCATGTCCACAA AGAGGTAATAAATCCATAAATTTGTATGTACTATTCTAGTCACAA TAAATTTGTGTCGTACTGTAATGCTGGGTATCCATTTTAAACG GGGGGCATCGGCTGAATCTGGGTCAATACAGTAGGAAATGCATA TATATAATCATTTACTCATGAATATTAATGTATTTAATGAGGGT AAAAGATATTACTTAAAGCAAAGTATTCGTTCCAGCTACTGTTG GATTTGTTCACTACTGTTTCCCATGCAGATATTACCTGTGATTT ACCTGCATATCAAGCATCTGGAAGTAGCTCAAATCCACCTGTGG GTAAATTAGGTTAGCC [A/G] TTTGTTGGCAAAAATTACAGTGT TAACTAATTTCCAGGGTATGCTTGCAAGTCAGTAGTTTTCATACTT AGGTACATGACTTGCAATTCACATCATCTGGTTAATGGTGTGAAC AGAGATTTTCTTTATGGTTTTTGGAAATACAGTAAGATAATGTTA AGCTAACGTAAGTCTGTTAACAGTACCTGGTTCTGAACTGTATT TATAAGGTGTATCATAAAACCATTACTTTGGAGTTTGCCAATCT TAAATTCAGAACAAATTCAAAAATGAGCCAGAATCTAGTTTGCAT CATTACCACTTATAAAAATAAGGATCTGTAAGTTGGCTGGATAA AATATATTACAAAATAATGACTTAAGTGGCTCTGGAGCCAGCAC AAAAGATAAAAATTGGGTATACTCAAATACCTTCAAATATC TTAAGTCATTCTTAAATACATGTAAATATGCCAACTCAAATA CATCCAACAAAATAATATTTTTCCCAATTTGTTGGA	SEQ ID NO. 184
KCP_1648	TCGACGTTTCCAAAGTCATGGGGCCTATGGTTTGTGAGCTTATT	SEQ ID

97	<p>TAGGTTGTCCCCGGGCCCAGCATCAAAGCATTGAGACACGTAC  TGAGGGACTCTTTTCTAGCCTCTCAGTCCTGACTGCTCAAGGA  CCAAGTGGTACTTCTTGCTGCGTTCTTTAATGCTTGCCTAAT  ATGAGCTAGTCTTCTCTGATCACTTTTTTTTTTAATCCAAAGTA  GGTGGGCATTGTCCCAAGAGCCTTTGGAAAGCAGCTGCCTCTCA  CTAGGACTTCACAGCATCATTTTGCTTTGCTCTCTTTGTGGTTA  AAATTACCTTCCATTCTGCTGGTGGGTGTATGTCAGGATCCCCACA  AGAAACAGAGGGACACCCAAATTAGGGACATACTTCAGAGGGAC  TAATGACAAAGGCATGGGTGGGAGTAGAGGGGAATACAAGGGAG  ACTTCAAGAACTCTTGGCCTTTATTATAAATGCAATGTATGTCCA  CTATGGAAAATTTGGG [A/G] AAAAAAGCAAAGTAGAAAGAAGA  AAAACCACATGCTTGAATTCCTACTGCATGGAGAGAAGCATCA  TAAACACCTTTTGGAGGAGTCTCTTCTTCTTCTCCCTTTCTC  CTTCTTTGTATAGAGAGGTCTTCTCTGAGGACTTCCAGAATCT  TGCAGATCCAAAATCTTAAGAATTTGCAGAGGCAGTGAGGAGTT  AACATGCACAGCTCAGGGAATATTCTGCTTTTATCTGGAACCA  GGCTCGGAACAAGACTCCTTGCTTTTCTGCTCTGTGTTTTCATC  TTCTCTCAGAACCCTAATTTGAGATAAGATCTTTGACTATTAT  TAGGCGGGTGCAAAGTAATTGTAGTTTTTGGCATTATTTTAA  TAGAACTGCTTCTGTGCTCCTCAGATCTCCATCGTTCATCTCCTG  ATAAGTCCCTGAAAATTTCTGGCCCCCTTGGAGCTCCTTCCAGG  AGTAGAATGATCACAAGAGCTGCCATGTATTGCTTAT</p>	NO. 185
KCP_1692 34	<p>TTGCTTATTCCAACCTTGGACTTGCCGGAGTCCCATAGACAGAGG  CTACTCTCCCACCGTGCTGAAGCTGGTGCATGCCATGTTTCACT  AAGAGAAAGGAGGGTGCCTGGGCTTTCGTCTCCACCCAGGTGCCT  CTCCCCCAGCAGCTGCACCAGGCCAGCTGAGGGGGATTTTAGCC  CGAATCCAGGGTTTCTCCTACAGAAGACAAGGAGTTTGGGCACCT  GCCAGAATTAGAAGAACAGAAAGAAAATGTTCTGGATTCTTCAT  CAAATGCCCCCTAGCCTGAGAAATATAACTAAATTCACCCCTAGG  TCATCTTACAATCTGTCTGCCCCAGTGTTCCCCACTCAGGGAA  CTGCTCCACCCACATCCTGGTCCCCAAACCAGAGGCCTGGGAGT  CACCCCTTGACATTTCCTCCCCTACACCCCTAATCAATCAAAATCC  TGTTTATCCTGCCCCCTGAGAGTCTGCACCGAAATCTCTCTCT  CTCCTTCCACCTACC [A/G] TGGCCCAGCAGCTTTACCATCAT  GTCTCACGGATCTCTGCACCGCTCCCAACTGGCCTGTGCGTTCA  CTCCTGCCCCCTCCTCCAGCCCTGTGTACACTCCCTTCCACCAT  CCTTTCTATACTCTCCTCAATCCTATCTGCACCCCTCCTTCAACC  CTGTCTGTACTCTCCTCCAATCCTGTCCACACACTCCAAACAAA  GTCATATTTCCAAGACAAATTTGACCATGCCACTTTCTCCACA  GCTCTCCACCACCTCCAGGATCCCATCCTCAGTGTTAGCCAGAC  ACTCCCAAGGCCTTGTGATCTGCCCTGCCTATGTCTCCAGCCTC  ATCCTGCAACTCCCCCTACACTCTGTGTTCTGGCCATCAAACCA  ATGGGCTCCTCTTCTGACCCCCATCCACTCTTGACATCCTG  CACTCTATGTCTGAACAGCTCGGTTTCTCTTCTTTCTTCTGGC  ACATGTCTGCTCTACCTGCAGGTCATCTTAGATGTCA</p>	SEQ ID NO. 186
KCP_1738 48	<p>AAAAGGGAATTTATTGGCTCATGTAAGTGAACCTTCAACATTTTA  CAGAATCTCATTGGCTCCAATGGGCTCATACGTCCATCCCCAAA  CCAATCACAGTGACTGAGGGATTATCCAAGGATCACACTGGCCA  CTTTTACAGGTTTTATCCCTAAAGGAAATCACAGGTAATAGATG  TGGGGCTGCAGAAATGCAACATGCACTTTTCTTGAACCTGCAT  CCCTTTTCCCTGAAGATGAAGCTTGAAGAAGTCTAAGAGGTTA  AGCATGGAGCTGATGGGCAAGCCACAGGCAGAAAGAGTAGCTGT  GCAGCCAGGCTCCTGGCCAGGGAGGGCAGATAAGGAGGGGAGGC  AAAGTTTGGTAAACAGGAAGCTAATCTATGGGCAAGAATCATTT  TCTTCAGCATCCTGACCTCTCCTAAAAATGTTCTCCACTGGTCCC  TGCTAGGACAAAGGAATTACCACCAGACTAGAGTCAGGAGTCTC  GGGCTGGTTCTGCTGT [A/G] TGACACAGGACAGGTGGCTTGCC</p>	SEQ ID NO. 187

	TGGTCTGGGGCCACAGCCTCCTCCCCCTGTTGATGAGCATGTTGGT TGTTCCAGCACCATGTCAGCCCTAGAAATCTCTGAATTCTTGAC CAGATCAGTAATTGCTCTCTTGCGTTTACTTTTCCTTCAAATAA AGAGATTGGCATAACAGGGGAGGAGCCAGTACAGACGGCATGCT TGGCTCAGGTTCCAGAACCAGAAACCAGACAAGAGTTGGGAAA CCATGATGGTGGAGGAGGGTGTGCCACTCCTTACTAGTGCCTAA TCTCTTCGAGACACTAATGTTTCAGTATTATCCACAGATTCTGA TGCCAGGCAGCCAGATGACTGGGGTCAGTTATTAGCATGCTTC CTGGAGGTGGTTCCAGGTGCAGGCTACCTGCAGTCTGGCTGGA TGGGCCCTGCACCACACTTGCTTCTGGGAAGCTGGTTTTGGGGT TGCCACAATCTCTGAAAGAATCACTAGGCCACCCTCT	
KCP_1739 82	TTCACAGGTTTTATCCCTAAAGGAAATCACAGGTAATAGATGTG GGGCTGCAGAAATGCAACATGCACCTTTTCCTTGAAACTGCATCC CTTTTCCCTGAAGATGAAGCTTGAAAGAACTCTAAGAGGTTAAG CATGGAGCTGATGGGCAAGCCACAGGCAGAAAGAGTAGCTGTGC AGCCAGGCTCCTGGCCAGGGAGGGCAGATAAGGAGGGGAGGCAA AGTTTGGTAAACAGGAAGCTAATCTATGGGCAAGAATCATTTTC TTCAGCATCCTGACCTCTCCTAAAATGTTCTCCACTGGTCCCTG CTAGGACAAAGGAATTACCACCAGACTAGAGTCAGGAGTCTTGG GCTGGTTCTGCTGTATGACACAGGACAGGTGGCTTGCTTGGTCT GGGCCACAGCCTCCTCCCCCTGTTGATGAGCATGTTGGTTGTTCC AGCACCATGTCAGCCCTAGAAATCTCTGAATTCTTGACCAGATC AGTAATTGCTCTCTTG [A/C] GTTACTTTTCCTTCAAATAAAG AGATTGGCATAACAGGGGAGGAGCCAGTACAGACGGCATGCTTG GCTCAGGTTCCAGAACCAGAAACCAGACAAGAGTTGGGAAACC ATGATGGTGGAGGAGGGTGTGCCACTCCTTACTAGTGCCTAATC TCTTCGAGACACTAATGTTTCAGTATTATCCACAGATTCTGATG CCAGGCAGCCAGATGACTGGGGTCAGTTATTAGCATGCTTCCT GGAGGTGGTTCCAGGTGCAGGCTACCTGCAGTCTGGCTGGATG GGCCCTGCACCACACTTGCTTCTGGGAAGCTGGTTTTGGGGTTG CCACAATCTCTGAAAGAATCACTAGGCCACCCTCTGAGTGGGTG CTTCTGTAGGAATTATGGATAAAAATTGTTCCACTAGTCTTACCT TCTTGGGGAACCCTTCTTGATTTCCAGGCTGGGCTGGGTGTCC CTGCAGCCTAGCCCCACAGCCCTCCTGCTTCTCTTTT	SEQ ID NO. 188
KCP_1742 43	TGACCTCTCCTAAAATGTTCTCCACTGGTCCCTGCTAGGACAAA GGAATTACCACCAGACTAGAGTCAGGAGTCTTGGGCTGGTTCTG CTGTATGACACAGGACAGGTGGCTTGCTTGGTCTGGGCCACAGC CTCCTCCCCCTGTTGATGAGCATGTTGGTTGTTCCAGCACCATGT CAGCCCTAGAAATCTCTGAATTCTTGACCAGATCAGTAATTGCT CTCTTGCGTTTACTTTTCTTCAAATAAAGAGATTGGCATAACAG GGGAGGAGCCCAGTACAGACGGCATGCTTGGCTCAGGTTCCAGA ACCCAGAAACCAGACAAGAGTTGGGAAACCATGATGGTGGAGGA GGGTGTGCCACTCCTTACTAGTGCTAATCTCTTCGAGACACTA ATGTTTCAGTATTATCCACAGATTCTGATGCCAGGCAGCCAGA TGACTGGGGTCAGTTATTAGCATGCTTCTGGAGGTGGTTCCCA GGT [A/G] CAGGCTACCTGCAGTCTGGCTGGATGGGCCCTGCAC CACACTTGCTTCTGGGAAGCTGGTTTTGGGGTTGCCACAATCTC TGAAAGAATCACTAGGCCACCCTCTGAGTGGGTCTTCTGTAGG AATTATGGATAAAAATTGTTCCACTAGTCTTACCTTCTTGGGGAA CCCTTCTTGATTCCCAGGCTGGGCTGGGTGTCCCTGCAGCCTA GCCCCACAGCCCTCCTGCTTCTCTTCTCATCACAGTCTTGTTA TCTCTACCAACTGTAGGCCTGCCCCACTGATGGTGTGAATAAAG GGACTGGGTCTCTCTAGCACCTAGCATAGATCTGATACATAGTG GGTGATCTCTATTGAATGAACGATGAATGAATGAATGAATGAAT ACATTTAGATAATTCAGATTACTTTCTAGCTCAGCAGTGATAA AGCAGGAAGACATGCTGTCAATATGATTTAGGGCAAGTTT	SEQ ID NO. 189
KCP_1751	AACGATGAATGAATGAATGAATGAATACATTTAGATAATTCAGA	SEQ ID

06	TTACTCTTTCTAGCTCAGCAGTGTAAGCAGGAAGACATGCTGT CAATATGATTTAGGGCAAGTTTTCAAATCTCTCTGGACCTCAGT TTTACCTCTTGAAAAATAAATAATAAATTTGTCCTTACTTCAT GAGACTATTTTGAAGATTAAATGAGATAATGTATACACTACTAC TCACTGTCCTTACTTGAATATTCCTAGGTCCTTGGTGCTACATT AGGCTACATAGAATGTATTTAAAGTAATAGAGTGGTATTTAATA AATATTCATTTTCTTTCCCCAGAACTACCTTAAATTAATTTGTT GAAAGGACAGATGGATGGATGGTTGATGGAAGTAGCAGGCTTCC AGCAGCAGGGGATGGAGTGAGTGTGTGGATACCGCTGGATCAGC AGAAGGTTATACCATTTTAGAGTAACATCTCGGACTTCGGAGA GTTCTGCGGTATGAAG [C/G] TTTGGCTTTAATTAAAGTCTCAG CACAGTGTTAAATGCCATTTTATTTTAGGTCATAATTAACACTA ATGAGATGAGTGGATTACAAAGAGCACACATTTTGAGAAAGTGA AAAACAACATCTGAGCTTGGTGGTTTCCATTTTCGCTTTTCCCC CTCCCATGCTCTGTTCAATTAAGTTTGGAGAAAATATTACAA CCATACTCCTTGTCTTTGTGGTAATGAAGCATATTAATTTGAAT GTGATGAATACAATATTCCTGACTTTTTTATTCCCTTATCTA CAAAAGTTTAAATAATGGACCAATTAAACCAGGAGAGAAGAAT GCAGGGTTTGCCTGGGGATCCAATTCAGCAACCAGAGAAGTGAA AGAACAAAATTTTGTGACGGAGTCTGGGCCAGACTTCATCCCTT ACCTATAGCTGACAAACAGTAAGTCAAATTTGGGCAGATGTGGAC CAGCGCAGAACACATACTATATTGAGGATCGAAAGGC	NO. 190
KCP_1751 70	GTGTAAAGCAGGAAGACATGCTGTCAATATGATTTAGGGCAAGT TTTCAAATCTCTCTGGACCTCAGTTTTTACCTCTTGAAAAATAAA TATAATAATTTGTCCTTACTTCATGAGACTATTTTGAAGATTAA ATGAGATAATGTATACACTACTACTCACTGTCCTTACTTGAATA TTCCTAGGTCCTTGGTGCTACATTAGGCTACATAGAATGTATTT AAAGTAATAGAGTGGTATTTAATAAATATTCAATTTCTTTCCCC AGAACTACCTTAAATTAATTTGTTGAAAGGACAGATGGATGGAT GGTTGATGGAAGTAGCAGGCTTCCAGCAGCAGGGGATGGAGTGA GTGTGTGGATACCGCTGGATCAGCAGAAGGTTATACCATTTTAG AGTAACATCTCGGACTTCGGAGAGTTCTGGGTATGAAGGTTT GGCTTTAATTAAAGTCTCAGCACAGTGTTAAATGCCATTTTATT TTAGGTCATAATTAAC [A/G] CTAATGAGATGAGTGGATTACAA AGAGCACACATTTTGAGAAAGTGAAAAACAACATCTGAGCTTGG TGGTTTCCATTTTCGCTTTTCCCCCTCCCATGCTCTGTTCAATT AAAAGTTTGTGAGAAAATATTACAACCATACTCCTTGTCTTTGTG GTAATGAAGCATATTAATTTGAATGTGATGAATACAATATTTCCA CTGACTTTTTTATTCCCTTATCTACAAAAGTTTAAATAATGGA CCAATTAAACCAGGAGAGAAGAATGCAGGGTTTGCCTGGGGATC CAATTCAGCAACCAGAGAAGTGAAGAACAATAATTTTGTGACGG AGTCTGGGCCAGACTTCATCCCTTACCTATAGCTGACAAACAGT AAGTCAAATTTGGGCAGATGTGGACCAGCGCAGAACACATACTAT ATTGAGGATCGAAAGGCCAGGTTCCAGACCGTCTCTAATATTT TCTTAGTGAATATTTGTTGGATGAATGCATGGATGGG	SEQ ID NO. 191
KCP_1752 52	CTTACTTCATGAGACTATTTTGAAGATTAAATGAGATAATGTAT ACACTACTACTCACTGTCCTTACTTGAATATTCCTAGGTCCTTG GTGCTACATTAGGCTACATAGAATGTATTTAAAGTAATAGAGTG GTATTTAATAAATATTCAATTTTCTTTCCCCAGAAGTACCTTAAA TTAATTTGTTGAAAGGACAGATGGATGGATGGTTGATGGAAGTA GCAGGCTTCCAGCAGCAGGGGATGGAGTGAGTGTGTGGATACCG CTGGATCAGCAGAAGGTTATACCATTTTAGAGTAACATCTCGG ACTTCGGAGAGTTCTGGGTATGAAGGTTTGGCTTTAATTAAAG TCTCAGCACAGTGTTAAATGCCATTTTATTTAGGTCATAATTA ACACTAATGAGATGAGTGGATTACAAAGAGCACACATTTTGAGA AAGTGAAAAACAACATCTGAGCTTGGTGGTTTCCATTTTC [A/G] ] CTTTTCCCCCTCCCATGCTCTGTTCAATTAAGTTTGTGAGAA	SEQ ID NO. 192

	AATATTACAACCATACTCCTTGTCTTTGTGGTAATGAAGCATAT TAATTTGAATGTGATGAATACAATATTCCTGACTTTTTTATT CCCTTATCTACAAAAGTTTAAATAATGGACCAATTAAACCAGG AGAGAAGAATGCAGGGTTTGCCTGGGGATCCAATTCAGCAACCA GAGAACTGAAAGAACAAAATTTTTTGACGGAGTCTGGGCCAGAC TTCATCCCTTACCTATAGCTGACAAACAGTAAGTCAAATTGGGC AGATGTGGACCAGCGCAGAACACATACTATATTGAGGATCGAAA GGCCAGGTTCCAGACCGTCTCTAATATTTCTTAGTGAATATT TGTTGGATGAATGCATGGATGGGTGGATGAATAGATGGATGGAT GGACAGATGGACGGAGAGAGATGGATGAATGGATTGTTGG	
KCP_1768 36	GCAGGCCTGTGAACCTGACACATGGTCCAGGTGTCTCCCTGAGG ACTTCTGGAAGTCTCCCCACCTCTCTGTGGTCTTTAGGCATTA ACACCACCTTGTCACTGTGTCTCTGAGGCAGTCTGGAAGTTCA TACCCCACAATCTCTGTGTACCTTGTCCCCATTCTGTTCTCTG CATTCAGATGGTTTAAACACACACACATACACGCGCAAAATG TTGTTCTTTTCTTAAACCCATTGTGGCCAGGCTAGACAAATC CTTAACACGGTCTACAATATTCTGCATGGCATGGCCCCCTGGGTG CCTCCCAACCTGATCTGTGCACACACCACCTCCACCTTTGCGTGT TCCCTGGGCCCCTAGCACTAACCTTTGGTTTCATTCCTAGACACCT TTTCAGCACTTAGGCCCCACAGCCCTCAGAACCTTTACACTTG CTGTCTCTTTTGCTTAA [A/G] TGTTCTTGCCCCACCTACCAC CTAGTTAATGCCTTTTCTCCTTCAGCTCTTAGTTGAAGCATCA CTTCCTCAAGGAGGGCAGCCCTGATGAACTCATATGCAAACCT CCAGCCTGGGTGGGCCTTATCTTTATGCTGTGATGGCCCTGAG TATCTTCCTTTATGGCACCAATCACGGCTTATATGATATACTT ATGCTATTATTTGAGTTATGTCTGTCTCCCCAGTAGGCCACTA GTATTAGAATCATTGATTTTTAATCATTGTATCCCTAGTGCTTA GCACAGAGCCTGGCTCATAATAGATGCTTAATAAATATTTGTTG AATAAATGAATGAGTGAATGAATAAATGCCTCATTCAAGAGCTT TGGCTCTTTCTGTACTACTACATTACTTCTATTTTTTAGCTCTT AATTCTCAAAGCACTTTCTTTGTGCTGGGCTTATGCTGGGAGCT TAGACAGTAAAGCTTAGA	SEQ ID NO. 193
KCP_1801 73	TTACATCCACAGGTTTGATTATAAATGTGTGATTGAATTGGAA TTTCTGTTGAAATTCTGATCCCTTCTAGACAAAGAAGGTAAAAA TTGAAACATGTCAATGGATATCTAAATATCATTACTCACTGGCT TTATTTGCAATGGCTTTCCATTGACAACAGTTACATTTTGTTC AAAGCAACAAATGATTGGCGCTGACAATCCACAGGAACATGGTG CAGTCATTAATGAATGTGCTCATTATTCCTCCCTGCCGGGAGGC ATCGACTCCCGTTCTCCAGCCTGTTTTAAGCAGACAGACCTACA TCTGCACCTGTGAGCTTGGAACCTTAGTAGGGGAGGGGGATGCT GATGTGATGGAGAATGAAGAATGGGCCCTGCAGGCTGACATTTT GGGAGAGTAGGTTCTGAAATTTATCCCAAAGGACATGGAATCCT GGAAGCAGGGTTCAAGATCCTCCCAAATTTGATCTCCAGGATG CTTGGAATGATTGTTT [C/T] GAGGGTTTTGTAAATGCCAGGG GAAAACCAGGAAGCTTCTCTCCAGTTGTCTTGCCCTCCTTCTCT CCAGTCTCCATGGAGCTGACTTTGAGAATTAACCTCTGAGGGAC AGAGACCCTGGGATGGAGAGCCAGCCCTGCTGGATTCCACAAGG TGCTGCTTAAAGCACACACCTCTTCCCAATGACAGGTTCTGAA AGAAGGCCTTGTAGCTAGATGCACAGAGGGTTTTGTTTTGTTTT TTTTTTTTTAACTTTTACATCTGTCTAAAATGCTCTGGGCT GGGTACAGTGGCTCCACCTGTAATCCCAACACTTTGAGAGCTG AGGCAGGAGGATCGCTTGAGCCCAGGCGTTCTAGACCAGCCTGG GCAATATAGTGAGATCTCTATGTCTAGAATGTTTTTTAATTAGC TGGGCTTGCTGCCTGCACCTGTAATTCAGCTACTTGGGAGGCT AAGGTGGGGGATCACTCGAGCCCAGGGGGCTGAGGC	SEQ ID NO. 194
KCP_1802 37	CCTTCTAGACAAAGAAGGTAAAAATTGAAACATGTCAATGGATA TCTAAATATCATTACTACTGGCTTTATTGCAAATGGCTTTCC	SEQ ID NO. 195



	<p>ATTGACAACAGTTACATTTTGTTCAAAGCAACAAATGATTGGCG  CTGACAATCCACAGGAACATGGTGCAGTCATTAATGAATGTGCT  CATTATTCCTCCCTGCCGGGAGGCATCGACTCCCGTTCTCCAGC  CTGTTTTAAGCAGACAGACCTACATCTGCACCTGTCAGCTTGGGA  ACCCTAGTAGGGGAGGGGGATGCTGATGTGATGGAGAATGAAGA  ATGGGCCCTGCAGGCTGACATTTTGGGAGAGTAGGTTCTGAAAT  TTATCCCAAAGGACATGGAATCCTGGAAGCAGGGTTCAAGATCC  TCCCAAATTTGATCTCCAGGATGCTTGGAAATGATTGTTCCGAG  GGTTTTGTAAAATGCCAGGGGAAAACCAGGAAGCTTCTCTCCAG  TTGTCTTGCCCTCCTTC [C/G] TCTCCAGTCTCCATGGAGCTGAC  TTTGAGAAATTAACCTCCTGAGGGACAGAGACCCTGGGATGGAGAG  CCAGCCCTGCTGGATTCCACAAGGTGCTGCTTAAAGCACAAACAC  CTCTTCCCAATGACAGGTTCTGAAAGAAGGCCTTGTAGCTAGAT  GCACAGAGGGTTTTGTTTTGTTTTTTTTTTTTTAACCTTTCAGC  ATCTGTCTAAAATTGCTCTGGGCTGGGTACAGTGGCTCCACCT  GTAATCCCAACACTTTGAGAGCTGAGGCAGGAGGATCGCTTGAG  CCCAGGCGTTCTAGACCAGCCTGGGCAATATAGTGAGATCTCTA  TGTCTAGAATGTTTTTTAATTAGCTGGGCTTGCTGCCTGCACCT  GTAATTCAGCTACTTGGGAGGCTAAGGTGGGGGGATCACTCGA  GCCCAGGGGGCTGAGGCTGCAGTGAACCATGATTACACCACTGA  ACTCCAGCCTGGGCAACAGAGTGAGACCCTGTCTCAA</p>	
KCP_1840 80	<p>CTGATGGAACCTGGGATGTGAGAAGAAGGCAGGTTTTCTGATAAA  CAATTCCTGTATCTTTCACAAATGCCAAATCACAGACTCAGCTT  GGGACATATGAGGACAGCACAGACTTTGGAGGCAGGTAGATTTT  GGGTTGTACGCAGACACCCACTACTATGAGACCTGGATTTCTT  TCTGACGTTATTGGGGATAAGAAGTGGCACCTCACCATTTCCTAG  GAAATAGTAGGTAAGTCTTCTGGTTGCCACTGAGGTGACTCAC  CTGAGACACAGTTGCTCCTAAAGTTCAAGGTTAGGAGACAATCC  AGAAGGGGAGCTGTCTGTGAAGTCAGAATTCTTGGAAGAATGTA  AGTCTTTACACAGTAACAGCAAAGCAGACAGTGGGAACCACTAC  TCTGCCTTCTTGATCATTCTTTCCTAGAAATACCAGAAAGCAG  TGAGGGATTAAGTCTAATTCTTGGCACCTGACCTTATATCTAAC  AGATGCTCAGTATTAC [C/G] TGTTGATGGGACCTCACTGGGAA  TGTTTTGTGTGCAGTACAAAAGGGCAATAGATGAAACTTTGGGA  CGGGAGCCCAGGAAAATGGCTGAGAGGAGAGCTTATGCCTAGCT  TATGCATGAGCTTGCAAAAGGGAGAATACACGGGAGGGAAGAT  CAGCAACAGCATGAGTTTTATAAGGCAGAGAGTTGTTGGGAAGG  AAGCAGCAGGGAGAGGGGAAGGAGTAAGTAGAAACCTAGAAGAG  ATACAGCTAAGATAAGCCAAGAGAACAAAGTATTGACTTACCAG  AAACATGGAAGTCTTCTGCTTCTAATTTAGTTCCGCATATCTG  GATATGTGAATGCCTAAAATCCCATTAAGCCCAGTGGGTTAATT  ATTACACTTGCTAGGGCCCCAGAGGAGAGGAAAACACAGTAAGTC  AGAAAAACCTCTGGGCAGGTGAATTTCTCAGGTTTTCTTCTGGG  CAGATGGGATCTGGAATGGTAGCGTGGCATCCTGGTA</p>	SEQ ID NO. 196
KCP_1855 79	<p>CCTTTCCAATATTAAATAATATTAACATTGGTAATAGTGGTAC  TAAACAACCTAGGGTGTTTTTTTTTTTTCATTTAATAGTATATTTT  TAGTATCTTTCCAGGAAAAGATACATGGATGTGCCACATTATTT  TTAATGGCTCACATGGTACTCCTTTTATGTATGCACTATAATTT  ATGGAACCAGTTTTCTCACCGATGAGCATGTAAGTTCTTTTCAGT  CTTTTACTGTTATAAACGAATGATGCAATGAATATCCTTGTA  TATATATTTGTGCGCATATGTAGGTATCCTTACAAGTGGAATTT  CTGAATAAATGGATATATACAATTTATTTATGAATTTACCTTCC  TACAAGTGATTCAAGAGAGTGTCTTTGCTCCACAGTGTTGTCAA  TATAGTGTATTCTCAAAATCTGACACCAATATGTGTGAAGTGCC  TGCTCTGTTCCACACTTTACACAGGTTCTCTTATTTG [C/A] G  TTAAGTTTATTTAAGAAGAGGAACTGGGCCTCATGGAGATCTA  GGAACCTTGCCCAAGGACAGGTCTCTGTGACTCTAAGAGTGCAAT</p>	SEQ ID NO. 197

	CTTCCCTTTTCCCATGTCAAGCACCTTTCCCCACCAGGCTCAC TGCTGACAATCCAGTGACGAAGAAGGGAAATTACCCCCACAGA GCCCAAAGTTTAGGACATGCCGACAGCATCACTCTTTTGCCTC CTCATTCTCTCTTTTCAATTTCCAGAACATTTGCTCACTCAGTGCT GCCCAGTGATACTTAGCCAGCCTGATTACCCATCTAATAATTTT TGATACTAATATAAAACCTTTCCCAAAGACAAATATAACTGAGAC GCACTCCAGCTTACCATAGCTTTTCTGGTGGTACAGTTTCCAGG GACATTTCACTGTGTCAAAGCAGGGACCACATATGTTCCAGACC AGCTTGTTGGGTTTTTCACTGGGAAGTGAAGACAAATTGTTGTC CCTT	
KCP_1860 48	TTCCACACTTTACACAGGTTCTCTTATTTGCGTTAAGTTTATT TAAGAAGAGGAACTGGGCCTCATGGAGATCTAGGAACCTGCC AAGGACAGGTCTCTGTGACTCTAAGAGTGCAATCTTCCCTTTTC CCCATGTCAAGCACCTTTCCCCACCAGGCTCACTGCTGACAATC CAGTGACGAAGAAGGGAAATTACCCCCACAGAGCCCAAAGTT TAGGACATGCCGACAGCATCACTCTTTTGCCTCCTCATCTCTC TTTCATTTCCAGAACATTTGCTCACTCAGTGCTGCCAGTGATA CTTAGCCAGCCTGATTACCCATCTAATAATTTCTGATACTAATA TAAACCTTTCCCAAAGACAAATATAACTGAGACGCACTCCAGCT TACCATAGCTTTTCTGGTGGTACAGTTTCCAGGGACATTTCACT GTGTCAAAGCAGGGACCACATATGTTCCAGACCAGCTTGTTGGG TTTTTCACTGGGAAGT [A/G] AAGACAAATTGTTGTCCCTTTGA AAAAGCATCTTTCATCTCTCCATCTATCTGCGATCTAAAGCAAT GGGGCTCTTTCTGTATGTCCTTCAAATGGTCTACACTGACACAC GTTTTCTCTGAGCTGCCGAGAGAATATGCCATGAGATGTTGCCA GTGATGGTTACACTCAGCTAGCAGAAGATTAGGGACTGGTTAAA CCTTTGGAGAAATTGCCCTTGGGAAAAGAGGAAATAAAAGCAAAT ATTACTATGAAACATAGAGATTACCAGGTAGGAGGAGAGAGAG GTGGAGGGAGGGGTAGGAGTGGAAGGAAGGGAGGGAGGCAGAAA GAGGAAGGCAGACTGGTGGAAAATAAACCGTGCACTTTAGAACA GCAGGAAGGGAGGCTTGGAAGCCTGGTTTTCTGGCTTTGAATGA CCGCTTAGCGCTTGCCGGTGCGCCAGGGTGCTGTGAGGATGTGG GCAGAGGGCGAGTCCGAAGGGCTCCAGACACTGGGAA	SEQ ID NO. 198
KCP_1866 79	GAGAATATGCCATGAGATGTTGCCAGTGATGGTTACACTCAGCT AGCAGAAGATTAGGGACTGGTTAAACCTTTGGAGAAATTGCCCTT GGGAAAAGAGGAAATAAAAGCAAATATTACTATGAAACATAGAG ATTACCAGGTAGGAGGAGGAGAGAGGTGGAGGGAGGGGTAGGAG TGGAAGGAAGGGAGGGAGGCAGAAAGAGGAAGGCAGACTGGTGG AAAATAAACCGTGCACTTTAGAACAGCAGGAAGGGAGGCTTGGA AGCCTGGTTTTCTGGCTTTGAATGACCGCTTAGCGCTTGCCGGT GCGCCAGGGTGCTGTGAGGATGTGGGCAGAGGGCGAGTCCGAAG GGCTCCAGACACTGGGAATAGTGGTGGTTCGTGTGCTCCTCCCTG AACTTTTTGCACTACCTCGGACTGATTGACTTGTGACAGCGGTAA GCGAACCTTGGAGCTTCCCCGTTTTCTGTGAATGTGTTTTGTG GCTTCGGTTGCTGTGA [C/G] AGTCGTTTCGAAAATGCACGGAA ATGAGGGCGGAGACCCGAGAGATTTGAAAAAGCCGGGTGAAAC AGCGTGGTATTGGTCCCCGCTCCCCAGTCGCGCCCCAGTGCTG CGCTGTCCGTGCTGTGAAATGTGGTGCCTGGGGAGTGCGGG AGCCAGGAAGTTAGGGTCTCCTGCTCCGGCCCTATGAGCATGTG AGTCTTGATGGATTATTAGCTATGGGTGAGGCCAGCACACAACA TCACAATTCTCTGAAGCTGTCTGGTAACCTACGTATATTGTTG ATGGAAGCCAGTGACTTTTAAAGCCATTATGTTGATTAACTTT TTTAAAGAAGTTTAGGAGATTATATGGAGGTAAACCTTTGTA AAATGCTAATCACAGTGTCTGACAATTAGAACACATTTAATAAA TGTCAGTTTTCTTGCTCAACCCTTATAAGAACCTTTATTCAAA GCCACCTCCTCAGCTCTGACTTCAGCTCCATTCCTTA	SEQ ID NO. 199
KCP_1871	TGCTGTGACAGTCGTTTTCGAAAATGCACGGAAATGAGGGCGGAG	SEQ ID

16	<p>ACCCGAGAGATTTGAAAAAGCCGGGCTGAAACAGCGTGATTG  GTCCCCGCCTCCCCAGTCGCGCCCCAGTGCTGCGCTGTCGTCG  TGCTGAAATGTGGTGCGCCTGGGGAGTGCGGGAGCCAGGAAGTT  AGGGTCTCCTGCTCCGGCCCTATGAGCATGTGAGTCTTGATGGA  TTATTAGCTATGGGTGAGGCCAGCACAAACACATCACAATTCTCT  CTGAAGCTGTCTGGTAACTACGTATATTGTTGATGGAAGCCAGT  GACTTTTAAAAGCCATTATGTTGATTAACTTTTTTAAAGAAGTT  TAGGAGATTATATGGAGGTAAAAACCTTTGTAAAATGCTAATCA  CAGTGTCTGACAATTAGAACACATTTAATAAATGTCAGTTTCTT  TGCTC [A/G] ACCCTTATAAGAACCCTTATTCCAAGCCACCTC  CTCAGCTCTGACTTCAGCTCCATTCTTAGTGAGAATGGGGTTA  TAAATCCAGGTTAACCAGATTGTTTAGGATTAGAAAGTGATTG  GTTTCCAACGTTGAAGGAGTTCAAGAAACAAAGAGTTTATTTT  TCCTCCTTATGAGATATTGTTCCAAATAGAACACAGTTTGTCTA  GATGATTTTGTCACTTAAAATTAGGCTCCAGGAAAGATTCCAA  ATTTTCATGAGCAATTGGGCTCATAAAACAAGATCAAACCTCCAAT  AGTGTATATCCAAAGTATGTATAATGTGTATTTCGGTGTATATTC  TTCCACCACTGCATGGTGTAGACAGAATTTCTCTTCCAAGGGGC  ACCACATGACAAAACCGTACATAATAATGAAATGCATTGTAGA  CAAAGGACTAGCTAAAATACCAACTGAAAGTGGGAAGACCAGAA  ACTGAAG</p>	NO. 200
KCP_1872 58	<p>AATTGCCTTGCGAAAAGAGGAAATAAAAGCAAATATTACTATGA  AACATAGAGATTACCAGGTAGGAGGAGCAGAGAGGTGGAGGGAG  GGGTAGGAGTGGAAGGAAGGGAGGGAGGCAGAAAGAGGAAGGCA  GACTGGTGGAAAATAAACCGTGCACTTTAGAACAGCAGGAAGGG  AGGCTTGGAAGCCTGGTTTTCTGGCTTTGAATGACCGCCTAGCG  CTTGCCGGTGCGCCAGGGTGCTGTGAGGATGTGGGCAGAGGGCG  AGTCCGAAGGGCTCCAGACACTGGGAATAGTGGTGCTCGTGTGC  TCCTCCCTGAAACTTTTGCACTACCTCGGACTGATTGACTTGTCT  AGACGGTAAGCGAACCCCTGGAGCTTCCCCGTTTTCTGTGAATGT  GTTTTTGTGGCTTCGGTTGCTGTGACAGTCGTTTCGAAAATGCA  CGGAAATGAGGGCGGAGACCCGAGAGATTTGAAAAAGCCGGGCT  GAAACAGCGTGATTTGGTCCCCGCTCCCCAGTCGCGCCCCAG  TGCTGCGCTGTCCGTCGTGCTGAAATGTGGTGCGCCTGGGGAGT  GCGGGAGCCAGGAAGTTAGGGTCTCCTGCTCCGGCCCTATGAGC  ATGTGAGTCTTGATGGATTATTAGCTATGGGTGAGGCCAGCACA  ACACATCACAATTCTCTCTGAAGCTGTCTGGTAACATCGTATAT  TGTTGATGGAAGCCAGTGACTTTTAAAAGCCATTATGTTGATTA  ACTTTTTTAAAGAAGTTTAGGAGATTATATGGAGGTAAAAACCT  TTGTAAAATGCTAATCACAGTGTCTGACAATTAGAACACATTTA  ATAAATGTCAGTTTCTTTGCTCAACCCTTATAAGAACCCTTATT  CCAAAGCCACCTCCTCAGCTCTGACTTCAGCTCCATTCTTAGT  GAGAATGGGGTTATAAATCCAGGTTAACCAGATTGTTTAGGATT  AGAAAGTGATTTGGTTTCCAACGTTGAAGGAG [G/T] TCAAGAA  ACAAAGAGTTTTATTTTTCTCCTTATGAGATATTGTTCCAAT  AGAACACAGTTTGTCTAGATGATTTTTGTCACTTAAAATTAGGC  TCCAGGAAAGATTCCAAATTCATGAGCAATTGGGCTCATAAAA  CAAGATCAAACCTCAATAGTGATATCCAAAGTATGTATAATGT  GTATTCGGTGTATATTCTTCCACCACTGCATGGTGTAGACAGAA  TTTCTCTTCCAAGGGGCACCACATGACAAAACCGTACATAATAA  TGAAATGCATTTGTAGACAAAGGACTAGCTAAAATACCAACTGA  AAGTGGGAAGACCAGAAACTGAAGTGTAAGATGAGGTAAGCCCT  GGAGTAAGAGTCAAGAAATCCACTTCTATCCATAATCTGTCTC  GGTTTAATGTTGGTCAAGTCATTTTTTAAAAAATTCTAGGTCTT  GGTTTCCTTATGATGACTTTAGATCTCTGTTTCTTGGAAATCTA  GAGTGATCCAAAGGTTTCTTTGAATTCAGTTTTGTGGGTTGAGA  CGGGCAGCCAGACTGTGAGTCCCTCAGCTCTGCTTCAACCAGAA</p>	SEQ ID NO. 201

	CAGCTCCACTTTACTGTTTCAGCATGTTAGCCCTGTATGTAAGGA TGTTTTTTAGCTTTAGCTAAAATTTAGTGACTCTATGACCCATA GGCCCTGCTTCCCTGAGATTTTGAAAGCTGAAGCACATTCGGAA AACTTTTTCTTCCCTAAAATCACCTGAAATCTGACAATCTGGA AGACTAGTTCTGTCTGCTCCAGCCCTTGGTCCCTTAGATGTGCT TTTCTGAAGATCCAACTCAACCTGCCAGTCAATATACCAACTG AGCAGAGCCCTGTCTCCACCAGATTTCAAGAGAACATGTTCC ATTCTGTTCAGAGCTTCAGAGCAGCTTCCGCTAAGATTGCACA TTAATGCAACAGCGTCTATTTTCTTTGTTTCTTTTTTTTTTTT TTTTTTTTTTTTTGATGAGACAGGG	
KCP_1876 88	ATTTTTCTCCTTATGAGATATTGTTCCAAATAGAACACAGTTT GTCTAGATGATTTTGTCACTTAAAATTAGGCTCCAGGAAAGAT TCCAAATTTTCATGAGCAATTGGGCTCATAAAACAAGATCAAAC CCAATAGTGATATCCAAAGTATGTATAATGTGTATTCGGTGTA TATTCTTCCACCCTGCATGGTGTAGACAGAATTTCTCTTCCAA GGGGCACCACATGACAAAACCGTACATAATAATGAAATGCATTT GTAGACAAAGGACTAGCTAAAATACCAACTGAAAGTGGGAAGAC CAGAACTGAAGTGTAAGATGAGGTAAGCCCTGGAGTAAGAGTC AAGAAATCCACTTTCTATCCATAATCTGTCTCGGTTTAAATGTTG GTCAAGTCATTTTT [T/A] AAAAAATCTAGGTCTTGGTTTCCT TATGATGACTTTAGATCTCTGTTCTTGGAAATCTAGAGTGATC CAAAGGTTTCTTTGAATTGAGTTTGTGGGTTGAGACGGGCAGC CAGACTGTGAGTCCCTCAGCTCTGCTTCAACCAGAACAGCTCCA CTTTACTGTTTCAGCATGTTAGCCCTGTATGTAAGGATGTTTTTT AGCTTTAGCTAAAATTTAGTGACTCTATGACCCCTAAGGCCCTGC TTCCCTGAGATTTTGAAAGCTGAAGCACATTCGGAAAACTTTTT CTTCCTTAAAAATCACCTGAAATCTGACAATCTGGAAGACTAGT TCTGTCTGCTCCAGCCCTTGGTCCCTTAGATGTGCTTTTCTGAA GATCCAACTCAACCTGCCAGTCAATATACCAACTGAGCAGAGC CCCTGTTCTCCACCAGATTTCAAGAGAACATGTTCCATTCTCTGT TCAGAGCTTCAGAGCAGC	SEQ ID NO. 202
KCP_1893 31	CTCTAAAATTTACCCTCTGTTCTGTACACCAAGTACCTCAGCA AGTAATCCAGTTCCAGATGGGATCTGCAGTCTGCCATTAAGTCT TTACCACACATAGGCTCTTATGTAGAGCCCTTACCATATGGTC CAAAATGCCATTTTAAATGTGTATTTGATATGGAGACTCTGTTT ACAATTTGAGTACTAAAGAGAGAATAACACCTCCTAGTAGATAC ACCAGGACCAATGTAATGCTGTCAATCTAAGGAGAGCAGTGGA CATCTCCAAAGAACCCTCTGTAGTCTTCTTCCGCTTGTATC TTATTCCTATTTTATTTTAAAGGTTTTTTTTTTTTTCTTCGAGA CTAAATCTCACTCTATCACCAAGCTGGAGTGCAGTGGCATGAT ATCAGTTCAATTGCAACCTCTGCCTCCCGACTCAAGCGATTCTC CTCACTCAGCATCCCAAGTATCTGGGACTACAGGCATACACCAC TATGCCCAGCTAGTGT [A/G] TGTGTGTGTGTGTGTGTGTGT GT GCCAGGGTGGTCTTGAACCTCCAGAGCTCAGGCGATCCACCTGC CGAGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACAGCG CCTGGCCAATCTTTTAGGGATAATTTTAGAACAGTATACAGATA TTGAGCCAAGAGTCAAAGAGCTGGGTTGCAATTCTGGTTGTGC CATTTATCAGTTGTGTGAGGTGGGACAAGTCTCTTTTCTCCCT AGCTTTCTCTTCTCCTCATTTATAAAATAAAGAAATGAGAATGAT AGTTGTATTAATTTCTGAGGACTGCCAGAACAAATTAACAAA CTGGGTGGCTTAAACAACAAACATTTATTCTCACATAGTTTCA GAGGCTAGCAGTTTGAATCAAGTTCTTGACAACTCCCTTAGA GTCTAAAGTCTCTAGAGAAGGATTCTCCTTGCCTCT	SEQ ID NO. 203
KCP_1927 42	GAGCAAGCACTGCAGCCATCCTCCTTTATTTCCCTCAAGGCAAT ATCCAAGGATTAAGTCAAGAGCCGTCTGCAGATTCTCCTCTCT CTACCTTGCCCTGCATTTTTTGTGCCCTTCTCTTCCCCCTCTC	SEQ ID NO. 204

	<p>CAGCCCCAACCTCTCTCCTGATCCACGGTACTCCTCCTGGGAT  GTCCACTGGGGCTGATCCTCCCCATTCTCCCCCTGAGTTCCCT  GCTGTTAATCTGTCTCCAGCAAAATTAACCTAGCCTATGTCCCA  TGCCCTCTGGACTCTGGCTGCTCGTCAATCACTCTTAAAAATCC  GGTTTCTCCTTAGGCAATCATTTTGTGTTTATGTGTAAA  AAAACCTGAGTAAATTTTTTTTTTTTGGAGATGGAGTCTTGCT  CTGTTGCTCAGGCTAGAGTACAGTGGCATGATTTCTGCTCACTG  CAACCTCCGCCTCCCGGGTTCAAGCGATTCTCCTGCCTCAGCCT  C [T/C] TGAGTAGCTGGGACTACAGGTGCCACCACCATGCCTG  GCTAATTTTTGTATTTTTGGTAGAGACAGGGTTTCATCATACTG  GCCAGGCTGGTCTCAAACCTCTGACCTTGTGATCCACGCACTTC  GGCCTCCCAAAGTAATCACTGCTGGGATTACAGAAGTGAGCCAC  CGTGCCTGGCCAAACCTAAGTAAATGTTTTAAAAATTATACTACT  AACATAGCATACAGGCTTTAGACTGTTGGTTGCTTTTAAAGTTTG  CTTACTTTTAAAGCTAGAGAGAAGATGGTTGAGGTGATCTTGTC  TCCTTCAGTATTCACCTCTGAGCCATGCCTCCTGAGGAAGTTTGC  TTTAGGGGAGGCATTGCTATGTTATACACTCTACGATGCACCAG  CCCTTGCTCAGAAAGGCAAGGTTTGAACCCCAACACTGTCTTTT  GCAAACCTGTTACCTTAGGAAATAGATTTTATCTCCTTAACTCAC  TTTTTA</p>	
KCP_1931 93	<p>GTTCAAGCGATTCTCCTGCCTCAGCCTCTTGAGTAGCTGGGACT  ACAGGTGCCCCACCACCATGCCTGGCTAATTTTTGTATTTTTGGT  AGAGACAGGGTTTCATCATACTGGCCAGGCTGGTCTCAAACCTCC  TGACCTTGTGATCCACGCACTTCGGCCTCCCAAAGTAATCACTG  CTGGGATTACAGAAGTGAGCCACCCTGCCTGGCCAAACCTAAGT  AAATGTTTTTAAATTTATACTACTAATAGCATACAGGCTTTAG  ACTGTTGGTTGCTTTTAAAGTTTGCTTACTTTTAAAGCTAGAGAG  AAGATGGTTGAGGTGATCTTGCTCCTTCAGTATTCACCTGAG  CCATGCCTCCTGAGGAAGTTTGCTTTAGGGGAGGCATTGCTATG  TTATACACTCTACGATGCACCAGCCCTTGCTCAGAAAGGCAAGG  TTTGAACCCCAACACTGTCTTTTGCAAACCTGTACCTTA [G/A]  GAAATAGATTTTATCTCCTTAACTCACTTTTTACATTTGCAAAA  TGGGTAAATTGTGACTACCTCACATGGATGTCATGAGATGAAAT  GTAAGAATGTGTGTCCCTGGCATATAGTAACCACTTTTCGCCAAA  GACTGAGTTATCCAACCTACAGACAGAGAACAGCTGGTGGCCTAA  TCAAAGGGAGATACAAAATAACAATGCCAAGACTGGAAAAGGAA  GTTTCATCTTAGGATTTCCAAGAGAAAAAGAAATATGACTGTATT  ATAATAGGTATATTTATTAAGCTCTTACCATGTGCCAAGCAAAG  TTCTTTATATACATGATATACTTCATATACATTATTTTCAATTTAG  TCCTCATGGCTACCAGGTGAGCACCATTATTTTCCATTTTACA  GATGAGGCACAGAGAAGTTAAGCCACTTACCTAGGAAGGGCAGT  CCTAGTTAAGAAGCTGGGATTCAAATCCAAGAGGCTGGATTCCA  GACCTCAGG</p>	SEQ ID NO. 205
KCP_1939 56	<p>TTATAATAGGTATATTTATTAAGCTCTTACCATGTGCCAAGCAA  AGTTCTTTATATACATGATATACTTCATATACATTATTTTCAATTT  AGTCCTCATGGCTACCAGGTGAGCACCATTATTTTCCATTTTA  CAGATGAGGCACAGAGAAGTTAAGCCACTTACCTAGGAAGGGCA  GTCCTAGTTAAGAAGCTGGGATTCAAATCCAAGAGGCTGGATTTC  CAGACCTCAGGCTCTATTATGAGAAGTACCTAAATAGAGATTGG  TTTAACCAAAGCCTGAGTCCCAACTAAGGGCAAGACTGTGACAC  AGAGGTCACTAATCAGAATGAAAGATTGAGCCAGAGTTGAGTTG  TTGGAATGTATTTTGGTACATTTAGGTTGTTTTAAGTATATCAA  TCTCCATTCCACTCAATGGTTGAGTTCAAGTTTCAAGTTTCCAA  ATGCTTTATGGGAAAGTCATATTTTCTCCATTGCAGCAGGGA  TGCCAGCGCAGCCATG [C/T] TTCTCAACCACCAAGTAGAAGCA  AAGCCAACTGACCCAAGAAGATGAACAGAGGGAATCCAGGGAG  TTCCAACCTTGGGTTTACAGCTGCAATTCTCAAAGGATGGACTAA</p>	SEQ ID NO. 206

	GCCATGTCACCCCTCCAGATAACACAGTCATATTAATAGTGACC TTTTGGAGGCCTCCCTAAACAGCAGGTGAAGTCCCAAAATCATT AGATTATTCCTGGCCTCAATTGTGGCCCAGAGGGAGAGCCCTAA GATTTTTCATGGGAACAAAGATCTAAATTCTGGGACTATCTGG GCCATGTCCACCCTGCACCATTACTACAAAATGGGCTGATCCT ATGGAAGCACACTACCTGTGTGTGGTCATATAGATCATCACCT GGCTTCTCCAGGGCTAACCAGTTAGCATGGAAATGGGACACCCA AGAACAAGAGGATAGAAAGAAGGGAAGGGTGGAAAGAAGGAAGG AAGAAAGGGTGGGAGGGGAAGAGTGGTAGTTTTG	
KCP_1946 16	TCCTGGCCTCAATTGTGGCCCAGAGGGAGAGCCCTAAGATTTTT CCATGGGAACAAAGATCTAAATTCTGGGACTATCTGGCCATGT CCACCCTGCACCATTACTACAAAATGGGCTGATCCTATGGAAG CACACTACCTGTGTGTGGTCATATAGATCATCACCTGGCTTCT CCAGGGCTAACCAGTTAGCATGGAAATGGGACACCCAAGAACAA GAGGATAGAAAGAAGGGAAGGGTGGAAAGAAGGAAGGAAGAAAG GGTGGGAGGGAGGGAAGAGTGGTAGTTTTGGAAGGAAGGAGGGA ATCAGAGCTAAAGATAATACATGATATGAGTCAGTGTTCATGT CCCTGAAGATTAGGGGAATCAAGCTTTGCTTCCAGGAGAATTAA CACAGGAGAGCCAACAGAGATGTGGAAATTTAGGAAGTCAGAGG AGACATTCTTTCA [T/C] TCATTCATTCTGTTTATTTCATT GCTCATTTTTACATGAATTGACTCTAGAACAGATGCTGGAGATA CAAAGATGCATGAGACTTGCCCCCATCTCAACAGTCATTCACA GTCTAATCAGAAAGAGAGCCTTGCAATTTGGAATACAATATGGAG TAATAATACCTCTGTGTTCAGCCTGCACAAAATACTCTGTATGC ATGGTCATATGTCCCTTGAAACAAC'TTATGAGGAAGATACTAC TATAGTCTCCATTTGACAGATAAGGAACTGAGGCTTAGGGAGG TCAAATAAATTGCCCAAGTAAACAAC'TAGTAAGTAGCTGAACC ACAAAACAGAGATTTCATGCAGAAAGCTGTACAACAGAAGAAACC AGGACTACATCTGCCTCAAAGGAACCAGAGAAGGCTTCAAAGA AGGCAGCATTTTAAATGGGTTTTGAAGGATGTATAGCA	SEQ ID NO. 207
KCP_1965 48	CCCAGCCCTCAGGCACATCAGTGCCCTCTCTAGGCTCTCTCTCA CCAAC'TTTAGAATTGAATTACATCAGTTGTTTCCAGATGGTGAT CTGCAGAATTCCTTTAAAGACCACCTGTGGGATTTGAGGGAGGA AACTTACACTCTCCCAATCTCCCTCTTTAACCCAAGCATCTGAT TGCTTTCATCTGTTTACATACTTAGCTTCTGTGCACAACTTCC TTTGATTAAAGAGTTCCCTTGCCCTTATAGTAGTGGATGATATCT AAGGATGATGTAAATACTGGGTGTAGCTAAGGTTTTTACCAA CTTAAAGCCTTTATGCTTCATAATTCCACTTTATTGATGTAGGA AGACAAATGATAGACTTACTTTCAAGGTGGATAGAAGGGATGCG ACCTAGCCAAGGCTACAGCATTTCTCT [A/G] TGGCACCCTGC CATGACAACCATCAGTTTGAATGCCTTATGGGTGCATCCTATGG GTTATGCACTGGCCCCAAGCCATAACCCCTAGGACTCTAGAGCC AGCAGCAAACACAAAACACTGAATTAATAATGAGTGAGATCTCT GTTCCCATAGCTGCCACAGGCTAAATAAGTTGAGGGGGTATTGT AAAACCCAAGATGAGATCACTGAGCCTCTGGTATCAAAAAGGTG TATTTACAGAAATGTTTAGTTGGACGAGAGCTTGAAGAGCATGG AAACGATCTGGTATCATTCTGGTCAAAGACCAGAATTTAGACCC CAGTTCTGCCATTTGCTGACTAATGACTTTGGGCAAAATACTTA ACTTTCTGAGAGTTAGTTTCTCATCTATAAAGTGGGGTAATA TAACCCACCTTGCAGGATACTGGTAGGATTA	SEQ ID NO. 208
KCP_1976 78	AGCAGGGTCCCCTGAGCGTTTCTCTCAGCTCCCAACACTTCCC TCCAGGCACAGTATGCAGGGCAAGGTCTGGAGGGGGCGCCGA AACACCACTCGAGATCCTCACTCTCAGGAATTCAATATAGAAAA CACATTAAGACCTGTTTACATGGAAGTCTGTTTATAATTATTG TTCCCTATGGGATATTCCCACTGCTTCTCCAATCCTCTTTTA AACTGCTCAACTAATAGAGTTTTCTGGCTTCCCAGGGAGACA TTCACAGATGCTAATAGAGACATAATTCAAAAATTGCTTGATAT	SEQ ID NO. 209

	ACATGCCCTCAATTTTCCCCAAGAACCACCTAAGTAAAGAGCCC CAGACATGCAACACATTTCATTGGCCAGATGCAATTTAACATGCG TGGGATTAAATATACAGGCTACTACAGCCAGGTTGTCATCAAGC AGCAGCAGGCATGGCATTTCCTAAGGTACCACCA [T/C] GG CCAAATGCAACAGGAAAGAAGCAGGCTGCTGGGTGGGACCCCTG GAAGATCCCCCTCTCTGTAAATTTCCACTGCAAGCTTTTCCCAGG CCTTTTCAGGCAAAGCGGGGAGTTTGGAAAATAAATCCCCCAGG CTTGGAGAAGCAAAGAATCAATGCTAAGCAGCTCCGGAAATAAT AGCTTCCATCTCTCTGATATATAAAGAGGATAAGGAAGGCAGAA AGAAGGGGCATGATATTATGAGATTGCAACAATACATTGCAACA TTACATTAAAGAATTACAGAAAGCAAGATCTAGCTTCAGATGCC AGTTCATGCACTTACTCCCTGTGTGACCCTGGGAATCACTTAAG CTGTCTGAGACTTAGCTTGTCTAATGACAACTGGGGATACTAA TATCACCTCCCAGGATTGTTGGGAAGGTAAATGGAGATTGACAA ATGTGAACACACTTAGTATGTCTTT	
KCP_1977 75	TGTTTACATGGAAGTCTGTTTATAATTATTGTTCCCTATGGGA TATTCCTCCACTGCTTCTCCAATCCTCTTTTAACTGCTCAACT AATAGAGTTTTCTGGCTTCCCCAGGGAGACATTACAGATGCT AATAGAGACATAATTCAAAAATTGCTTGATATACATGCCCTCAA TTTTCCCCAAGAACCACCTAAGTAAAGAGCCCCAGACATGCAAC ACATTCATTGGCCAGATGCAATTTAACATGCGTGGGATTAAATA TACAGGCTACTACAGCCAGGTTGTCATCAAGCAGCAGCAGGCAT GGCATTTCCTAAGGTACCACCACGGCCAAATGCAACAGGAA AGAAGCAGGCTGCTGGGTGGGACCCCTGGAAGATCCCCCTCCTCT GTAATTTCCACTGCAAGCTTTTCCCAGGCCTTTT [C/T] AGGCA AAGCGGGGAGTTTTGAAAATAAATCCCCCAGGCTTGGAGAAGCA AAGAATCAATGCTAAGCAGCTCCGGAAATAATAGCTTCCATCTC TCTGATATATAAAGAGGATAAGGAAGGCAGAAAGAAGGGGCATG ATATTATGAGATTGCAACAATACATTGCAACATTACATTAAAGA ATTACAGAAAGCAAGATCTAGCTTCAGATGCCAGTTCATGCACT TACTCCCTGTGTGACCCTGGGAATCACTTAAGCTGTCTGAGACT TAGCTTGTCTAATGACAACTGGGGATACTAATATCACCTCCCA GGATTGTTGGGAAGGTAAATGGAGATTGACAAATGTGAACACAC TTAGTATGTCTTTACATAGTAGGTATTCATAAACTCTTCTATA TATCTTCTCTTTCTGAAAATCTGAATATGGGGAGCATGGATATG	SEQ ID NO. 210
KCP_1989 33	GTCCCCACCCTCCTTTTTATTGAGAGGGAATTGACATTTCAGG GAATGGAAATGCCAGCCAGCAATTGGGGATGTGGTCTGGGAAC CCAGGTCTCCCATCCACTCCCTCGCCCTCTCACCCCTCCCGC TGGTCAGTGTTCCTTTGCTCTGCTGGCATCCCTGGGGACGGGC CAGCCCCCATCCCCCGACACACACATTGTCCCTTCAAGATG GAGCCAGGCTGACACCACGTAGAATGACCTGGAAGCCCCACTC AGTCTACCAGTCCCTCCCTCCTCACACAGGAATAGATGGGAGGGA AATGAAATAAGCTGCCATCTGCTGTGCATCCTCTGTGTGCCATG CTCTGGGTACCCATCTAATCCTCGTGAAGACCCTGAGAAGTGAG TGTTCTTCACAGACTAGGCAACACCAGAAGGCAG [G/A] TGAAG AACGTACAGAAGCTACAGAGTGACAGGTGACAGGTATGAGAGC CAAGCCATTCAAACCTCCCTGGGTATAGGACCCAGCTCTTCCCAC GTCTCTGCCTTTACCGAATCAAACACCTGAGCACGGAAGACCCT CCATCAACATGAACTGCTTTGAATTGACATGAACAAGCTTCAAT CAAACATAAATGCTGAAATTTTTCAATTATAGAAAGTATTTGA AAGATCCCATAAATTCCTGTGCATATCACGTGAGCTGCATTTA CTGCAGCAGACACTTTTTATCTCGGGCTTGGAGGAAGGATTAGC AAGAAGAAAGTGGAGGGGGTCTGAGGAAGGGCTGGCAGCCTAGA GGAGGACAGCAGCAAGAAGCAGGCTGGAGGCAGTTCTGTGCTGC CGGCCTTCATGGGTGTGGCCTTTGGACAGCACCTTAGCAGGAAT GTGGTGGAGAGCAGCCCCATTCACTCCAGAGGAGAGC	SEQ ID NO. 211
KCP_1993	AAGACCCTGAGAAGTGAGTGTTCTTCACAGACTAGGCAACACCA	SEQ ID

65	GAAGGCAGGTGAAGAACGTACAGAAGCTACAGAGTGACACAGGTG ACAGGTATGAGAGCCAAGCCATTCAAACCTCCCTGGGTATAGGAC CCAGCTCTTCCCACGTCTCTGCCTTTACCGAATCAAACACCTGA GCACGGAAGACCCTCCATCAACATGAACCTGCTTTGAATTGACAT GAACAAGCTTCAATCAAACCTATAAATGCTGAAATTTTTCAATTA TAGAAAGTATTTGAAAGATCCCATAAATTTCCCTGTCTATATCAC GTGAGCTGCATTTACTGCAGCAGACACTTTTTATCTCGGGCTTG GAGGAAGGATTAGCAAGAAGAAAGTGGAGGGGGTCTGAGGAAGG GCTGGCAGCCTAGAGGAGGACAGCAGCAAGAAGCAGGCTGGAGG CAGTTCTGTGCTGCCGGCCTTCATGGGTGTGGCCTTTGGACAGC [A/G] CCTTAGCAGGAATGTGGTGGAGAGCAGCCCCATTCACTC CAGAGGAGAGCCTCAAACCTCTCAGGCAGATCTAGCCTAGGTAG AATCTTGGCCTGGCCCCTCCGGGATGACAGGTGCCATTGCCCAA GAATGGGGAAAAGGCTGAAGTGCTCCAGCCAAAGACCCCAATTT ATCTTCAGGACAATTTTCACTGGAAACCTTGCCTCACCCTGCC CACTTTTTTCAAGTAATTAGAATGCTAATCTATAAGAAAGATG ACTATTAATAAATAAATTAATAATAGATAATACATTTTGGCCTTAC AATTTTGAATAATATAGCCATCCCATCTTAAAGTAAAAATTCAT ATATTTTTAATAAGCCTGAGACATGTTTTCCAATGAACCACAGA TGGTTCATTTTTATTATCCTATAAAGAGACATTATGGGCAAGTG TTTTTTAAATGGTAAACAGAACCTTAGAGCAGCTCTCTTTT	NO. 212
KCP_2002 41	GGCAAGTGTTTTTTTAAATGGTAAACAGAACCTTAGAGCAGCT CTCTTTTGAAGATCTCTAAGCACTTTCTAAGCATCAGGACCCCC TTCTGTCATCACAGAGACTGAAATGAGGAGATGGTCTCTGTCTCAC CCCCTCACTCACCAGTGAGCCCCAGACCTTCATCCCTGATCAGA TGGAAGCAGTGTGGCATGATTACAGTTCATATTTCAACTCTGCC ACTCAATGACTAATAGCCAAGCACTAATAATGCAGAAAAATGTAA ATTTAAAAAATAATCTTCTGAGATTGGTTATGAAATGCACTCA ACACAGCACCATCCACAGAGAGGTTCTTTTAAATTGCTCTTTTC TTTCCTCTCGACACCCAGAATCACAAGCATGCCTGAAAGCGTC ACACATATATGTCTGTGACCATAACATGGCATTGCACATGCAAA GGAAATAA [A/G] TAGGTGTTACCCATGTGACAAAGGTCCATGA GCTCTGTCCGCAAAAAGCTGTTGAGTTTAAAGAACAAATAATTC TGAAAAATCTTCCAGGAGATGAAATTTGTAGAACTCAAGGGCAG TAAACTAGCTGCTTTCCAAGGACTTGTCTAGCTTTATTGACTT ACAATAGCCAAAGATAAGTCAGTATTAATCAAACCCATTCTCTA GAAAAACCTCATCATCACTGGGGCCAGGGCAGAGAAGTGTGACA CAGCTCTCTCCAGCTTCCCCACTTCACAGCATGGTTCCACCATC CACCCAATTGCTAAAGCCTGGATAGTCTTCTTGTACCTCCCCG ATCCCCCTCTCTAACACCCATCCCCCGGCCACCCAACATCAGCA AGTCTGGTGGTTTCTCTCTGTCTCAGAGATTCAAGATCTTCCC	SEQ ID NO. 213
KCP_2019 85	TCGTAGTGTTTCATAGACTCTCCTTCCTTCTTAACCTTAAAGAGG CTCCTTCTGGTTTTTCTCTTCATACACTTCCCTCACTCTTTTCTT TCACTGCACTAAAGATGATTTCTAATTGCATAGTCATTGATGCC AGTATTTGTTTATTGTGTCTATTCTGCTGAACAGAGGATGGGCC TGACTTATTTGGGACCATGTTGCTGATGCCTGGACCTAAGCCTG GCACAGAGTAGGAGCTCAACAAATTTGTTAAATGAGTGGCTGAA TGGCCATACTCTCAAAGGACCCACAGTCTAGGAGAGACAGAAGA ATCTTTGTCTTTTGTCTTGCAGTGGGATGGAAGCTGCAGGGAG GGGTCTGTCTCATTTGATACTGTCTGGGAAGACAGAAAACTT CAGTTTCAGAGGAGGTAGCCCTTGAAAC [G/A] AGATTGAGAG AGGGCAGCACATTGTACAACCTCATGGGCACCATGCAATTGTA GTCCAGATAAACAGAGCCCCCTTGGAGATATGTGAGGCATGGGAT AGACTCAGAGAAACCCAGGAAATAACCCCTTCAGGCATCTGACA TGCAAAGATGTGGAAGTGTCAACCAGGAAGTCATGTTGGGGGAA CAGCAAGTATTTACAGAAAGTGACTGTGTGTGTCTGTGTAGGAG GGTGACTTTGTATAGGAGAGATAAAACCTGTGAGCTAATCAAGG	SEQ ID NO. 214



	AGAAGATCATAAAAGACCTTCATAAAGAGCATGGCCTTTTTCCT GCAAGCAGTGAGGAGCCATTGAAGGCTTTAGCATAAGGACAGTC AGATGTACTTCCCTAGAATGCACATTTCTTCTGCTCCAGAACT TCTGCACAGGAGGCTCCTAAAAGCTCTCCCCATCCTCCCTGTAC ACGTAGAATCTGCCTCTGTCTCTCTTTCTCTCT	
KCP_2020 67	CACTTCCCTCACTCTTTTCTTCACTGCACTAAAGATGATTTCT AATTGCATAGTCATTGATGCCAGTATTTGTTTTATTGTGTCAATC CTGCTGAACAGAGGATGGGCCTGACTTATTGGGACCATTGTTGC TGATGCCTGGACCTAAGCCTGGCACAGAGTAGGAGCTCAACAAA TTTGTAAATGAGTGGCTGAATGGCCATACTCTCAAAGGACCCA CAGTCTAGGAGAGACAGAAGAATCTTTGTCTTTTGTCTTGACAG TGGGATGGAAGCTGCAGGGAGGGTCTTGTACATTGTACTGT CTGGGGAAGACAGAAAACTTCAGTTTCAGAGGAGGTAGCCCTT GAAACGAGATTTGAGAGAGGGCAGCACATTGTACAACCTCCATGG GCACCATGCACATTGTAGTCCAGATAAACAGAGCCCCCTTGGAG [A/G] TATGTGAGGCATGGGATAGACTCAGAGAAACCCAGGAAAT AACCCTTCAGGCATCTGACATGCAAAGATGTGGAAGTGTCAAC. CAGGAAGTCATGTTGGGGGAACAGCAAGTATTTACAGAAAGTGA CTGTGTGTGTCTGTGTAGGAGGGTGACTTTGTATAGGAGAGATA AAACCTGTGAGCTAATCAAGGAGAAGATCATAAAAGACCTTCAT AAAGAGCATGGCCTTTTCTGCAAGCAGTGAGGAGCCATTGAA GGCTTTAGCATAAGGACAGTCAGATGTACTTCCCTAGAATGCAC ATTTCTCTCTGCTCCAGAACTTCTGCACAGGAGGCTCCTAAAAG CTCTCCCCATCCTCCCTGTACACGTAGAATCTGCCTCTGTCTCT CTTCTCTCTCCTCCTCCTCCTCCATCTCCTCCTCCTCCTCCTC	SEQ ID NO. 215
KCP_202 795	GCTCCAGAACTTCTGCACAGGAGGCTCCTAAAAGCTCTCCCCAT CCTCCCTGTACACCTAGAACTCTGCCTCTGTCTCTCTTTCTCTCT CCTCCTCCTCCTCCATCTCCTCCTCCTCCTCCTCCTCCTCCTC TCGCTGTCTCACACACACATACACACACTCCTTCTTCTCTAT CTAGTCAGATTCCACTCCTTGGGATTTAGGCCCCACCGTCACTC CTCAGGGAAGCCTGCCCTGAATGCCTGCACTACACAGGGCCCC TTTCCCCCTGCCCCCATCCCAGAGCACCAATAGCTTTCCCTTGC AGCACTTCTCACAGCTGTCAATTTATGTTTGTGTCTGTGATTCT TAGGTTAAGTCCCTCATGCACCAATCATAAGATCTGGGAACAA GGACCACACCTGTCTG [C/T] TCATCACTGTAATCATCACT GCCTGCCAAAGTGCTTGCACATATTAGATACCTTAGTAGTTATG TGTTCCATGAATGACTCTTTAAGAGATCTTCTAGCTGTTCTTGC AAAGAACCCATTGGTAAGGTTGAACCTACAGGCTGATACTTGC ACTAGTCTCAGGAAGAGATGGTGAGTACATGAAATTGAGTCCCC CAGAGGTTAATGCCCAGTGCCCCAGCTAGGAAACGTCCAAGGAG GCAATTTGAACCCCATCTGTCTGGCTGCAGAGCCTAGCCCTCTA ATGCATTACAGGGTCTTAGCTCCTCGAGGATGCCACTGTGCCGT GAACCTTCTTCTGACCTCATGGCTCCAGCACAGCATCCACAC TCAGAAGTGCAAGATGAATGTTTGCAGATAATGAACATAAGCT. CTCAGGAACCTCATCTCCTGAGAATCTGCTTTGGCCCCCACAG CAGGTCTGGGTGTGGACCTTCCCCA	SEQ ID NO. 216
KCP_2042 42	GTGGCAAAGTTGGGATCTTAACCCAGTTCTATGTGGCTATAAAG TTCATGGAATAGAATGCTGCAGTTAAGAACATGGGCTTTGGCAT CAAGCAGACCTGTATTTGAGCCCCACCTCTGCTGTTTATTAAC GTGGCCCTGGGCAGATGACCTTACATCCTTAAGTCTCTAGTTCT TTGTCTTTAAAGGGTGGCAGAATGTACCTCACTGGTTTTAGGA AGGTCAATGAGATAGTGACATGAAGCCCTAGGCATGGGAAAA TTCTTCTAAATGTGAGCTGCCATTCTGATCACTGCAAGACCC CACCCCAATACTCCCAATTGTACCACCCACCCCACTCACCAG TGTCTCAGAAATGCCTCCTCCAGAAGGAAGGCATCCTGTCTAAC CCACTGCTTCTAGCCAAGCTGTCTTTCTTCAAGGTAGAAAAA GATTGTTAGTCATTGTTTAAATCTTTATTGAGTATATACCGCCAC	SEQ ID NO. 217

	<p>ACCAATTGCACTGCCA [C/T] TCATTATCTCATTTAAATCTGAC  AAGAGCCTTGTAAGTAGGGATTATTCCCACCATTTCCCAGATG  TTGAAACTGAAATTGATAAACACGACATGTTGCCATGGCTACAT  GAAGATCTCCAAGCCGGAGGATCTCCACCCTCACCTGCCTAGCT  TCCCAGACCTCTCTGCAGAAAAGGGACTGACCCCAAGACAGCC  CTGGCCTCTGGGCTCCACCCCTTCCACATCCATCCCAGGGCCGC  TGAGGACTGAAGAGTTCTCCACGTTTGCCCTTTAAAGTGACTTA  AAAATAATCTTTATGAATTTCTTCATATACAAAATTTGTACTTA  CTCATTGCAGCAAATTTAGAAAATACACATAAGCAAAAAAGAAC  GTAACAGCCATCCATAACCCTAACTCTCAGAGATCACCCTATT  AAAATGTTTATTATCTAAGAGAGAGATGATATAGACAAAGATGA  GACAGATTGACACAGAGAAGATGGGTACATGATAGAT</p>	
KCP_2062 67	<p>TGCTCAACTGTAATCAAACATTATTTTTAAAAAATCATTCCAGC  CTGGGAAACAGTGAGAAACCCATCTCTACAAAATAAAAAATAAA  AATTAGCTTGGCATTGTGGCATCTGCCCCGTGGTCCCTGCTACTC  AGGAGGCTGAGATGAAAGGATCACTTGAGCCTGGGAGGTTGGGG  CTGTGGTAAGCCGTGATTGCCCATTTGCACCTCATTCTAGGCCAA  CAGAGTGAGACCCTGTCTCAAAAAAATATTATTCAATTAATAT  CTGTTGCCACCACAGGACTGATCCCTCTGTGAGGGCAGAGATTG  TTCATGCATGGAATTGTGATTATAAGCACTGGCTCTGGAGCCA  GGTTGCCTGAGCACGGAGCCAGCTGTGCCCTGCGGGACACCTGT  GGCACACTTCACTCCTGGGACACCTGGGACACGCACACAATAGA  AATGTTTACATTTTACTAGGCAATGCCAGTCACATAGTCCCTACC  TAATTTCAAAGGGTA [A/G] AAGGTACACCCAACACGCATCAG  GAAGGAGGAGGACCAGAAATTGTTGGTGACAAGCACAAATGACC  ACCCAATATAATATTTTGTGTTGGAAGGCATTTTATTCCACAAA  AACACATTACAATAAACACAACAACAAACACTGGTTGCAGTA  GAACCAACTTTCCAGACCTATCTGCACAGCACAAACATTATCCC  ACTCAAAATGTCATGTTTTTACCCAAAAACATTAAAATTTAAAA  GCAATTCAAACCCATAGCTTAAAAAATGTTCCAACCAGTAATAA  AAGGAAAAGTGTGCCTCCTCCTCCCAACTTCCCTACCCACAAT  CGCAAGATATTATCCTTATAGGCGAAAAGGGTTTCAGGATTTGA  GATGCAGGCTGGGAGGTCTGAGAAGACTTCCTATAGAAGACATG  ACTTCAAACCTCTTTCTTGTATGTGAGATTTAATTTTCAAAGACT  CCTCTGATCCAACCTTAAGCTTTATGGTAAATCACCTT</p>	SEQ ID NO. 218
KCP_2076 61	<p>ATATGCCAGCGCTCTATCTGCAGGGGTTCTTTTGATAGCAGCAG  ACTGAGAGATGATGTTACTGTCCCCTTTTCTCTGTTGTTGGCAA  CTGAGACTCAGAGGATGGAAGTGACTTGCTCAGGTCCACCACCT  CTTCAGCTGTGGAGCTGCGACAGGAGCCTTTGTTTGACTTCAA  GCTCACCATCACTCCTCTCTCACTGATGCTCAAGTGGGCTATCA  CCTCGCCTTTCTTGAGCCTTCTTTCGCTATCCTAAAACAGCGCC  TCCCGAAATCACCCTAAAGAACTTATTCATGTAACCAAACACC  AGCGGTTCCCCTAAAAACCTATGGAAATAAAAAATTAATAATAA  AACAGTGCCTCCCATGACCCATGTCTCTCCAGTCCCATAACTCT  GCTCTATTTCCATTACAGCTCCATCCCCACCTTTATGTCTTTT  GTTCACTGCTTTATCCCCAGTGCCTAGAAGAGTGCTTGGCACCT  AGTAGACACTCAGTAA [C/G] TATTTGTGGAATGAGTTAATAAG  GTTGTGAAAAGAACGTTAGATTACTGGAAGGATTCATCTGAGTT  TAATTCGTCTATGCTGGGAATCCAGTGTGCGGCCCTGGATGAAG  CCAGTTCCCTCCCTGGGCCCCAGTAGCCACATCTGTACATTTAG  AGGGCAGGAGAAAAGCCACACGCTCTGTGACTTATACAATTTGT  TGCCCAGAGTGGAGGCTGCTTTGATGCTCAGAAAAAAGAAACAA  ACATGGAAAATGCTAAATGGGTGGCAGAGAGCTTGAGGGAGGAAG  GAGATGGGGAGGGTACTCTTGAAACTGTTTGGTGTCTTCCCTCC  TGCCCCCTCAGTACCAATTGTCAAGTACAGAAAGTGAAGGAGAC  TTGTATTAGTGGAATTTGGTCCCTGACTTGTATAGAGACACAA  TTACAAAGACACAAGAGTGGGCCAGCAGAGACCCCTTAGGGTGG</p>	SEQ ID NO. 219

KCP_2079 65	<p>TCCCTTGAGGTTCCAAAGCATCTGCCCATCAAGCAGA</p> <p>CACCAGCGGTTCCCCTAAAAACCTATGGAAATAAAAATTAAAAA  TAAAAACAGTGCCTCCCATGACCCATGTCTCTCCAGTCCCATAA  CTCTGCTCTATTTCCATTACAGCTCCATCCCCACCTTTATGTC  TTTTGTTCACTGCTTTATCCCCAGTGCCTAGAAGAGTGCTTGGC  ACCTAGTAGACACTCAGTAAGTATTTGTGCAATGAGTTAATAAG  GTTGTGAAAAGAACGTTAGATTACTGGAAGGATTCATCTGAGTT  TAATTCTGCTATGCTGGGAATCCAGTGTGCGGCCCTTGGATGAAG  CCAGTTCCCTCCCTGGGCCCCAGTAGCCACATCTGTACATTTAG  AGGGCAGGAGAAAAGCCACACGCTCTGTGACTTATACAACCTGT  TGCCCAGAGTGGAGGCTGCTTTGATGCTCAGAAAAAGAAAACAA  ACATGGAAATGCTAAATGGGTGGCAGAGAGCTTGAGGGAGGAAG  GAGATGGGGAGGGTAC [C/T] CTTGAAACTGTTTGGTGTCTTCC  CTCCTGCCCCCTCAGTACCAATTGTCAAGTACAGAAAGTGAAGG  AGACTTGTATTAGTGGAATTTGGTCCCTGACTTGTATAGAGAC  ACAATTACAAAGACACAAGAGTGGGCCCAGCAGAGACCCCTTAGG  GTGGTCCCTTGAGGTTCCAAAGCATCTGCCCATCAAGCAGATGA  TGTGATTAGTCTCTGTGACCCCAAGGATGCCTCCTGAAATTGCT  GATTCAATTTCTCCTAATAAAATAGGAACAATAATTAGCTAATA  AGAAATCAACAATTAAAGCTATGAGAGAATTAAGTGAGATCATG  TAAGCAAAGTACATGTCACAGTGCTCTGCAAATAGGCAGTGCTC  AGAAGTGTACCTTTTCTCTTTCTCTCTGAGCCTCCGTCTTCT  CTTCGGTAAAAATGAGAATAATATTATGCATACCTCACAGGGGTT  AAGCAATGTGAAAGTACTCTGTAAAGTATAAGGCTGA</p>	SEQ ID NO. 220
KCP_2115 25	<p>GAGATGATCAACAGTCTTTTCATCCAGAGGGTTGTGTTTGTCTGGT  GGCCATTACCTTTAACATAAAACGATCATATTTACTTTATCCTA  TTCATGTCCAACCTCAACTGACAATTGAGTTGTGTCTCTGACAA  TAAATAGCAGAAAAAGGAAATCTTCCTATACTGAAGAGAAACAC  AATTAATTAAGTAGATCCATCAGGAAAGGTACAATCATGATTGA  GACAGTGTTTAACAGATGTGACTATTGGATTCTGTTGTTGAGAA  TGACCCTTAAAATCACAGTCAAAATATACGACAAGATGGAAATA  ACATTTTTGAGCACCTACTATGCATGTAGAGCATCTTACATACC  TTATCTCACTTAGATTTACAGCTGCAAGGTGGGTATGATTCTAG  CTTGAATTAGTCTAATAACCATATACCTCCTAGGGGCAGTGAGA  TGATTAGATCAATTCTAAAACCTATTACCATGCTCTCTGAGCTCA  CCAAGACAGGCAGTTA [A/G] TACAAGGATACATTAATACCGAA  TCCAGCAAAGCTCACATGGCCAGCTTCCATTATGTTTCTATTT  GTGATTATTCTGTATCAAGCACAGAAATGTATGTTACACGAAC  AACAAAGAAGGGGTTTATTAGTGTGATTACAGGGCCTAAGCCT  ACCTCTGAAACTGGTTTTTGGAGTCTTTAGCACGCTTGTGTTGGG  ACAGTTAAACATGTGCCAGCTATTCTAAAACAGTAGCAGTAATG  TGATAGAGCTGGGTCATACCGTGCTTCCCAAAGTATGATCACTT  CATTTCAACAACCTTCACTAACAAGCCTGAACTGGGCTGTGAAG  GGAATATTTAGACCAAGGAAACTGGAAAACCTGTATCAATCAGGC  TTTTCCACCCTCCCCAAGAGCCAGTTGTCAGATATCTACCAGCC  TACCAACGCTAGCTCTCTAATCAGAAACCATCACTTAGCAAGTT  CCCAAATTATCTGCAGAGCAATGAACCTCTCTCTTC</p>	SEQ ID NO. 221
KCP_2118 50	<p>CTATGCATGTAGAGCATCTTACATACCTTATCTCACTTAGATTT  ACAGCTGCAAGGTGGGTATGATTCTAGCTTGAATTAGTCTAATA  ACCATATACCTCCTAGGGGCAGTGAGATGATTAGATCAATTCTA  AACTATTACCATGCTCTCTGAGCTCACCAGACAGGCAGTTAA  TACAAGGATACATTAATACCGAATCCAGCAAAGCTCACATGGC  CAGCTTCCATTATGTTTCTATTTGTGATTATTCTGTATCAAGCA  CAGAAATGTATGTTACACGAACAACAAAGAAGGGGTTTATTAG  TGTGGATTACAGGGCCTAAGCCTACCTCTGAAACTGGTTTTTGG  AGTCTTTAGCACGCTTGTGTTGGGACAGTTAAACATGTGCCAGCT  ATTCTAAAACAGTAGCAGTAATGTGATAGAGCTGGGTCATACCG</p>	SEQ ID NO. 222

	<p>TGCTTCCCAAAGTATGATCACTTCATTTCAACAACCTTCACACTA  ACAGCCTGAACTGGGC [C/T] GTGAAGGGAATATTTAGACCAAG  GAAACTGGAAAACGTATCAATCAGGCTTTTCCACCCTCCCCAA  GAGCCAGTTGTGATATCTACCAGCCTACCAACGCTAGCTCTC  TAATCAGAAACCATCACTTAGCAAGTTCCCAAATTATCTGCAGA  GCAATGAACTCCTCTTCTTCAGAAAGCAGGCTGAAAGATACACT  GTTACATCTTAGCCTGACCTGGACCCAGTGAGTTTCCATCAGT  GAGAAAATTCTGTGCTAACTTGAGATAATACTATTCTTGTGGCA  ATTTTACTTTTCTTTGAGCGATTCTTCAACCTCTCTCTGCCC  CTTCATTTTTCCGTCTTAAAACTAAAAGTGCCCTTTCTCCCTGG  ACACTCCTCATTTGCAATGAATTGTCATTTTCAGCTCCTCAGTCA  AGAGGAGTAATGAAATCCCACCCGTGTTAATCCTCTTATATCCC  GCAGAAATATTGTAGACCCACTCACCCCTAGGCAACAT</p>	
KCP_2127 75	<p>AGTAATGAAATCCCACCCGTGTTAATCCTCTTATATCCCGCAGA  AATATTGTAGACCCACTCACCCCTAGGCAACATGCCCTCTCTCTT  CAACACAGGTCATCAATTGTTCACTTTACTGGCTATCTCCATGTA  CTGGAACTTCAGGGTGGTGTCCAGCTGGGTTCAAAGGAGAAACA  GTGGGAAGTTTCTCCACTGCCACCTGAATTAGATGAGAAAGAGT  TGTCTACTGAAATACACTAGCTGGTGGCAGGATTGGGACGTCAT  TTGACTAATTGCCTCCTAGAGCTGCAGAGACTGCTGGAACTACC  TAAGTAAATCATCAAAAAAAAAAAAAAAAAAATCATCCCAGGG  CACTTTTTTCCAGACAAAAAGGTCCACTTAAACATCCTCTAGAG  ATCTGTGCCTGAAGCTGAGCTGCTGCAATGAACTGACATTTCT  GCCTTGCAGCCTGGCCATGGGCTTAGCTGGACTAAAATGCTGCT  GCAGTGGTGAGGGCAC [A/G] TGAGAGTCCCTAATGTACATGGC  CTTGCTCCTTGTCTGACACATCTTTTAGGGCTGCTGCTTTCTC  TAGTGCTGGAATCTAGATAATTCCTTTCCAGCCGTTTGTCTCT  TCAATCTTGGAAAATATCTGGATGAATGTAACACTGTCACACAC  AAACAGAATTATGACTTACGTCACATTCTATGTCGTGATTTTGT  GGACTTTTAATAATTGCATTACATTTGTGACCATTAATTTCCAC  CATCGCCCTGCTCCTGAGAATCTGTAAGGGACATTTGACACTCC  TCTCCCCACCCACCTCAACATTTGTGCTGACCTGAAGGTACAT  TAAAAACATACCCATTTGGAGAGAAAGATCTGTCTACTGAAATA  CACTAAATATTGAAGAAATTTCCAAGTCATTTGATCTTGAAACT  CCATCTAATGGAAGCAGAAACACTCAAAGGTTTTTTTTTTTGA  CTCCCTTTTTTTCAGGACACTTTTCAGGACTGAGGTATAT</p>	SEQ ID NO. 223
KCP_2217 99	<p>TCAGACTTTGAACAAACCTCAGAAGGAAGTGTCAAGGAGGCTCC  CCACGGGTTACGCTCTTCTCTCCTCCTGCACACAGGGAACAGG  GCCATTCTCCTTCTTTACTGGGACTACCTGGGCTTCATCCAGG  GAATCCCCAGGTGGCAACAGGAGGGTGGTGAACCCGCTGCCCG  TCACCTGTAAAGTTTCTGTGAATGTGTCTACAGCGGCCAGCAC  CACAAGGCATACAAAGAAAGGGAAGGGAGAGCTGATGTGAGAGC  GGCAGCGTGGGCACTCCTGTGAGGTTGCCACAGCTGTAGACAAG  TTAAATCAGTGCAGTTCAATCAAAGTCATGACCCATGAGCGTC  ACAACCAGCAGAGTCTACAAAGGAATACATTAATACTAAGACC  AGAGCACAGCTCACATTAGTGAGGGATGGGATCATTTTCATGGAG  TTTTTGTTCAAAAATATTTCAATTAACATTTCACTTATATACATG  TGTGTATACTGGGTTGTGAT [A/T] TAAATTACAATTCTTACTA  TAAATACAGCAAAAGAAAGAAAGAAACAAAGAGAGGGCCACTGG  TTTACCTAACATCCACAGGCAGGCTACTTCCCAGCATCTTGAGC  CCCAAAGAAGTAAATTTCTTCCACAACCGATGTTACCAAGCC  TGACACTTAGCCAATGATGAAAACGAAAAACAAAACAAAAGCTT  GGCAGTCAGTATCCAAATATGCAGATACTACAGAATCTGTTTGA  TGTAGAAGTTGATCCTGCTACCCAGACAGCAAAACACTCATTTA  TTAATAAAGTCCAGTTCCTCCTTAATGAAGTGGGTTAATAGTT  GATATCTCAATAATTACTTAGTGCATTTTTTATGAAGGTGATGG  GAAACAAGTGCTGTTTCTTGAGTCGGAAGAGTCTCTCAAGCTC</p>	SEQ ID NO. 224

	CCACAAAGAAATTTCCCGAGCTTGTGAGGAATTCAGTCACAGGA AGATCAAGGAATT	
KCP_2235 68	GATCTAATGCTAGGAGATTCAAACCAACAATTAATTTCTCTGTT AAAATGGGTTAAAATAGATGTAAAATATTAATATGTATATAAGC ATTCTGAATTAGACTTATGTGAATTTTTCTCCTTTTCTTTCTTT CTTTTTGAGAATAAGCCCTTTCATTTACGTAGAAATGCTTCAGC GTTTAGATAATTGCTACTTATCTTGTTAGCTACAAACACAACCA TAATTAAAGGCTCTGTAAGAATTATGAATTCTGGGGAAATTGGC CACTTGTCTCTGTGGCGTAAACAGTATCTAATTTATAACAAATC ATCTGCCTTAGTCCCAGCAGGATAAGGTGATATGTATTGCCAG CACATGAGAAAGATGGCAATTAGGAATTGTTACCAAGTTACGGG AGCCTCACACGAACATCCATCACCTTTGGGGATATGTACAAGAT ACAACTTAATTTGATGGATTCTTTTGTATTGGGATCAAAGTC TCAAAGGGAAAGTGACAATTTCAAGGAAATCTGGTGCAATGA GACCAACACTGATGAGAGAAAATGCACACAATTTAATACACCTGC TCACCTGATGTGGCAACTCAGCCTGTGCTTGTGTGGGTTGCCA CAGGATGAGACATGGTCTGTGCATATTTCCAGCAGCCACCCATC TCATCACTATTCTTGCCAGCCAGATTACAGTTGTTCAATAGA TGGATTTGGTAATATCTGCATGACAACAACAGGCAGAGAAGGTT AGATGGCAATTGATTCTTGATTGGTGTAAGTTTATAGAACACAT TCTGGCAGGGCCCCAAAGGAAATCACTCACCTACCCCTCTGTGAT GGTAAAACGTTGAAAATTCCACGACTTGGACCTTGTGATCCTT CAGTGAAGATGGGCAGATTCTTGTCTTTAATTGACAGACACTT TCTAAATAACTAATGCAATCTTATATTACATTATAGTCCATAAG GGAGACATACTTAACTACTACTTACAACAAC [G/T] GTTTTTTA GAGCCTTTCAAATGGTGTGTACAAAGTAGCTCCCATTTAAGATA TTTTCTTAGTATTTTAAGGCTATCTAGTAGACATTACAAAACAAT ACGCTGTAAATACATTAGATTTTTTATCAGTAATACTTAAACATG CCGTAATTTGAACTTTCTGCTAAATCATGCTATCCATTCTTAGT TGGCCCCAATGGTGAGAGTTTACTGTTCTTTAAATAATTTTGT TTCCCTTTGCTGTCTAGAGGTGTTTATCATCTGCTTACTTGCC TGTGTCTCTGGAATATTCAGAAGGTTCCATGGGAAACAAATTTGA ATATGCAAAGAAGTTATTTTTAAAGCAAGGAAAATGTTTTCATA TGGATTTATTTTGAGCACTTCTGCCTTTGCCTCCACTGGGAACA TGTTTCTCTCCAACGCCGAAGCCCCCTCCCTGTGTGGTGTGTA CGCAGAGGCTGACAGGGCAGGGAAGTGGGGTTCAAGATAGGAAG GCCATTGGCAGTGTGACCCAGCCACAGTCCTAGATCCCAGGT CGTGACACCACTCTTTTGACAGCCAGATTGTTACCTAACAAGA ATGACTCCCAAGCTCAACCATTCCAATGCCATCTCCTCTGGTTC CAGATAAGATTGAAGATGAGCTGGAGATGACCATGGTTTGCCAT CGCCCCGAGGGACTGGAGCAGCTCGAGGCCAGACCAACTTCAC CAAGAGGGAGCTGCAGGTCTTTATCGAGGCTTCAAAAATGTAA GACCCGTGCACGCTCTGAAGGCCTGGGGGGGGTTCCACGTGAG GCTACACTCTCCCCAATGCAAGGGAGCTCATAAGGCGTTTCCC ATATGTGAGGCTGTACAAGGAAGGCCAGCTCTATAAAGGGGGCA TGAGAGGGAGATCACCTGGCTAGAAAGGAAGGCTCCAGGCGAGG ATGGAGCAACCTCAGGAGACAGTAAACGGCCAACCTGCCAGAAA TTTCACAGGGTGGCACATCCTCAAG	SEQ ID NO. 225
KCP_1152	GATTTTTATCAGTAATACTTAACATGCCGTAATTTGAACTTTCT GCTAAATCATGCTATCCATTCTAGTTGGCCCCAATGGTGAGAG TTTACTGTTTCTTTAAATAATTTGTTTCCCTTTGCTGTCTAGA GGTGTATTATCATCTGCTTACTTGCTGTGTCTCTGGAATATTC AGAAGGTTCCATGGGAAACAATTTGAATATGCAAAGAAGTTATT TTTAAAGCAAGGAAAATGTTTTCATATGGATTTATTTTGAGCAC TTCTGCCTTTGCCTCCACTGGGAACATGTTTCTCTCCAACGCCG AAGCCCCCTCCCTGTGTGGTGTGTTGACGCAGAGGCTGACAGGGC AGGGAAGTGGGGTTCAAGATAGGAAGGCCATTGGCAGTGTGACC	SEQ ID NO. 226

	<p>CCAGCCCACAGTCCTAGATCCCAGGTCGTGACACCACTCTTTTG  ACAGCCCAGATTGTTACCTAACAAGAATGACTCCCAAGCTCAAC  CATTCGAATGCCATCT [C/T] CTCTGGTTCAGATAAGATTGAA  GATGAGCTGGAGATGACCATGGTTTGCCATCGGCCCCGAGGGACT  GGAGCAGCTCGAGGCCCAGACCAACTTCACCAAGAGGGAGCTGC  AGGTCCCTTTATCGAGGCTTCAAAAATGTAAGACCCGTGCACGCT  CTGAAGGCCCTGGGGGGGGTTCCACGTGAGGCTACACTCTCCCC  AATGCCAAGGGAGCTCATAAGGCGTTTCCCATATGTGAGGCTGT  ACAAGGAAGGCCAGCTCTATAAAGGGGGCATGAGAGGGAGATCA  CCTGGCTAGAAAGGAAGGCTCCAGGCGAGGATGGAGCAACCTCA  GGAGACAGTAAACGGCCAACTGCCCAGAAATTTACAGGGTGGC  ACATCCTCAAGGAATTCACCTGGCCCAGGGTCAAGCCTTAGCC  CTTAACATAATCATACCTTCCAACCTGGTGGTGCCCCACAATA  ATGGGATTTGGCCCTGCTGACTTATGCTAACCAGGCT</p>	
KCP_1333	<p>GGCAGGGCCCAAAGGAAATCACTCACCTACCCCTCTGTGATGGT  AAAACGTTGAAAATTCACGGACTTGGACCTTGTGATCCTTCAG  TGGAAGATGGGCAGATTTCCTTGAATTGACAGACACTTCT  AAATAACTAATGCAATCTTATATTACATTATAGTCCATAAGGGA  GACATACTTAAACTACTACTTACAACAAGTGTGTTTAGAGCCTT  TCAAATGGTTTGTACAAAGTAGCTCCCATTTAAGATATTTTCT  AGTATTTAAGGCTATCTAGTAGACATTACAAAACAATACGCTGT  AAATACATTGAGATTTTATCAGTAATACTTAACATGCCGTAAT  TTGAACCTTCTGCTAAATCATGCTATCCATTCTAGTTGGCCCC  AATGGTGAGAGTTTACTGTTTCTTTAAATAATTTTGTTCCTT  TGCTGTCTAGAGGTGTTTATCATTCTGCTTACTTGCTGTGTCT  CTGGAATATTCAGAAGGTTCCATGGGAAACAATTTGAATATGCA  AAGAAGTTATTTTTAAAGCAAGGAAAATGTTTTCATATGGATTT  ATTTTGAGCACTTCTGCCTTTGCCTCCACTGGGAACATGTTTCT  CTCCAACGCCGAAGCCCCCTCCCTGTGTGGTGTGACGCAGAG  GCTGACAGGGCAGGGAAGTGGGGTTCAAGATAGGAAGGCCATTG  GCAGTGTGACCCCAAGCCACAGTCCTAGATCCCAGGTGCTGACA  CCACTCTTTTGACAGCCAGATTGTTACCTAACAAGAATGACTC  CCAAGCTCAACCATTCGAATGCCATCTCCTCTGGTTCAGATAA  GATTGAAGATGAGCTGGAGATGACCATGGTTTGCCATCGGCCCC  AGGGACTGGAGCAGCTCGAGGCCCAAGCAACTTCACCAAGAGG  GAGCTGCAGGTCTTTATCGAGGCTTCAAAAATGTAAGACCCGT  GCACGCTCTGAAGGCCTGGGGGGGGTTCCAC [A/G] TGAGGCT  ACACTCTCCCCAATGCCAAGGGAGCTCATAAGGCGTTTCCATA  TGTGAGGCTGTACAAGGAAGGCCAGCTCTATAAAGGGGGCATGA  GAGGGAGATCACCTGGCTAGAAAGGAAGGCTCCAGGCGAGGATG  GAGCAACCTCAGGAGACAGTAAACGGCCAACTGCCCAGAAATTT  CACAGGGTGGCACATCCTCAAGGAATTCACCTGGCCCAGGGTC  AAGCCTTAGCCCTTAACATAATCATACCTTCCAACCTGGTGGTG  CCCCACAATAATGGGATTTGGCCCTGCTGACTTATGCTAACCA  GGCTCACCGAGACTGATGTGTAAGCCGAATGTCGGTGTATTAAT  TTACCTTGGGAAATGGAAGTACAGTGGAAACAGACACTCCTCT  CCCTTCGCTGGGACCCGCTCTCCTTGGAGCCACATGGAAGCCA  GGTTACAATCAAAAGTGGAGTCAGAGGACGGGAGTTCTTGTGTT  AGTTGTTACTTTAAATACATTAATGTGTTCTGAGTCTCAGGC  CAGTTTGAGAGCTCTCAGATACAATCCTGGATATTAATTTATTT  TTTAAGTTTAACTCTCAGAGTGCAATCTTATCCCAAATCCTGG  AGTGGTGTGGAGTGGGGTGGGCTACAGCGACATGCACCTGGTCA  CCCTCCCTCCAGGTGCAGTCTGTAGGTAGAGCTGAGCTGGGTCA  GTTCCAACTGACCACAGCCTCAATGTTCTCCAACTGCTGACC  CACAGGGATTCCAGCCCCCTCCTGGGAGTTATCTGACAGGTGCTG  GGATGCCTCTTCTTCCACACTAGCCTTGACTGCACATGCCAAG  TGCCCAGTTTCTACCATTAGGGCTTCTTTCCTTCGATGGCAGC</p>	SEQ ID NO. 227

	ATTAGCAGTGGGCAGCCGAGTTGGAGAAGGATCCTGTGGGAAAG TTTTCCAGGCAGGCACTGGGCTCAGAGGGAACAGCATCCAGAAA AGAGAAGAAATCTACACTGCTTGGC	
KCP_2252 20	AATTTACCTTGGGAAATGGAAGTGCAGTGGAAACAGACACTCC TCTCCCTTCGCTGGGACCCGCTCTCCTTGGGAAGCCACATGGAAG CCAGGTTACAATCAAAGTGGAGTCAGAGGACGGGAGTTCCCTTG TTTAGTTGTTACTTTAAATACATTAATGTGTTCTGTCAGTCTCA GGCCAGTTTGAGAGCTCTCAGATACAATCCTGGATATTAATTTA TTTTTTAAGTTTAACTCTCAGAGTGCAATCTTATTTCCAAATCC TGGAGTGGTGTGGAGTGGGGTGGGCTACAGCGACATGCACCTGG TCACCTCCCTCCAGGTGCAGTCTGTAGGTAGAGCTGAGCTGGG TCAGTTCCAACTGACCACAGCCTCAATGTTCTCCAAACTGCTG ACCCACAGGGATTCCAGCCCCCTCCTGGGAGTTATCTGACAGGTG CTGGGATGCCTCTTCTTCCACACTAGCCTTGACTGCACATGCC AAGTGCCCAAGTTTCCT [A/G] CCATTAGGGCTTCTTTCCTTCGA TGGCAGCATTAGCAGTGGGCAGCCGAGTTGGAGAAGGATCCTGT GGGAAAGTTTTCCAGGCAGGCACTGGGCTCAGAGGGAACAGCAT CCAGAAAAGAGAAGAAATCTACACTGCTTGGCATCTACCATGGA CTCAATACCACCTAACATAGGTTTATAAGATACCTTGGGGAAAG TTATTGTTACCCCCATTTTACAGGTAAGGATATTGAGGATCAGA GACTGGCTTGGCCAAAGTCACAAAGCTTAGTATTGGCTGAGCCA GGATTTAAACCCAGGTTTTTCTGATCTTAAAGCCCCAAATCTCT CCACCTCACAGTGGCCATTCTCTGACAATGTCTCATATTTTGC AAAGCAGCTCCAGTCTGAGATGGCACTACTTGGGAGAAGTGGA AATGCACAGGTCCCTGTCCCTGGGGATCATGAGGAACCCAGAC ACCAAGGCTGGGCCAGTCTTCTCCTAGTGCTGGCCC	SEQ ID NO. 228
KCP_2649	GGCTCACCGAGACTGATGTGTAAGCCGAATGTGGTGTATTAAT TTACCTTGGGAAATGGAAGTGCAGTGGAAACAGACACTCCTCT CCCTTCGCTGGGACCCGCTCTCCTTGGGAAGCCACATGGAAGCCA GGTTACAATCAAAGTGGAGTCAGAGGACGGGAGTTCCCTTGTTT AGTTGTTACTTTAAATACATTAATGTGTTCTGTCAGTCTCAGGC CAGTTTGAGAGCTCTCAGATACAATCCTGGATATTAATTTATTT TTTAAGTTTAACTCTCAGAGTGCAATCTTATTTCCAAATCCTGG AGTGGTGTGGAGTGGGGTGGGCTACAGCGACATGCACCTGGTCA CCCTCCCTCCAGGTGCAGTCTGTAGGTAGAGCTGAGCTGGGTCA GTTCCAAACTGACCACAGCCTCAATGTTCTCCAAACTGCTGACC CACAGGGATTCCAGCCCCCTCCTGGGAGTTATCTGACAGGTGCTG GGATGCCTCTTCTTCCACACTAGCCTTGACTGCACATGCCAAG TGCCCAAGTTTCTTACCATTAGGGCTTCTTCTTCCGATGGCAGC ATTAGCAGTGGGCAGCCGAGTTGGAGAAGGATCCTGTGGGAAAG TTTTCCAGGCAGGCACTGGGCTCAGAGGGAACAGCATCCAGAAA AGAGAAGAAATCTACACTGCTTGGCATCTACCATGGACTCAATA CCACCTAACATAGGTTTATAAGATACCTTGGGGAAAGTTATTGT TACCCCCATTTTACAGGTAAGGATATTGAGGATCAGAGACTGGC TTGGCCAAAGTCACAAAGCTTAGTATTGGCTGAGCCAGGATTTA AACCAGGTTTTTCTGATCTTAAAGCCCCAAATCTCTCCACCTC ACAGTGCCCATTTCTCTGACAATGTCTCATCATTTTGCAAAGCAG CTCCAGTCTTGAGATGGCACTACTTGGGAGAAGTGGAATGCAC AGGTCCCTGTCCCTGGGGATCATGAGGAACCC [C/T] AGACACC AAGGCTGGGCCCAGTCTTCTCCTAGTGCTGGCCCTCAAATGCCT CCCGCTGACTCTCTCCCTTCCCACAGGAGTGCCCCAGTGGTGT GGTCAACGAAGACACATTCAAGCAGATCTATGCTCAGTTTTTCC CTCATGGAGGTGAGTCTGACCTTGAAATCTATCTTGCCAGCTC CCTCTCTGGTAAGCAGCCTTCCCTTCTCCAAGTCTCTCTTCC TTGCCATTTGCTTCTTCTCGAGGAAGAGACAAACTCAGGGCAG GACACCTCCCTCATCGTGAGAGGTGGGAGTCTCCAAAGCTTTAG CAGGAAAGAACTCTGAAAATGAACCCACCTGGAAGGGGAAGAA	SEQ ID NO. 229

	<p>GGGCTGATAATGCAACATCACAACGTCTCAGAACAGCTCTAGAA  AGCAGGTATTATAATCCCAGATGGAGTAAGTGGGTTTCGGGGAA  GATAAGCAGTGTACTCAAGATTGCACAGCTGGTGAGTAGCAAAC  CAGGATTAGATTCCATAAGGGTCTGAAACAGGTTTTGCCATGCT  GGCACCACCATTGTGCAGGGCACTTTTGAATCTTTTCTTAAAA  TAGCTGAGACAAGCTGGAATTTTGTAAAAGAACTTCAGTAAATA  CCGAAGACTATAAAAAATAAATAAATGAAAAAGAGGCAGGAAAC  ATAAAGTTGTGCTTATTAAGCCAGTTTACAAGTGTGCCAGGCCC  ACAACAGCTGCTCTGTGTGCCCTGCCCGACTCCTGTGGGAACCA  CTGTGTCCCATGGGCTGGGACCACATCGGTGACTCCTCCTGT  GGCCTCCATGTGTACATGCCACTTTGCATCCTGTACCAAGAG  CTGTCTCCTGCAAGACATCTTCCCTGGATCCTGACAAAATGCAA  ATCCAAGTATTCCAAACACTTCTTGGGCCCTGTTTCTCATGGGC  CTTTTTGGCAGCAGACAGATGCCCTTCTTGGTGTGTGGGGCCCC  TACCAGATCAGGTGGGGGAGGCAG</p>	
KCP_2278 71	<p>CCTCTGGTTCTGCATCACCTCCCCCTCTAAATCTCAAGGCATTG  GGGGAAGGTCTGGACCATCAAAGCTCTCAGTCAGACCAAAGAC  ATGTTTATCCATTTGTAAAGCATTTTCTTAAAGATGGGAAAAGCA  GCAGCAACTTTCCCTGGCCTGCAGGAACTCAGGGACTCAGGGGA  CTAATAACAACAGTGTATGAGCTTCCGGGCACACTGCTTCCCAG  TGGCAGCCCCCTGTACTTAGGGCTTTGTATGTATTAATTCAATTA  CTCCAATTCCCACAATAACCTATAGGGTAGGGTTTTATTATTG  ATTACCTTTTTACAGAAGAGGAGAGTAAGGCAAAGAGAGATAGA  GTAGTTTTCCCAAGGTCAAAGAGCACATAAATGATAAAGGATGG  ATTTGAATGTAGGCAGAATGACCCTCAATACAGACTGTTCTCTAC  AGTCCACGTCTCAGCCACTAGACCATACGGCCACTGGGATGAT  AGACAGACCCTGCAG [C/G] CATGGATAAGGCAAACAGGGC  TGGCTGTGTGATCTGTGTCTCTCAGAGCTCCATTCTTCTCAA  GGGGGCACCTTGCAAAAAAACAACAAAAATGGGGCAGGGTAGG  GAACTGAAGGCAGGAGCTCTTACAGAGCATAGCCACATCCTCC  AGGCAGACAAGAGGACGCAGGAGGCACCATTTCTGTGAGAGTATC  ACAGTCTGACCCAAAGACACAGCTTCAACTGTCTGATGGCTTG  ATGGTTAATGTCACTCTGCCTTTTCCCCTTCTCAGGACTTTGTA  ACCGCTCTGTGATTTTATTGAGAGGAAGTCCACAGAGAACT  AAGGTGGACATTTAATTTGTATGACATCAACAAGGACGGATACA  TAAACAAAGAGGTAAGTGAAGTGGGGCCAGGGGTGTGAGAGGGC  TCCAGTGAAGGTAACCTAACCAACAGAAAACAGCCCCAGGCATG  AGGATAGCACTGTCTGAATGAGGCAGGCTCTGCTTTG</p>	SEQ ID NO. 230
KCP_2279 87	<p>TGTGCCATTTCATACACCAACGACTCCATGCATAGACAGGCAGGA  GAATGGTTTTCTCATGATGGCTAGAGGGAGGGGCAAGGGCTCAT  CTCACTTTTTGCTAGATCTAAGTTTCAACCCAAACCCAAAGAGT  TGAGTCAATGGGCCCCACTCCATAATTTCTCCTTTCCATCACC  CTAGCATCACTCTCCTCTCTTTCTTGTGGAAGCCCTGCCTTGT  TGGAAGGTTCTCCCTGTGTGGAATTCCTGCCCCCATCACCTGCC  CTCCTTTTCTGCCTTGTAGATGCCAGCACGTATGCCATTACCT  CTTCAATGCCTTCGACACCACTCAGACAGGCTCCGTGAAGTTCTG  AGGTACGCTCATCTGGGGTCCACTCTAGGGGTCTCTGTTTCTG  CATCACCTCCCCCTCTAAATCTCAAGGCATTGGGGGAAGGTCTG  GACCATCAAAGCTCTCAGTCAGACCAAAGACATGTTTATCCAT  TTGTAAGCATTTCTTAAAGATGGGAAAAGCAGCAGCAACATTC  CCTGGCCTGCAGGAAGTCAAGGACTCAGGGGACTAATAACACA  GTGTATGAGCTTCCGGGCACACTGCTTCCCAGTGGCAGCCCCCTG  TACTTAGGGCTTTGTATGTATTAATTCATTTACTCCAATTCCCA  CAATAACCTATAGGGTAGGGTTTTATTATTGATTACCTTTTTTA  CAGAAGAGGAGAGTAAGGCAAAGAGAGATAGAGTAGTTTTCCCA  AGGTCAAAGAGCACATAAATGATAAAGGATGGATTTGAATGTAG  GCAGAATGACCCTCAATACAGACTGTTCTACAGTCCACGTCTCT</p>	SEQ ID NO. 231



	<p>CAGCCACTAGACCATACGGCCACTGGGATGATAGACAGACCACT  GCAGCCATGGATAAGGCCAAAAACAGGGCTGGCTGTGTGATCTG  TGTCTCTCAGAGCTCCATTCTTCCTCAAGGGGGCACCTTGCAAA  AAAAAACAAAAAATGGGGCAGGGTAGGGAAAC [C/T] GAAGGCA  GGAGCTCTTCACAGAGCATAGCCACATCCTCCAGGCAGACAAGA  GGACGCAGGAGGCACCATTCTGTGAGAGTATCACAGTCTGACCC  AAAGACACAGCTTCACACTGTCTGATGGCTTGATGGTTAATGTC  ACTCTGCCCTTTTCCCCCTTCTCAGGACTTTGTAACCGCTCTGTCTG  ATTTTATTGAGAGGAACGTGTCCACGAGAACTAAGGTGGACATT  TAATTTGTATGACATCAACAAGGACGGATACATAAAACAAAGAGG  TAAGTGAGCTGGGGCCAGGGGTGTGAGAGGGCTCCAGTGAAGGT  AACTAACCCCAACAGAAAACAGCCCCAGGCATGAGGATAGCACTG  TCTGAATGAGGCAGGCTCTGCTTTGGGGCTAACAGAGCTGGTCC  CTGGCAAAATAAAGAAGGCCTCCCTCATTGCCCTACCCTGCCCT  GTTCCCAAGCGCCAGAAAGGATTAAACAGATTCACTCTCACTG  GGTCACCTAGATTTCAGTAGATATTACACAGTGGATAAAAAATGAC  TTGTTTCAGTGTGAAGAGTTACTCTTCCCTAGGGAACCTGCATT  TGGAAGGTTAGGAGCCACAAGTCAAAGCTAAAAGTTGAAATGG  TGGAATTGTAGGCAGCACCTAGAATAGAAAAGAAAGATTTTAA  GGAAGAGGAACCTACAATTGGGTCAATTTGGCCTTAACTATTT  TGCCTATTAATACAACCGCCAAGGGGGTAATGGAAGGTACAGCT  GTCTTTACAGAAATTATCACAATAATTTCTGAATCTTCACTGC  TTTGCACTTTTGAACCTCAGAGGACATGTCTCTAGCCAGTGAA  ATACCCTCAGGTCTATCTCAAACTCACTTTGGTATCCACTGTA  TCCTGGTATCTCAGTGGAGCTGGAAATTGGCATCCTGTAACAC  TCCACTTGCTGAGCTCCTGTGTGCCAGGCACGGTGCCTGGAGGT  ATAGATATCAGACCAATCTTCACC</p>	
KCP_2281 07	<p>TAGGGCTTTGTATGTATTAAATTCATTTACTCCAATTCCACAAT  AACCCTATAGGGTAGGGTTTATTATTGATTACCTTTTTTACAGA  AGAGGAGAGTAAGGCAAAGAGAGATAGAGTAGTTTTTCCAAGGT  CAAAGAGCACATAAATGATAAAGGATGGATTTGAATGTAGGCAG  AATGACCCTCAATACAGACTGTTCTTACAGTCCACGTCTCTCAGC  CACTAGACCATACGGCCACTGGGATGATAGACAGACCACTGCAG  CCATGGATAAGGCCAAAAACAGGGCTGGCTGTGTGATCTGTGTC  TCTCAGAGCTCCATTCTTCTCAAGGGGGCACCTTGCAAAAAAA  AACAAAAAATGGGGCAGGGTAGGGAACTGAAGGCAGGAGCTCT  TCACAGAGCATAGCCACATCCTCCAGGCAGACAAGAGGACGCAG  GAGGCACCATTCTGTGAGAGTATCACAGTCTGACCCAAAGACAC  AGCTTCACACTGTCTG [A/T] TGGCTTGATGGTTAATGTCACTC  TGCCTTTTTCCCCTTCTCAGGACTTTGTAACCGCTCTGTCTGATTT  TATTGAGAGGAACGTGCCACGAGAACTAAGGTGGACATTTAAT  TTGTATGACATCAACAAGGACGGATACATAAAACAAAGAGGTAAG  TGAGCTGGGGCCAGGGGTGTGAGAGGGCTCCAGTGAAGGTAAC  AACCCAACAGAAAACAGCCCCAGGCATGAGGATAGCACTGTCTG  AATGAGGCAGGCTCTGCTTTGGGGCTAACAGAGCTGGTCCCTGG  CAAAATAAAGAAGGCCTCCCTCATTGCCCTACCCTGCCCTGTTC  CCAAGCGCCAGAAAGGATTAAACAGATTCACTCTCACTGGGTCT  ACCTAGATTTCAGTAGATATTACACAGTGGATAAAAATGACTTGT  TTCAGTGTGAAGAGTTACTCTTCCCTAGGGAACCTGCATTTGGG  AAGGTTAGGAGCCACAAGTCAAAGCTAAAAGTTGAAA</p>	SEQ ID NO. 232
KCP_2325 21	<p>ATTTCTTAAAGTAGATAAAATTTGACTTTATCAAAGTTAAAAATT  TTGTGCTTTAGAAGACACCTTTAAGAAAATGGAAATGCAAGCCA  TGGACTTGGAAAAAATGTTTGCAAATTATATACCAGATATATAA  AGATACCAGGATACCAAACCAATATAAAGACTGGCATCCAAAAT  ATATAAGGGACATTTATAATTTAATACAAAGATAAACAACCTTCA  TATAAATAGGCAAAAGATTGATGAGATATTTAAGAAAAGAAG  ATATATGAATGGCCAGTAAACCCATGAAAGGTTGCTCTATATCA</p>	SEQ ID NO. 233

	<p>CTGGTCTTCAAAGAAATGCAAATTATAACTATAATGAAATACAA  TTGCACAGAATGGCCACAATTAAAAAGACTGATAATACCAAGCA  TTGCCAAAGATGTGGAGCAATAGAACTCTCATAGATAGCTGGC  AGAAATGTAAATGGTACAAACACGTTGGGAAACATTTTGGCATC  TTTGATAAAGCTCAGCACACACTTAACATACAACCCAGAAATCC  CATTCAGTCAGGCATGGTGGCTTACGCCTATAATCCCAGTACT  TTGGGAGGCTGAGGCAGGCGGATCACTTGAGCTCAGGTGTTCAA  GACCAGACTGGGCAACATGGCGAGACACTGTCTCTACTAAAAAT  ACAAAAAAGCCAGACATGGTGGTAAACACCT  GTGGTCCCAGCTACTAGGGAGGCTGAGGTGGGAGAATTGCTTAA  CCCTGGGGAGTGGAGGTTGCAGTGAGCTGAGATTGCACCACTGC  ACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCAAAAAAGA  AAAAAGAAGAAGAAAAAGTCCCACTCCTGGATATTTACCCC  CAAAAGAAAAATATGTAATTCATAAAGACTTGTACAAAGATGT  TCATAGCAGCTTTATTCATAGTAATCTCAAACTTAAATGACCC  AAATGTCTGTCAACAGGACAAATGGGTAAATAC [A/T] TCATAGT  CTGTTTCATCCAATGGAATATTACTCAGCAGTAAAAAGGAATGTT  ATAGTTGCATGCAGCAATGTGTATGAAGCTCATAAACCTCATGC  TGAGTAAATGAAGCCAGACGCAAATGAGTTTACACTGTTTTACT  CCATTTACATGAGATTTTAGAAAAATACAACTAATCTATAGTAA  CAGAAATTAGATCTGTGGTTGCCTGGTGTCAAAGCTTGAGAGGC  ACTCACTGCGAAGAAGTGTGAAGGGATGTCTTTTGGTTGTGAAA  ATGTTCTATATCTTGAGTGTGGTGGAGGTTACATGGGTGGATAC  ATTTGTCAACATTCATCAAACAGTACACTTAAATGGGTGAATT  TGTTATAAGTAAATTATGCTCCAATAAATTTGATTTATTTGTTG  AAAACTTGGTGTAAGGGGGGAAGTGCCTAACCAATAGAAGACAC  TCAAAAAATGTGTTGAAGGAAAAAATCCTGTGAAATAAAGCAG  GTAAGAGAAAAATAAGAACTCAATATCATCCAAATATAGATTAC  AAATCCTAAATGAGATAATAGGAAATTAATCCCAGTGCTCTGTT  TAAAGGCTCATACCTGTAATCCCAACACTTTGGGAGACTGAGGC  AGGAGGATGGGTTGAGCCCAGGAGTTCAAGACCAGCCTGGTCAA  CATAGGGAGAGCCTGTCTCTTCAAAACAAAAATTTAAAAATTAC  CTGGGTGTAGTGGCACGTGCCTGTGCTCCCAGCTACTCCAGAGG  CTGAGGCAGGAGGATAGCTTGAGCCCAGGAGTTCAAGCCTGCCC  TGAGCCATAATCACTGCACCACACTCCAGCCTGGGCAACAGAAC  AAGACCCTTCCTCAAAAAAGCAATAAAATAAAATAAAGAAATGC  ACATGACTAACATAGGGTTTATTCCAGGAATGCAGGAATAGCCC  AGTAGCAGAGAAAGCCTATTAAATAATTTATCACATTAATATAT  CAAAAGATCAAACCATTTGATGCTA</p>	
KCP_2336 55	<p>TTTACTCCATTTACATGAGATTTTAGAAAAATACAACTAATCTA  TAGTAACAGAAATTAGATCTGTGGTTGCCTGGTGTCAAAGCTTG  AGAGGCACTCACTGCGAAGAAGTGTGAAGGGATGTCTTTTGGTT  GTGAAAATGTTCTATATCTTGAGTGTGGTGGAGGTTACATGGGT  GGATACATTTGTCAACATTCATCAAACAGTACACTTAAATGGG  TGAATTTGTTATAAGTAAATTATGCTCCAATAAATTTGATTTAT  TTGTTGAAAACTTGGTGTAAGGGGGGAAGTGCCTAACCAATAGA  AGACACTCAAAAAATGTGTTGAAGGAAAAAATCCTGTGAAATA  AAGCAGGTAAGAGAAAATAAGAACTCAATATCATCCAAATATA  GATTACAAATCCTAAATGAGATAATAGGAAATTAATCCCAGTGC  TCTGTTTAAAGGCTCATACCTGTAATCCCAACACTTTGGGAGAC  TGAGGCAGGAGGATGGGTTGAGCCCAGGAGTTCAAGACCAGCCT  GGTCAACATAGGGAGAGCCTGTCTCTTCAAAACAAAAATTTAAA  AATTACCTGGGTGTAGTGGCACGTGCCTGTGCTCCAGCTACTC  CAGAGGCTGAGGCAGGAGGATAGCTTGAGCCCAGGAGTTCAAGC  CTGCCCTGAGCCATAATCACTGCACCACACTCCAGCCTGGGCAA  CAGAACAAGACCCTTCCTCAAAAAAGCAATAAAATAAAATAAAG  AAATGCACATGACTAACATAGGGTTTATTCCAGGAATGCAGGAA</p>	SEQ ID NO. 234

	<p>TAGCCCAGTAGCAGAGAAAGCCTATTAAATAATTTATCACATTA  ATATATCAAAAGATCAAACCATTTGATGCTAAAATCACATTTGA  TATAATTTACCATTTATTCATAATAATTTTCAGGATTCAATTAA  TTAGGAATAAAATACTTCTTCAGCATAATAGAAAATACCCAGC  CTGGTACACAGCTTCATACTTTATGGTAACAC [A/G] CGGAGAT  TCTCACTGAAGAAAAGATGAGGCAAGAAAAGATGATGAAGAAAA  GATGAGGCAAGAAAAGATGATGTCTGCACACTGTCAGACATCAC  CACTGTTTTAAATTTCTGAAAAGCTCTTCAAACACAGTGAAACA  GAAAAGGAAATGCGATCTAAATAGGAAAAATTACAACATTCCTT  GTTAATGACATGATTTTCTATCTGAGAAAAAGACAGCAAGAAA  ATCAACTTAAACAACACTAGAACTTTTAAAAAGCTGGCAAAGTGA  CTGGTAATAAAATACATATGCAAAAAGAAATGTGTAGCCAATA  TATCAGTTGTGACTAGCTAGAAAATTGTAATACAAATATTCTCA  TTGTGATCACAATAAAATTTAAAGCACATGGGCATTTTAAATA  TCCATAATTTAGATGAAGAGAAAGAAAATTTTGATAAGTAGAGA  AACATACCATCTTCTGAAAGGATGTATATTATAAGATAGCAAT  ATTATAATGACAGCAATTCTTCTCTAATTAAATTTATTTTATTT  TGAATCAAAATGGAAGTGTTATTTGGGAAGGAAATTTGGCACAA  TTGTTATAAAGTTACATTGGAAGATTAATCAGATGAAAATAGCA  AAGATAATTTTCAAAAAGAAGAAAAATGGTGGGATTTGTTCTAC  CAGATACTGAAATATATTATAAAGCTGAAACTATTAAATATTA  TAATATCAGAGAAGGAACAGGTAGATCAATGGAACAAAATAGAA  ATCCCAGGTACAAATACCATCTTGGTTCATAATAAGGGAGCAT  ATTGAATAGAGAGGTAATGAATCATTAAATGATTCTTGGAAC  TGGTTAACTATTTTGGCAATAAGTAAGTAAATATTCTTACTCGG  TACCATAAACACAAAATCACTATAGATATGTACAGTTGCTTTTT  AACTAAAAAGAAGCTAAAAATCATATGTGAATATCTGATCAAAG  AATGGAAAAAGCATAAAATCAAAGT</p>	
KCP_2375 05	<p>GCCTGTAGTCCCAGCTACTTGAGAGGCTGAGGCGGGAGGATCAC  TTGAACCCGGGAGGTGAGGCTGCAGTGACGGGGATTGTGCCAC  TGCACTCCAGCCTGGGTGACAGAGCAAGAACCTGTCTCAAAAAA  AAAAAAAAGAAAAAGAAAAAGAATGAGAACTCATAACAGA  TTAGAAGAGACTAAGGAGACACAACAAATAAATGCAATGTAGAA  TCATTGAAGGGAAAAAATATTAGTTGAAAAGCTGAGATCCCGC  CACTGCCTCCAGCCTGGGCCACAGAGCGAGACTCCGTCTCAAA  AAAAAAAAGAAAAAGAAAAAGAAAAAGCTGATAAAATTT  TGAATAAGCCCTGTAGTTTGTAGTTAATAATAGTGAAGCATGTTA  ATTTCTTGGGTTTGGTCTATGTGCTCTGGTTATGCAAGTTGTTA  ACATTAGAGGAGACTGAGTGAAAGGTATGCATGAACTCTCTGTA  CTAATTTTGTAATTT [C/T] CTGTAAGTCTAAAATTATTCATA  ATATGCAAAAATTAACAAAAAATAAAATAAAATAAGCACATGG  AATGAGACTGTCCCTGGGTCTCTGTAGAAACCAGGTCAAACAT  CCCAAATGCTCTTTTACCCCATTCCTGAGTTGGGCCAGAATGGT  CAGAATAATGGTTCCCAATGTACCTTGATAAACACGGAACTCT  CAGGACCGAGTCCTAAGGTTCTCTGATTCAATAGGTTTGGAGTG  GACTTGAGAACTGATCTTTTAAATAAGGGCCTCAGTCTGTGGAA  CTATTGGCCTCATGTGCCCTGTGGATAATCTTGGCTGTTGGTTC  ATTTTCTTAACTGAAAACAGTGGCAGAACTATGGGGATTTTT  AAATCTCTAGGCTAGAACATTAACTTTTTAAAAATTCAGAATAG  TATTTTATTTGCCCTCAAGCCTGTGAATGGGGATCCCAAAATCA  CCCCCACTGAAGACAATGCCATAACAAGGTAACCT</p>	SEQ ID NO. 235
KCP_1540 0	<p>TTATGCAAGTTGTTAACATTAGAGGAGACTGAGTGAAAGGTATG  CATGAACCTCTCTGACTAATTTTGTAAATTTTCTGTAAAGTCTAA  AATTATTCAATATATGCAAAAATTAACAAAAAATAAAATAAA  TAAGCACATGGAATGAGACTGTCCCTGGGTCTCTGTAGAAACC  AGGTCAAACATCCCAAATGCTCTTTTACCCCATTCCTGAGTTGG  GCCAGAATGGTCAGAATAATGGTTCCCAATGTACCTTGATAAAC</p>	SEQ ID NO. 236

	<p>ACGGAACTCTCAGGACCGAGTCTTAAGGTTCTCTGATTCAATA  GGTTTGGAGTGGACTTGAGAACTGATCTTTTAAATAAGGCGCTC  AGTCTGTGGAATATTGGCCTCATGTGCCCTGTGGATAATCTTG  GCTGTTGGTTCATTTTTCTTAAGTGAACAGTGGCAGAACTA  TGGGGATTTTTAAATCTCTAGGCTAGAACATTAACTTTTTAAAA  ATTCAGAATAGTATTTTATTTGCCTCAAGCCTGTGAATGGGGAT  CCCACAAATCACCCCCCACTGAAGACAATGCCATAACAAGGTA  ACCTACCCATGAGCTTCTGAGGGATTTAGGAATTGTCTACCATC  TCCTCTCTAAGAAGGGCTCCCACAATATATCCCCTTCTGCTTGC  TTCTAACTCCCTATCACCTGCTAAAGAAGGACCTCACCTTTTAA  TCACTTTTCATTGCCAAGGGGCACAAGGAGCCCCAACTCTGTCA  CCTAGGAAGAGCTTGACCTCATGGTTTCCACACTGTGTGCTTTT  ATGTCCCTGCTCCAGGAGATGATGGACATTGTCAAAGCCATCTA  TGACATGATGGGGAAATACACATATCCTGTGCTCAAAGAGGACA  CTCCAAGGCAGCATGTGGACGTCTTCTCCAGGTAAGTGCACAC  ACCCTGCACATGAGCTGTAAGCCAGCCTAGATCAAGTCAACCC  ACGAGCATCTGAGCAAATGATTGTGTCCAAC [C/T] CTGTACT  AAGCATGGTTGGTAACAGAAAAGAATTATAAGATACATTGTCTCT  CAAGAAACAGATGATCTCCTTAAGCTGCAAGTGTACATGACAGA  AGAGAACAAGAAAGTATATTATTAAACGCTAGTGGTATAGTATG  AACTCTAAATCCATAAAAAATTTGGGGATCAGGGTAACACGAAA  GACTTCATTAATTACAACCTGTGGAGGTGTTAAGCATTGTGTCT  GGGAAGTAAGGGGAAATAAGATTGGAACCTAGGATAGGGCCAGA  TTATGAGACCTTTAAATGGAAGAGTTTGGCCTTGCTCTGGTACA  GGATGGGCAGCTAGTGTGATCCTTGACTAAGGGAGTGGTATAA  TCATTGGGGCATTTTAGGAAAAAATTAATCTAGCGGTGGAGTAT  CAGAGAATATCAAGAGTTCACTCTAGTTCAACCTCCCACCTTGC  AGATGGGAAAAGAGAGTCTCTGTCCTTGTCAGGTTTGTAC  AGCAAGTAACAGGCCAGAAATCAGAACCTCTTTTGCCAGTGTTC  TGCCAGATGGACAGGGTAGCAGGGAGTCTACAGAAGAAGCAGAA  TAAGCCAGCAGTGAGGTGATGAGTGTCCAGAGCAAGTCTTTTGA  TTTAAGGAAGCTCATGGGGCTCAAAGTGTGTGAATCAGGACCTA  ATTGGAGTTGTCTGGCCAGTGAAGACAACTCTCATTCTCAGGG  CAAAGTTGGTTAATGAATGAATGAATGAGCTCCAGCTCGTTA  CTCTGAGCTCCAGCAAGAAAGCAGGGGAGTAAGCTTTGGAATGG  AGATCACCAGATTCTGTAAAGTGCTTTCTGTTATGTCTTTCAGA  AAATGGACAAAAATAAGATGGCATCGTAACCTTTAGATGAATTT  CTTGAATCATGTGAGGAGGTAAGGAGAGATCTCAGGGCACAATA  ACTCTACATCTGGGAAAGGAAACCTGGGGCCTGGGGACCTGCAG  AAGGAAGGTGATGAGAAACCTGCAC</p>	
KCP_2385 91	<p>TCTAACTCCCTATCACCTGCTAAAGAAGGACCTCACCTTTTAAAT  CACTTTCATTGCCAAGGGGCACAAGGAGCCCCAACTCTGTACAC  CTAGGAAGAGCTTGACCTCATGGTTTCCACACTGTGTGCTTTTA  TGTCCCTGCTCCAGGAGATGATGGACATTGTCAAAGCCATCTAT  GACATGATGGGGAAATACACATATCCTGTGCTCAAAGAGGACAC  TCCAAGGCAGCATGTGGACGTCTTCTTCCAGGTAAGTGCACACA  CCCTGCACATGAGCTGTAAGCCAGCCTAGATCAAGTCAACCCA  CGAGCATCTGAGCAAATGATTTGTGTCCAACCTGTACTAAGCA  TGGTTGGTAACAGAAAAGAATTATAAGATACATTGTCTCAAGA  AACAGATGATCTCCTTAAGCTGCAAGTGTACATGACAGAAGAGA  ACAAGAAAGTATATTATTAAACGCTAGTGGTATAGTATGAACCTC  TAAATCCATAAAAAAT [C/T] GGGGATCAGGGTAAACACGAAAG  ACTTCATTAATTACAACCTGTGGAGGTGTTAAGCATTGTGTCTG  GGAAGTAAGGGGAAATAAGATTGGAACCTAGGATAGGGCCAGAT  TATGAGACCTTTAAATGGAAGAGTTTGGCCTTGCTCTGGTACAG  GATGGGCAGCTAGTGTGATCCTTGACTAAGGGAGTGGTATAAT  CATTGGGGCATTTTAGGAAAAAATTAATCTAGCGGTGGAGTATC</p>	SEQ ID NO. 237

	AGAGAATATCAAGAGTTCACTCTAGTTCAACCTCCCACCTTTGCA GATGGGAAAAGAGAGTCCTCTCTGGCCTTGTGCAAGTTTGTACA GCAAGTAACAGGCCAGAATCAGAACCTCTTTTGCCAGTGTTCT GCCAGATGGACAGGGTAGCAGGGAGTCTACAGAAGAAGCAGAAT AAGCCAGCAGTGAGGTGATGAGTGTCCAGAGCAAGTCTTTTGAT TTAAGGAAGCTCATGGGGCTCAAAGTGTTGTAATCAG	
KCP_1615 2	GGAAGAGCTTGACCTCATGGTTTCCACACTGTGTGCTTTTATGT CCCTGCTCCAGGAGATGATGGACATTGTCAAAGCCATCTATGAC ATGATGGGGAAATACACATATCCTGTGCTCAAAGAGGACACTCC AAGGCAGCATGTGGACGTCTTCTTCCAGGTAAGTGCACACACCC TGCACATGAGCTGTAAGCCCAGCCTAGATCAAGTCAACCCACGA GCATCTGAGCAAATGATTTGTGTCCAACCCTGTACTAAGCATGG TTGGTAACAGAAAAGATTATAAGATACATTGTCTCAAGAAAC AGATGATCTCCTTAAGCTGCAAGTGTACATGACAGAAGAGAACA AGAAAGTATATTATTAAACGCTAGTGGTATAGTATGAACTCTAA ATCCATAAAAATTTGGGGATCAGGGTAAACACGAAAGACTTCAT TAATTACAACCTGTGGAGGTGTTAAGCATTTGTGTCTGGGAAGTA AGGGGAAATAAGATTGGAACTAGGATAGGGCCAGATTATGAGA CCTTTAAATGGAAGAGTTTGGCCTTGCTCTGGTACAGGATGGGC AGCTAGTGCTGATCCTTGACTAAGGGAGTGGTATAATCATTGGG GCATTTTAGGAAAAAATTAATCTAGCGGTGGAGTATCAGAGAAT ATCAAGAGTTCACTCTAGTTCAACCTCCCACCTTTGCAGATGGGA AAAGAGAGTCCTCTCTGGCCTTGTGCAAGTTTGTACAGCAAGTA ACAGGCCAGAATCAGAACCTCTTTTGCCAGTGTTCTGCCAGAT GGACAGGGTAGCAGGGAGTCTACAGAAGAAGCAGAATAAGCCAG CAGTGAGGTGATGAGTGTCCAGAGCAAGTCTTTTGATTTAAGGA AGCTCATGGGGCTCAAAGTGTTGTAATCAGGACCTAATTGGAGT TGTCTGGCCAGTGAAAGACAACCTCTCATTCTCAGGGCAAAGTTG GTTAATGAAATGAATGAAATGAGCTCCAGCTC [A/G] TTACTCT GAGCTCCAGCAAGAAAGCAGGGGAGTAAGCTTTGGAATGGAGAT CACCAGATTCTGTAAAGTGCTTTCTGTTATGTCTTTCAGAAAAT GGACAAAAATAAAGATGGCATCGTAACCTTTAGATGAATTTCTTG AATCATGTGAGGAGGTAAGGAGAGATCTCAGGGCACAATAACTC TACATCTGGGAAAGGAAACCTGGGGCCTGGGGACCTGCAGAAGG AAGGTGATGAGAAACCTGCACATACCTGCAACCCCTCCCACAG AGCCAACAACACCAGCAACAACCTGTGAAGTCCACAGTTCCACTC CTCAACCTGACCTGCAGTTGGTCTTGGCTAAGCACAAGACTGAA CAGAGAGCCTAAGTAGGGGTCTGGGGGCATGTGAAAACCTCAGAG GGGGTCTCTGTGAAAATAGACTTCCCGAGAGGGCAACACCATTA TTTTTTAGCCTGCCTCTGGCTTGATGACCCATTTCCAGACTAC AAGGAAGCAGCTGGGGGGAAAAAACCTACAATTGTGTGATTCT CAAACCACAGTGTGCATAAAAATTGCCTGGAATGATTCTGAAAA TGCATATTTCCAGGCCTCAATCCCAGAGACTCTAGATCTGGGTC ACTTTAACACAAAATGTCTGGACCAATGCTTCTAACACTTTAAT GTGTGAAACAATATCCTTGATGATTTTGTGTTAAATGCAGATTCT AATTCCATAGGTCTGGGGTAGGGCCTGAGATGTTACTTTTCTCA CATTCTCCCCAGTCACACTGGTGATGCTGATCCTGGGAACACAA CTTTCATTAAGTCTAACCAATAGACCAGCCCCAGAGTCCACCAG AGACTGAACTGGAAATAATTGCTTCATCTACTTTTGAGAAATCC ATTTGTACCCCCACATTATTTTAGAAATGTTAGAGTTACTCTG AGCTCCAGCCAAGAAGAAATAGCAAATGTAAGAAAGCCGGGGAGA AGTTCCTAGCAGATACTGAGCCCC	SEQ ID NO. 238
KCP_1806 9	TTGAAAGAGAGCGCTTTGGGGGGTTTTCTTACTGTATGTCTCTA TTGCATGTTCTGTATTTTACATTTTCTATTATTTCTTCTCTGA GGTATAGTATTGAATGTAGAAAAATCCTCAAATGTTCCGTATTA AGCAATACACTTCTAATTCATGGTTCAGAGAAGAAAATATCTCG AATAAAAATAAAAATAAAAATATGACTTATCAAATTTGTAGGAT	SEQ ID NO. 239

	<p>CTAAAGCAGTATTCCAGGAATGCAAGGTTGGTTTAAACATTCAAT  AATTGGTCAGTGTAATTAATCACATTAATAGAATAAAAAGAGAA  AAAATATAATCATTTCAGTGGATGTAATTGTTTCAGAGCTTCTTA  AAAGAAGCAACTCACTATTTTACTAGATGATTGTTTCTTCTGA  ATTCTCTTTAAGGCTACAGGTGGTGCTTCTTACTTTGAACTGA  TCACTTTCTAGGTCCCCACCCTTACTTCTTGTTTTTCATACCCT  TGTAGAGTTTCTCCA [C/T] ATAGGAAACCCATGCTTGACATT  TGCTCACCAGAGTTACAGAGCTCTCAGGGAGGAGACTCAGAGTT  CTAACCCCTCTTGCCCTCCTTTTTTCCCAGGACGACAACATCATG  AGGTCTCTCCAGCTGTTTCAAATGTCATGTAAGTGGTGACACT  CAGCCATTTCAGCTCTCAGAGACATTGTACTAAACAACCACCTTA  ACACCCTGATCTGCCCTTGTCTGATTTTACACACCAACTCTTG  GGACAGAAACACCTTTTACACTTTGGAAGAATTCTCTGCTGAAG  ACTTTCTATGGAACCCAGCATCATGTGGCTCAGTCTCTGATTGC  CAACTCTTCTCTTTCTTCTTCTTGAGAGAGACAAGATGAAATT  TGAGTTTGTFTTGGGAAGCATGCTCATCTCCTCACACTGCTGCCC  TATGGAAGGTCCCTCTGCTTAAGCTTAAACAGTAGTGACAAAA  TATGCTGCTTACGTGCCCCAGCCCACTGCCTCCAAG</p>	
KCP_2415 27	<p>ACTTTGAACTGATCACTTTCTAGGTCCCCACCCTTACTTCTTGT  TTTTTCATACCCTTGTAGAGTTTTCTCCATATAGGAAACCCATGC  TTGACATTTGCTCACCAGAGTTACAGAGCTCTCAGGGAGGAGAC  TCAGAGTTCTAACCCCTTGCCCTCCTTTTTTCCCAGGACGACA  ACATCATGAGGTCTCTCCAGCTGTTTCAAATGTCATGTAAGT  GTGACACTCAGCCATTTCAGCTCTCAGAGACATTGTACTAAACAA  CCACCTTAACACCCTGATCTGCCCTTGTCTGATTTTACACACC  AACTCTTGGGACAGAAACACCTTTTACACTTTGGAAGAATTCTC  TGCTGAAGACTTTCTATGGAACCCAGCATCATGTGGCTCAGTCT  CTGATTGCCAACTCTTCTCTTCTTCTTCTTGAGAGAGACAAG  ATGAAATTTGAGTTTGTFTTGGGAAGCATGCTCATCTCCTCACAC  TGCTGCCCTATGGAAG [G/T] TCCCTCTGCTTAAGCTTAAACAG  TAGTGACAAAAATATGCTGCTTACGTGCCCCCAGCCCACTGCCT  CCAAGTCAGGCAGACCTTGGTGAATCTGGAAGCAAGAGGACCTG  AGCCAGATGCACACCATCTCTGATGGCCTCCCAAACCAATGTGC  CTGTTTCTCTTCTTCTTGGTGGGAAGAATGAGAGTTATCCAGAAC  AATTAGGATCTGTCATGACCAGATTGGGAGAGCCAGCACCTAAC  ATATGTGGGATAGGACTGAATTATTAAGCATGATATTGTCTGAT  GACCCAACTGCCCATGTCACTTTGTTTCCAGAAACGAGGACCAA  TAATCTCTCACACTGGCATTTGTGCTGGTAGTACAAGTCCTTT  AATATGTCCAGGAAGGGAGCCATTGCCCAGTGGTCCATATCTCC  ACCACATCCCCTGCTTGAGCCAGCGCTGCATGTCCCTCCCAAG  AAGTCCAGAATGCCTGCAAATTGCTGTAATTTTATAC</p>	SEQ ID NO. 240
KCP_2418 04	<p>CTGATCTGCCCTTGTCTGATTTTACACACCAACTCTTGGGACA  GAAACACCTTTTACACTTTGGAAGAATTCTCTGCTGAAGACTTT  CTATGGAACCCAGCATCATGTGGCTCAGTCTCTGATTGCCAACT  CTTCTCTTTCTTCTTCTTGAGAGAGACAAGATGAAATTTGAGT  TTGTTTTGGAAGCATGCTCATCTCCTCACACTGCTGCCCTATGG  AAGTCCCTCTGCTTAAGCTTAAACAGTAGTGACAAAAATATGC  TGCTTACGTGCCCCCAGCCCACTGCCTCCAAGTCAGGCAGACCT  TGGTGAATCTGGAAGCAAGAGGACCTGAGCCAGATGCACACCAT  CTCTGATGGCCTCCCAAACCAATGTGCCTGTTTCTTCTCTTTG  GTGGGAAGAATGAGAGTTATCCAGAACAAATTAGGATCTGTCATG  ACCAGATTGGGAGAGCCAGCACCTAACATATGTGGGATAGGACT  GAATTATTAAGCATGA [C/T] ATTGTCTGATGACCCAACTGCC  CATGTCATTTGTTTCCAGAAACGAGGACCAATAATTCTCTCACA  CTGGCATTTGTGCTGGTAGTACAAGTCCTTTAATATGTCCAGGA  AGGGAGCCATTGCCCAGTGGTCCATATCTCCACCACATCCCCTG  CTTGAGCCCAGCGCTGCATGTCCCTCCCAAGAAGTCCAGAATGC</p>	SEQ ID NO. 241

	CTGCAAATTGCTGTAATTTTATACCATGTTCTAACCAATAAACA GAACTATTTCTTACACTCTCAATCACTTCTTCATGACTCCGTTA GGTAAGAGAGGTAAGCTGTGAAAAGGGAAGGCTAGTCCATTCA TTGACACCCAATTATTAGTGCAGTTGTCCCTCCATATGTGTGAA GGATCAGTCCCAGGACTCTCCATACCAAATCTGCAGATACTCA AGTCCCACAGCTAGCCCTGAGGGACTCGTGTTCAGAAAATTT GGCCTCCATATATGCAGGTTTCACATCCTATAAATAC	
KCP_1324	CCCAAGCTCAACCATTCCAATGCCATCTCCTCTGGTTCCAGATA AGATTGAAGATGAGCTGGAGATGACCATGGTTTGCCATCGGCCC GAGGGACTGGAGCAGCTCGAGGCCAGACCAACTTCACCAAGAG GGAGCTGCAGGTCCTTTATCGAGGCTTCAAAAATGTAAGACCCG TGCACGCTCTGAAGGCCTGGGGG	SEQ ID NO. 242
KCP_1520 4	TTGTCTACCATCTCCTCTCTAAGAAGGGCTCCCAATATATCC CCTTCTGCTTGCTTCTAACTCCCTATCACCTGCTAAAGAAGGAC CTCACCTTTTAATCACTTTTATTGCAAGGGGCACAAGGAGCCC CAAACCTCTGTCACCTAGGAAGAGCTTGACCTCATGGTTTCCACA CTGTGTGCTTTTATGTCCCTGCTC	SEQ ID NO. 243
KCP_4957	ACCCTCAATACAGACTGTTCTACAGTCCACGTCCTCAGCCACT AGACCATACGGCCACTGGGATGATAGACAGACCACTGCAGCCAT GGATAAGGCAAAAACAGGGCTGGCTGTGTGATCTGTGTCTCTC AGAGCTCCATTCTTCTCAAGGGGGCACCTTGCAAAAAAACA AAAAATGGGGCAGGGTAGGGAAC	SEQ ID NO. 244
KCP_5011	GCCACTGGGATGATAGACAGACCACTGCAGCCATGGATAAGGCA AAAACAGGGCTGGCTGTGTGATCTGTGTCTCTCAGAGCTCCAT TCTTCTCAAGGGGGCACCTTGCAAAAAAACAATAATGGG GCAGGGTAGGGAACGAAGGCAGGAGCTCTTCACAGAGCATAGC CACATCCTCCAGGCAGACAAGAGG	SEQ ID NO. 245
KCP_5051	GGCAAAAACAGGGCTGGCTGTGTGATCTGTGTCTCTCAGAGCT CCATTCTTCTCAAGGGGGCACCTTGCAAAAAAACAATAATGGG TGGGGCAGGGTAGGGAACGAAGGCAGGAGCTCTTCACAGAGCA TAGCCACATCCTCCAGGCAGACAAGAGGACGCAGGAGGCACCAT TCTGTGAGAGTATCACAGTCTGAC [C/T] CAAAGACACAGCTTC ACACTGTCTGATGGCTTGATGGTTAATGTCACTCTGCCTTTTCC CCTTCTCAGGACTTTGTAACCGCTCTGTCTGATTTTATTGAGAGG AACTGTCCACGAGAACTAAGGTGGACATTTAATTTGTATGACA TCAACAAGGACGGATACATAAACAAGAGGTAAGTGAGCTGGGG CCAGGGGTGT	SEQ ID NO. 246
KCP_5202	GACAAGAGGACGCAGGAGGCACCATCTGTGAGAGTATCACAGT CTGACCCAAAGACACAGCTTCACTGTCTGATGGCTTGATGGT TAATGTCACTCTGCCTTTTCCCTTCTCAGGACTTTGTAACCGC TCTGTCTGATTTTATTGAGAGGAACGTCCACGAGAACTAAGGT GGACATTTAATTTGTATGACATCA [A/C] CAAGGACGGATACAT AAACAAAGAGGTAAGTGAGCTGGGGCCAGGGGTGTGAGAGGGCT CCAGTGAAGGTAACCAACCAAGAAAACAGCCCCAGGCATGA GGATAGCACTGTCTGAATGAGGCAGGCTCTGCTTTGGGGCTAAC AGAGCTGGTCCCTGGCAAAATAAGAAGGCCTCCCTCATTGCCC TACCCTGCCC	SEQ ID NO. 247
KCP_e1a_ 249924	CCACCAGGGTCCCTTCCAACCTCAGGAGCCTATGGTACTGAATG GCAGCCAGGTTTTTTATGGAGCAATAGCTGGACTTCACATTTGC ATAATGCCTTGCACTTTCAGTGTAAAGAGTACTGCATTGTATTC TAATTATATGAATCTCGGTCATTCCTTTATGACATTTCTGAGGA ATACTATCTCAATCAAGAAAAGCCCTAATTGCACTCCTCTCCTA TCCCGGTGAGAGAGCACAGACTCGTGCCTGCTCCGCAGGGGTGG AGGCTGGAATTCAGTAGTCTGAGTCGGGGATGCCTGGAGCAGGA GGTGGTCAGGGGCATTGTCTTTTCCAAGTCAGGAAGGCAGACAG CACCTGCTGTTGGTGCCAAGGTTACTGGACAGGCTGCAGGGCT CTGTCTGTCTGTCCGATGTTACAGGCCAGCTCCCCGGAGGCTC	SEQ ID NO. 248

	AGCACTCAGCCAGCTTCTCCGAGATGCAAACCAGGCCACTCTG AGGCTGCCTACAACTTTCTGCTGAGTGCCGACAGCTGCTTCCCT GCTCTGCGGGGAGTTCTTCCAGATCCTGATCAAGGCACAGAGAA TTGATCTATCAGATTAACCAGGAAGGAAAGAGTGGGAGAGCGAG TGTGGGAGGCTGTGGGGCTGAGTGTTTTCTGCGTAGCAGTCCCC TCCCTTCTGACTTGAGTATTAATTGCTACATTACCGCTGCCATG TAAGAAAGACAGTCAGCAAAGCCTGGGAGAGCTCCAGCTCCTCC CTCCCTGCTCTGCTCAACTTCACTCTCCTCCTCGGTTCCCTTGG AGTACCTTGTGCCCCGGCAGTGCTGTCCCGGCCCTGGCATCCTG AGGTCTTCCCGTGGTGAGGACTTAAGTGGACA [C/G] CAGGAGT GGGTGGAGAGAGGGAGGGAGAGTTTGGCCTGCAGGCTCTCTGGA TGCAGAAGCCAGACTCGCTGCAGAGGCAGCTGTGCTGTTCCCGG AGCCTGGCTTCAGGGGTGCATCCGTCACTCAGGGTTTATTACAC CAGGCAGGCTCCAAGTTCTTGGGGTGACAAGGTGGGCACTGTC CCTTCTGGGTGCTGACAGCAGAGCCTGGCTCCCCCTCCGCCACCA TGAGCGGCTGCTCCAAAAGATGCAAGCTTGGGTTCGTGAAATTT GCCCAGACCATCTTTAAGCTCATCACTGGGACCCCTCAGCAAAGG TATGGAACTGGCCTTGACCTTGCTTTCTGTCTTGATATGGCC TGGCTGGTTCGCATTGCCTCGGTGTGGTGAGCGTGACCATCTGG TGCACCCAGGTCTTGGAAAAAGCTGGGGAAATTGGTGGCTGGGA TTCGAGGTGTGCTGACAACCTGCGTCTGGCTTTGAGTAGGCGGG CACCCAGCCAGGGAACCTCAGCTGGCTGTAATTGCCTGGAACCTT GGAAATGGAGTTGGTGGTGTGTGGCTGATACGTTATGGGCGGGC AGAGGGATAGAACCCTTTCCAGAGCATTGGAAGTGGCTTAGCGT GACTGGAGTTTCAAGAAGTTATCCATGGAAGGTGTATTTTGT GATAAAAGAGAGATTGATGCAGTGGGTTGTGAGTAATTCTGCA GAACAGAGACGCTTGAGGGGGCCAGTGGGAGGTGGTGTATGGGCC GGCATCTGCTTTGCCCTGGTGGCTTCAGAAACCGGATCAGCTCT GCACCTCAAGTGCCAAGAGCCTCCTCTCATAGGGTTCCAGCGTC TCGTGCTTCTGGGGCTTCATTATCGTTCTGCTTTCTTGGATCC CTGTCCCTCCACATTTTCATGCCTA	
KCP_ela_250027	CAAGGCACAGAGAATTGATCTATCAGATTAACCAGGAAGGAAAG AGTGGGAGAGCGAGTGTGGGAGGCTGTGGGGCTGAGTGTTTTCT GCGTAGCAGTCCCCCTCCCTTCTGACTTGAGTATTAATTGCTACA TTACCGCTGCCATGTAAGAAAGACAGTCAGCAAAGCCTGGGAGA GCTCCAGCTCCTCCCTCCCTGCTCTGCTCAACTTCACTCTCCTC CTCGGTTCCCTTGGAGTACCTTGTGCCCGGCAGTGCTGTCCCG GCCCTGGCATCCTGAGGTCTCCTCCCGTGGTGAGGACTTAAGTGA CAGCAGGAGTGGGTGGAGAGAGGGAGGGAGAGTTTGGCCTGCAG GCTCTCTGGATGCAGAAGCCAGACTCGCTGCAGAGGCAGCTGTG CTGTTCCCGGAGCCTGG [C/T] TTCAGGGGTGCATCCGTCACTC AGGGTTCATTACCCAGGCAGGCTCCAAGTTCTTGGGGTGACA AGGTGGGCACTGTCCCTTCTGGGTGCTGACAGCAGAGCCTGGCT CCCCTCCGCCACCATGAGCGGCTGCTCCAAAAGATGCAAGCTTG GGTTTCGTGAAATTTGCCAGACCATCTTTAAGCTCATCACTGGG ACCCTCAGCAAAGGTATGGAAGTGGCCTTGACCCTTGCTTTCT GTCTTGATATGGCCTGGCTGGTGCATTGCCTCGGTGTGGTGAG CGTGACCATTCTGGTGCACCCAGGTCTTGGAAAAAGCTGGGGAA ATTGGTGGCTGGGATTGAGGTTGCTGACAACCTGCGTCTCTGGC TTTGAAGTAGGCGGGCACCCAGCCAGGGAACCTCAGCTGGCTGTAA	SEQ ID NO. 249
KCP_ela_250049	ACAGAGAATTGATCTATCAGATTAACCAGGAAGGAAAGAGTGGG AGAGCGAGTGTGGGAGGCTGTGGGGCTGAGTGTTTTCTGCGTAG CAGTCCCCTCCCTTCTGACTTGAGTATTAATTGCTACATTACCG CTGCCATGTAAGAAAGACAGTCAGCAAAGCCTGGGAGAGCTCCA GCTCCTCCCTCCCTGCTCTGCTCAACTTCACTCTCCTCCTCGGT TCCCTTGGAGTACCTTGTGCCCGGCAGTGCTGTCCCGGCCCTG GCATCCTGAGGTCTCCTCCGTGGTGAGGACTTAAGTGGACAGCAG	SEQ ID NO. 250



	GAGTGGGTGGAGAGAGGGAGGGAGAGTTTGCCCTGCAGGCTCTC TGGATGCAGAAGCCAGACTCGCTGCAGAGGCAGCTGTGCTGTTT CCGGAGCCTGGCTTCAGGGGTGCATCCGTCACT [A/C] AGGGTT CATTCACCCAGGCAGGCTCCAAGTTCCTGGGGTGACAAGGTGG GCACTGTCCCTTCTGGGTGCTGACAGCAGAGCCTGGCTCCCTC CGCCACCATGAGCGGCTGCTCCAAAAGATGCAAGCTGGGTTCG TGAAATTTGCCCAGACCATCTTTAAGCTCATCACTGGGACCCTC AGCAAAGGTATGGAACTGGCCTTGACCCTTGCTTTCTGTCTTG ATATGGCCTGGCTGGTCGCATTGCCTCGGTGTGGTGAGCGTGAC CATTCTGGTGCACCCAGGTCTTGGAAAAAGCTGGGGAAATTGGT GGCTGGGATTGAGGTTGCTGACAACCTGCGTCTGGCTTTGAG TAGGCGGGCAGCCAGCCAGGGAATCAGCTGGCTGTAATTGCCT GGAACTTTGAAATGGAGTTGGTG	
KCP_UTR1 _382206	TGGCCACCTTCAGGGTCATGAGGATTCATAAACCTATTCTGC GAAGTGCCTCCAGGAATCATCAAGGGAGCTAGGGCAGCTCTGAG TCTCCACCAGGCCACCTCCGCTCTCAGGGCTGAGCTTCACT TCCCTTCCCAAAGGGGCCAGGGAGAGGGGCTGCTGATGACATGA TCTCAGAGGAAGGCCAAGGCCTCAGGCTGCCTCTGGGCTGGC ACAGGAAGGAGGAGGAGAAAATAGGGAGCCCAAGGAAAGATCAA CCCAGCCCAGCCCAAGGACCCCCAGCCCCAGCCCCAGCCCCAGC TGGGCTCAAATAATTGAAAACAGACTGGAAAAGGCTGCTTTTG CCCTTCTCTAGACTCAGCATCATCAAGACTGGAGGGACAGAGC ATTTGAATCATCAGACGCTGGGCCAGA [C/T] GTCACCCACGC GTTTTCTCATTTTATCGTCCTAAGAAAGCCAGAGGTGCGTAAA ATGGCCTGTCCCAAACAGATGAGGACATTACCTTTCTCTCTTC CTCCTCCTCCTTCTTCTTCTTCTTTTGCTTCATTTTCTT TCATTTTTTCCCCAGATGTTGCATTTAGAGAGGCTGAGCGTG TTGACTAAGGTACACAGCTACAAACATCAGGGACCTGCGAAAA AGCTCTGTTCCCTGGTGACAGGTGTTCTGTGATCCTAACACAGC CGGAGGTGGGGACAACGTCCTTGAGTAACAAAGGCCCTGTTGC TCAACTCAGTGGACATCAGGCCCTGTTTTCATTATTAGCAGGT CAGGGATTCCAGTGTACCTGTGCCATGTATTCCAGCTGATCTA CCTGCAAGCCTCTACTCCCCATTTTCCAGCAGCAGCCGCAGAC ACCACCAACTGG	SEQ ID NO. 251
KCP_UTR1 _382272	GGGTGATGAGGATTCATAAACCTATTCTGCGAAGTGCCTCCAG GAATCATCAAGGGAGCTAGGGCAGCTCTGAGTCTCCACCAGGCC CACCTCCGCTCTCAGGGCTGAGCTTCACTTCCCTTCCCAAAG GGGCCAGGGAGAGGGGCTGCTGATGACATGATCTCAGAGGAAGG CCAAGGCCTCCAGGCTGCCTCTGGGCTGGCACAGGAAGGAGGA GGAGAAAAATAGGGAGCCCAAGGAAAGATCAACCCAGCCAGCCC AAGGACCCCCAGCCCCAGCCCCAGCCCCAGCTGGGCTCAAATA ATTGAAAACAGACTGGAAAAGGCTGCTTTTGCCCTTCTCTAGA CTCAGCATCATCAAGACTGGAGGGACAGAGCATTGTAATCATCA GACGCTGGGCCAGACGTACCCCCACGCGTTTTCTCATTTTATCG TCCTAAGAAGCCCAGAAAGGTGCGTAAATGGCCTGT [A/C] CCA AACAGATGAGGACATTACCTTTCTCCTCTTCTCCTCCTCCTTC TTCTTCTTCTTCTTTTGCTTCATTTTCTTTTATTTCCTTCC CAGATGTTGCATTTAGAGAGGCTGAGCGTGTGACTAAGGTCA CACAGCTACAAACATCAGGGACCTGCGAAAAAGCTCTGTTCCCT GGTGACAGGTGTTCTGTGATCCTAACACAGCCGAGGTGGGGAC AACGTCCTTGAGTAACAAAGGCCCTGTTGCTCAACTCAGTGA CATCAGGCCCTGTTTTCATTATTAGCAGGTGAGGATTCCAGT GTCACCTGTGCCATGTATTCCAGCTGATCTACCTGCAAGCCTCT ACTCCCCATTTCCAGCAGCAGCCGCAGACACCACCAACTGG CAGAAATTTCAAACAAGGGGTTCTGCCTTGCACTCCGGTGCAAG GGTTGGGCACGTGACTCACAT	SEQ ID NO. 252
KCP_3UTR	CACAAAACAAATCCGGGACTTTAAGCCTGATCTGCTTGACCTGA	SEQ ID

2_395068	<p>AACTCATATCTACTTCCCTGCCCTCTGAAGATCTATATGTCCTA  TGTCATCACTTCACTGTTTACACAAGGTGATACCTGGCTTCTCC  AAGCACCTGCTACCCCTGAACCTTACTGCACCACTCTTTCCTTCCCT  AGCCTGAATGCAATTTGCAATGAGGAGATGATTGATTTTCTTC  AGCCCTAGACCTCCAGCTTCTTGAGAGCAGGTACTCTTGCCCTCT  TCTTGCTCATTATTGATCCATATATTTAGAATAGCGCTGGCAG  GTAGATGGTGCTTAATAAATATTATTGAATAAATGAATGAATG  AATGATCCAATGAGCCCCAAAGCAAATAACAATAAAGGACATTT  GCAGAGTGCTCTACAGAGAGACAAGTGCTTTCCCTTT [A/G] CT  TTATCTTACCCCATTTCTCACACAATCCCCTGACATGATTGGGT  TCATGTTTACAGATGAGGAGGCTAACGGCCAGGTGTACATACC  AGGGGACATGGGACTGGGTTTATATGAGCTCAGGGGTAAATGAT  GACACCCCTTTCCCTGCCCTGAAGGATCTCAGTTTGAGTATTTG  TAGCACACTTAGGATGTTCTGGGCCAGGCTGAGTGGCGGTGGAT  GGGGGCGGTGGAGGTGGGGTATGCAAAGCAGGAACTCGGCCCTT  TGCTTTCTAAAAGCTCCCACTCTATTTGAGGCCAGACTTATGCA  TGCAGAACATTTGGGAAATGGTACAAGACAGCAGCAAGCATAGT  GCTGAATTGCACATAATCAGGTGCCAACTGCATTCCCTTCCCTTA  ACTAATCT</p>	NO. 253
KCP_3UTR 3_398480	<p>AACTTTCTCCTCAGCAAAGAGCTCTCCTCTGTTCCCTGAATCCT  GGATATCCCACTGGGTCTCTAGTGACCCCAAGCTTCAGCCTCG  CATGCCCTCTTCTCGAACAGAGAAGGCAGGAGGGAAGCAGGGAC  CAGCCCCCTGCTCCATCTTCCAGGATTCCAGGCCTCCCTGGCCTG  GACAAGCCCTGAGCTGGCAGTTAGGAGAGCAGAGGTTGTGAATC  TGGTGGGACCCCCAGCAGGTCTTCTGGCTCAGTGCCCTCATCT  GTGAGCAGGGGTTCCCCAGGAGACCACGACAGAGGCCTGGAACC  CAAGTTCTAATCCCATCTCTGGCTGGGCAACTTCAGGCAAATT  TCTAACACAAGGTAAGCCTCAATTTCTCTCTGGGGTAATGATCA  GGCACCTGCTTAATTCACAGGGGTTTGGTGGGCATCA [C/T] GT  GGACAATGTGGTTGCACAGCAGTGCGCAATGCAAAGGAAAGGAA  GTATGTTAGTAAGTGCCCCCTCCCCTGTTGCACAAAACAGGACAC  ATGCTGGGATTGCAGAAAAGCAATAAATGCTGCACAGGTGAAGA  AAACTATTCAAGGACCCTGGCCAAGTCACAGGCTACCTGTGGCC  CTGAGGGGACAGCTCATGGGTTGGCATTAGGGGAAGCAGCTCTC  AAGGGGCCCTGTATCCTGGGGATTCAACTCTGTGCCTATGTGGCA  TTGAGCCTGTGTGAATGTGGTGAATGTGCATGCTGTTTTGCTGTG  TGTGCGTCTGCATGCCTGTGTGTTTGTGTGTCTCTCCACCTTCG  TGGGGGGCAACTGTAGGTGTATTATGAGCCTTGGGTCTGTCTGT  GTGTACAATAGCAATGTCTGTGCGGACTTAAGGACCTGCGCCCA  TATGTTTGTGGGACTTTC</p>	SEQ ID NO. 254
KCP_3UTR 3_398605	<p>CAGAGAAGGCAGGAGGGAAGCAGGGACCAGCCCCTGCTCCATCT  TCCAGGATTCCAGGCCTCCCTGGCCTGGACAAGCCCTGAGCTGG  CAGTTAGGAGAGCAGAGGTTGTGAATCTGGTGGGACCCCCAGCA  GGTCTTCTGGCTCAGTGCCCTCATCTGTGAGCAGGGGTTCCCC  AGGAGACCACGACAGAGGCCTGGAACCCAAGTTCTAATCCACACA  TCCTGGCTGGGCAACTTCAGGCAAATTTCTAACACAAGGTAAGC  CTCAATTTCTCTCTGGGGTAATGATCAGGCACCTGCTTAATTCA  CAGGGGTTTGGTGGGCATCACGTGGACAATGTGGTTGCACAGCA  GTGGGCAATGCAAAGGAAAGGAAGTATGTTAGTAAGTGCCCCCTC  CCCTGTTGCACAAAACAGGACACATGCTGGGATTGCAGAAAAGC  AATAAATGCTGCA [C/T] AGGTGAAGAAAATATTCAAGGACCC  TGGCCAAGTCACAGGCTACCTGTGGCCCTGAGGGGACAGCTCAT  GGGTTGGCATTAGGGGAAGCAGCTCTCAAGGGGCTGTATCCTG  GGGATTCAACTCTGTGCCTATGTGGCATTGAGCCTGTGTGAATG  TGGTGAATGTGCATGCTGTTTTGCTGTGTGTGCGTCTGCATGCGT  GTGTGTTTGTGTGTCTCTCCACCTTCGTGGGGGGCAACTGTAGG  TGTATTATGAGCCTTGGGTCTGTCTGTGTGTACAATAGCAATGT</p>	SEQ ID NO. 255

	CTGTGCGGACTTAAGGACCTGCGCCCATATGTTTGTGGGACTTT CTGGGCATGCATGCTTGTATTATGAGGCCATACATCCGGGTATTC TGTGAACTGCTAGCATGGTGTGTATCTGTGTGGCAGACAGAAAA TGGCTGGGTGGGA	
KCP_e1b_ 399912	ATCTCAGCACTTTGGGAGGCCAAGGCGGTGGATCACCTGAGGT CAGGAGTTCAAGCCCAGCCAGCCCAACATGGCGAAACCCCGTCT CTATTAAAAAATACAAAAAATTTAGCTGGGCCTAGTGGTGGGC GCCTGTAATCCCAGCTACTCCGGAGGCTGAGGCAGGAGAATCGC TTGAATCTGGGAGGCAGAGGTTGCAGTGAGCAGAGATCGCACCA CTGCACTCCAGCCTGGGCAACAGAGCGGAGACTCCGTCTCAAAAA AAAAAAAAAAAAAGAAAAAGAAAAATGAGAGTGTAAAGGCCAGAG GGGCTGAGGGCTCCTTTCTCCTCCCAACTCCTGTCTCAGTAGAA GGTGGGCCCCGCCATAGGAGGATTCTGCAGAACCCCTCAAGGACC CGCGGAGCAGGACGGCACCTTCTTCCCATGACCACCCATTGGA TGTGTTTTTACCCCTTTCTGGGTGGGGCAGACTTTCCCCCTCC CCATGAGTTCAGGCAG [G/T] GGGTTAAATAAGATTTCCCTTGA AGTCGAATGAAATCACAATGCACCACACACAGGGACACACACAC ACACACACGCACGCACGCACATCACACACACACACACACACACA CACACACACACACACATACACACACACAGTCTCCCTGGGGCC AATCTACTGCCCCCTGAACCTCACCCATCAGCCAGGTGCCTGGC CCCGGCTGTCTCTTAGGGTTACATGCTCCCGGGCTCCCGCA CATACCCCGGCAGATGAGGGTGCGCAGGGGTGAGGGCGCAGGGC TGGGCGTCCCCCGCCCCACCGTGCAGCCCTCGCCCCGCCCCG CCCTCCGTAGTTGCCCGCCCGCCGCCCCCTCCGCCGCCCTC CGCCGCTCCGACTCTCGCCCCGAGCGCTGGCAGCAGGCAGCAGG CAGCAGGCGGGCGCGCTGTGGCTCCGCGCCGCGCGGTCCGGGCT CTGTTCAATCATGATTGGTACTCGGCCCTCCGAGACC	SEQ ID NO. 256
rs102685	AGCACTCCTGGGGCTCATTGTAAAGTTTATAAACTCAGAGCTG ATGAGTTGTGTGCACTGTGTGGGTCTGAGTGGGCTTATGACTCC CCTCCAAGCCTGGCTGTAAGAATCTAAGACTTAAAGCTGAAGGA CCAAATGGGACTTTCTGTCCCATCCCCTCTCTGCTCCATGCAAG CACCAA [C/T] GTGGATTTTGGCCCTAATTATATTAGGGAACG CTGTCAATCAAAAAGATGATGTTAAACTCATCCAGAACAAACCA AACCATGTTTAAGGGGAAGAAAAGATTACATCTTCAAATGCCAG CATGCCATCATTAATACAATGTCTAATGTAGTCAATATAGTTCA GGCAACATTGAAAATGAACCACTGCAATACTAGGAATACAATT TCAAGAGGAAGCACAAACATTCTGTGTTTCTATGCACACAGTCCT GTAAATTATTTGCAGCTCAAGTATGTATGTTCTTTTAAATTTT CCCCTGGGTACAGCTTGAACAACCTCCTACAAGTGTGATATGT CATATTCTCATTATCATTTAGTTCAAAATTACCATGATTTAATT ACCATGAGGTTGCTTTTGTGATACATGAGTTACTTAGAAATTGA ATTAggctaggcatgggtggctccacctataatcctagcacttt ggaaggccaaggcaggaggattgcttgagtttgaggccagtcta ggcaatatagtgagacctcatctccccaaaagtacaaaaaaact agccaggcatggggacacatgcctatagttccagctactcaaag gctgaggtggggaggattgctttgagcctggg	SEQ ID NO. 257
rs905808	GCCAGCTATCCCAGAGACATCACAGGAGAAGGAGCAGAAGCTG GAACATCATCCGGGAGCTGGACTAGAACGTCCCGGGAACCTTCA GCCTGGCTTCTGCTTTGTCCCGAAAACCCAGGGGCTCCAGCTCC AGGGCTGTGTCTTAGAATGAGGCAGTTTATCTGTTTCAGGGCTTC TCTTAGTTTTTAATCCCAATAGGACACA [C/T] GTTGTATTAAA AAGCCATGCGAGATGGAAGAAGGAAATTGAATGAAATTTGAGGG CAGGTAGGAGCAGAGACAATAAATAATTACAGCAGTGAAGGAAGC AGAAAAAAGATTGCACTCATTTGCGCCTTCAACAATTATACTAA ACACCTGCTCTGGGCCACAGAAGGGCCAGATCCCATTCCTGTGC TCAGGAAGCCACAGGCCGGCAGGGAGAGGCTGGTTGGAATGTG TGCTTTGCACTGTAACGGAGGCATCGAGCATGGTAAGGGACTGG	SEQ ID NO. 258

	CGGTGACTGCTGCCTGCGGACGTCGAGACAGGGGCCTTTGAAGA GGCAGGACCTGTCTGGAGTCTTACCTGGGCCTTGGCCTGGCAAT GGGG	
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Table 1. The Build 33 location of SNPs and microsatellites employed for the first-pass association analysis across KChIP1.

5

Start (B33)	Marker	Public Alias	deCODE alias	Variation
169788696	DG5S47			
169794522	DG5S1592			
169843903	DG5S119			
169869845	rs933656	rs933656	DG00AAFCS	A/G
169869955	rs2339091	rs2339091	DG00AAFCI	G/T
169961410	DG5S13			
169964087	rs905808	rs905808	DG00AAFCEG	C/T
170006645	rs883849	rs883849	DG00AAFCK, DG00AAIOG	A/G
170015858	DG5S123			
170037283	rs2135046	rs2135046	DG00AAFCJ, DG00AAIOH	C/T
170041996	DG5S124			
170056955	rs2339139	rs2339139	DG00AAFCE	A/G
170064881	rs329468	rs329468	DG00AAFCH	A/G
170070041	rs50057	rs50057	DG00AAFCE, DG00AAIOI	A/G
170070735	rs102685	rs102685	DG00AAFCE, DG00AAIOJ	C/T
170073252	rs50364	rs50364	DG00AAFCD	A/G
170081291	KCP_1152		SG05S176	C/T
170081473	KCP_1333		SG05S921	A/G
170082788	KCP_2649		SG05S923	C/T
170085115	KCP_4976		DG00AAGHK, DG00AAHUT, DG00AAINX	C/T
170085217	KCP_5077		DG00AAINZ	A/T
170095540	KCP_15400		SG05S946	C/T
170096291	KCP_16152	rs486818	SG05S948	A/G
170098209	KCP_18069	rs1363712	SG05S189	C/T
170105556	D5S625			

5 Table 12. The Build 33 location of SNPs found through sequencing across KChIP1(from exon 1b to exon 8).

Build 33 Pos	Project Pos	DECODE ALIAS	SEQ PROJECT ALIAS	PUBLIC ALIAS	SNP
169866787	9677	DG00AAHAP	KCP_9677		C/G
169867465	10355	SG05S229	KCP_10355		A/T
169867556	10446	DG00AAHA R	KCP_10446		C/G
169871957	14847	SG05S485	KCP_14847	rs486768	A/T
169872129	15019	SG05S1298	KCP_15019	rs4867973	A/G
169872417	15307	SG05S437	KCP_15307		A/C
169872421	15311	SG05S438	KCP_15311		A/T
169872435	15325	SG05S439	KCP_15325		C/G
169872949	15839	SG05S440	KCP_15839		A/G
169873539	16429	SG05S486	KCP_16429		C/T
169873680	16570	SG05S487	KCP_16570		A/G
169875123	18013	SG05S488	KCP_18013		A/T
169875568	18458	SG05S1002	KCP_18458		A/G
169876302	19192	SG05S489	KCP_19192		A/G
169878365	21255	SG05S490	KCP_21255		G/T
169878734	21624	SG05S491	KCP_21624	rs486769	A/G
169879678	22568	SG05S492	KCP_22568		A/C
169879717	22607	SG05S493	KCP_22607		C/T
169881496	24386	SG05S494	KCP_24386		A/G
169882681	25571	SG05S495	KCP_25571		A/C
169883265	26155	SG05S496	KCP_26155		A/G
169883333	26223	SG05S497	KCP_26223		C/G
169883413	26303	SG05S498	KCP_26303		A/G
169883465	26355	SG05S1171	KCP_26355		C/G
169883518	26408	SG05S499	KCP_26408		A/T
169883738	26628	SG05S500	KCP_26628		A/G
169883811	26701	SG05S501	KCP_26701		A/G
169884084	26974	SG05S1172	KCP_26974		C/T
169884145	27035	SG05S502	KCP_27035		G/T
169884439	27329	SG05S503	KCP_27329		C/T
169884682	27572	SG05S504	KCP_27572		A/G

169884707	27597	DG00AAJHT	KCP_27597		A/G
169884973	27863	SG05S505	KCP_27863		A/G
169885005	27895	SG05S506	KCP_27895		A/G
169888453	31343	SG05S507	KCP_31343	rs4867975	C/T
169889433	32323	SG05S60	KCP_32323		C/T
169889680	32570	SG05S508	KCP_32570		A/G
169890025	32915	SG05S509	KCP_32915		A/G
169890055	32945	SG05S1173	KCP_32945		A/G
169890089	32979	SG05S1174	KCP_32979		A/C
169890291	33181	SG05S510	KCP_33181		A/G
169892122	35012	SG05S1175	KCP_35012		A/C
169892332	35222	SG05S511	KCP_35222		A/G
169892524	35414	SG05S61	KCP_35414		G/T
169892619	35509	SG05S512	KCP_35509		C/T
169892687	35577	SG05S513	KCP_35577		G/T
169893157	36047	SG05S514	KCP_36047		C/T
169893169	36059	SG05S515	KCP_36059		C/T
169893871	36761	SG05S516	KCP_36761		A/C
169894061	36951	SG05S517	KCP_36951		A/G
169894358	37248	SG05S518	KCP_37248		C/G
169895507	38397	SG05S1176	KCP_38397		C/T
169895699	38589	SG05S953	KCP_38589		A/C
169896322	39212	SG05S519	KCP_39212		G/T
169896357	39247	SG05S520	KCP_39247		A/G
169896369	39259	SG05S521	KCP_39259		A/G
169896451	39341	SG05S1177	KCP_39341		A/G
169896647	39537	SG05S522	KCP_39537		C/T
169896750	39640	SG05S523	KCP_39640		A/T
169896914	39804	SG05S524	KCP_39804		A/G
169897484	40374	SG05S525	KCP_40374		C/T
169897594	40484	SG05S526	KCP_40484		A/G
169897621	40511	SG05S527	KCP_40511		C/T
169897856	40746	SG05S528	KCP_40746		C/T
169898205	41095	SG05S529	KCP_41095		C/T
169898252	41142	SG05S530	KCP_41142		C/T
169898371	41261	SG05S531	KCP_41261		A/G
169899446	42336	SG05S532	KCP_42336		A/G
169899693	42583	SG05S533	KCP_42583		A/G
169900156	43046	SG05S534	KCP_43046		A/G

169900425	43315	SG05S1178	KCP_43315		C/G
169900629	43519	SG05S535	KCP_43519		C/T
169902212	45102	SG05S536	KCP_45102	rs211261	A/G
169902400	45290	SG05S537	KCP_45290		G/T
169903206	46096	SG05S538	KCP_46096		C/T
169903615	46505	SG05S539	KCP_46505		C/T
169903676	46566	SG05S540	KCP_46566		A/C
169903766	46656	SG05S541	KCP_46656		A/C
169904530	47420	SG05S542	KCP_47420		C/T
169904757	47647	SG05S543	KCP_47647		A/G
169906262	49152	SG05S1179	KCP_49152		A/G
169906576	49466	SG05S544	KCP_49466		A/G
169906846	49736	SG05S545	KCP_49736		A/T
169907866	50756	SG05S1180	KCP_50756		A/G
169908937	51827	SG05S1181	KCP_51827		C/T
169909190	52080	SG05S1182	KCP_52080		C/T
169910099	52989	SG05S546	KCP_52989		A/G
169910133	53023	SG05S547	KCP_53023		C/T
169911784	54674	SG05S548	KCP_54674		A/C
169911823	54713	SG05S549	KCP_54713		A/C
169913086	55976	SG05S1183	KCP_55976		A/G
169913415	56305	SG05S62	KCP_56305		A/G
169913670	56560	SG05S954	KCP_56560		C/T
169913988	56878	SG05S550	KCP_56878		C/G
169914731	57621	SG05S551	KCP_57621		A/G
169914887	57777	SG05S552	KCP_57777		A/G
169915597	58487	SG05S553	KCP_58487		A/G
169917130	60020	SG05S554	KCP_60020		C/T
169917579	60469	SG05S555	KCP_60469		A/G
169917813	60703	SG05S556	KCP_60703		A/G
169919206	62096	SG05S557	KCP_62096		A/G
169919909	62799	SG05S233	KCP_62799		C/T
169921008	63898	SG05S558	KCP_63898		A/G
169921407	64297	SG05S559	KCP_64297		A/G
169921917	64807	SG05S560	KCP_64807		G/T
169922010	64900	SG05S1184	KCP_64900		A/G
169922309	65199	SG05S955	KCP_65199		A/G
169922397	65287	SG05S561	KCP_65287		G/T
169923449	66339	SG05S562	KCP_66339		A/G

169923611	66501	SG05S563	KCP_66501		A/G
169924005	66895	SG05S564	KCP_66895		A/G
169925422	68312	SG05S565	KCP_68312		A/C
169926039	68929	SG05S566	KCP_68929		C/T
169926454	69344	SG05S567	KCP_69344		A/G
169926756	69646	SG05S568	KCP_69646		C/T
169927013	69903	SG05S569	KCP_69903		A/G
169927893	70783	SG05S570	KCP_70783		C/T
169928063	70953	SG05S571	KCP_70953		A/T
169928076	70966	SG05S572	KCP_70966		A/C
169928444	71334	SG05S573	KCP_71334		C/T
169928522	71412	SG05S574	KCP_71412		A/T
169928555	71445	SG05S575	KCP_71445		C/T
169928665	71555	SG05S576	KCP_71555		C/T
169928700	71590	SG05S577	KCP_71590		C/T
169929635	72525	SG05S578	KCP_72525	rs4269297	A/G
169929849	72739	SG05S579	KCP_72739		C/G
169930171	73061	SG05S580	KCP_73061	rs4867613	C/T
169930506	73396	SG05S581	KCP_73396		A/T
169930538	73428	SG05S582	KCP_73428	rs4867978	A/G
169930644	73534	SG05S583	KCP_73534	rs4867979	C/T
169931073	73963	SG05S584	KCP_73963		C/G
169931425	74315	SG05S585	KCP_74315		A/G
169931663	74553	SG05S586	KCP_74553		G/T
169931670	74560	SG05S587	KCP_74560		C/T
169932137	75027	SG05S588	KCP_75027		C/T
169932696	75586	SG05S589	KCP_75586		A/C
169932998	75888	SG05S590	KCP_75888		C/T
169933181	76071	SG05S591	KCP_76071	rs386758	A/G
169933212	76102	SG05S592	KCP_76102	rs386759	C/T
169933256	76146	SG05S593	KCP_76146		A/G
169933389	76279	SG05S594	KCP_76279	rs4368746	C/T
169933420	76310	SG05S595	KCP_76310		C/T
169933699	76589	SG05S596	KCP_76589		C/T
169933756	76646	SG05S597	KCP_76646		C/T
169934348	77238	SG05S598	KCP_77238		G/T
169934429	77319	SG05S599	KCP_77319		C/G
169934556	77446	SG05S600	KCP_77446		C/T
169934663	77553	SG05S601	KCP_77553		C/T



169934751	77641	SG05S597	KCP_77641	rs4242157	A/G
169934936	77826	SG05S598	KCP_77826		C/G
169934949	77839	SG05S599	KCP_77839		A/G
169935134	78024	SG05S600	KCP_78024	rs4867981	A/G
169935240	78130	SG05S601	KCP_78130	rs4867614	C/T
169935254	78144	SG05S602	KCP_78144		A/C
169935713	78603	SG05S603	KCP_78603		C/T
169935892	78782	SG05S604	KCP_78782		A/G
169935939	78829	SG05S605	KCP_78829		A/G
169935989	78879	SG05S606	KCP_78879		C/T
169936272	79162	SG05S607	KCP_79162		C/T
169936275	79165	SG05S608	KCP_79165		C/T
169936329	79219	SG05S609	KCP_79219		G/T
169936495	79385	SG05S610	KCP_79385		C/T
169936910	79800	SG05S611	KCP_79800		C/G
169937029	79919	SG05S1189	KCP_79919		A/G
169937270	80160	SG05S612	KCP_80160		A/G
169937896	80786	SG05S613	KCP_80786		A/G
169938126	81016	SG05S614	KCP_81016		C/T
169938400	81290	SG05S615	KCP_81290		A/G
169938894	81784	SG05S1190	KCP_81784		A/G
169939578	82468	SG05S957	KCP_82468	rs4242158	A/G
169940311	83201	SG05S616	KCP_83201		C/T
169940995	83885	SG05S617	KCP_83885		A/G
169941106	83996	SG05S618	KCP_83996	rs4867615	A/G
169941897	84787	SG05S1191	KCP_84787		A/T
169942667	85557	SG05S619	KCP_85557		A/G
169942775	85665	SG05S620	KCP_85665		C/T
169942903	85793	SG05S958	KCP_85793		C/T
169943046	85936	SG05S621	KCP_85936		A/G
169943817	86707	SG05S622	KCP_86707		A/T
169944237	87127	SG05S623	KCP_87127		C/G
169945487	88377	SG05S624	KCP_88377		C/T
169945857	88747	SG05S625	KCP_88747		A/T
169945886	88776	SG05S626	KCP_88776		C/T
169945923	88813	SG05S627	KCP_88813		A/G
169946380	89270	SG05S628	KCP_89270		A/G
169946491	89381	SG05S629	KCP_89381	rs4867983	A/G
169947228	90118	SG05S630	KCP_90118		A/G

169947236	90126	SG05S631	KCP_90126		G/T
169947285	90175	SG05S632	KCP_90175		C/T
169947471	90361	SG05S633	KCP_90361		C/G
169947529	90419	SG05S634	KCP_90419		C/T
169947661	90551	SG05S635	KCP_90551		A/G
169947834	90724	SG05S636	KCP_90724		A/G
169948187	91077	SG05S637	KCP_91077		A/G
169948683	91573	SG05S1192	KCP_91573		A/G
169948703	91593	SG05S1193	KCP_91593		G/T
169948722	91612	SG05S1194	KCP_91612		A/G
169948755	91645	SG05S1195	KCP_91645		C/T
169948788	91678	SG05S1196	KCP_91678		A/G
169948798	91688	SG05S1197	KCP_91688		C/T
169948977	91867	SG05S638	KCP_91867		C/T
169949063	91953	SG05S639	KCP_91953		C/T
169949229	92119	SG05S640	KCP_92119		C/T
169949277	92167	SG05S641	KCP_92167		A/T
169949352	92242	SG05S642	KCP_92242		A/G
169949354	92244	SG05S643	KCP_92244	rs4867984	A/G
169949449	92339	SG05S644	KCP_92339		C/T
169950146	93036	SG05S63	KCP_93036		A/G
169950148	93038	SG05S645	KCP_93038		A/G
169950333	93223	SG05S646	KCP_93223	rs4867985	C/T
169950655	93545	SG05S64	KCP_93545		G/T
169950703	93593	SG05S1198	KCP_93593		C/G
169950754	93644	SG05S654	KCP_93644		G/T
169950844	93734	SG05S655	KCP_93734		C/T
169950855	93745	SG05S656	KCP_93745		G/T
169950892	93782	SG05S1199	KCP_93782		C/G
169950990	93880	SG05S657	KCP_93880		C/T
169951245	94135	SG05S1200	KCP_94135		A/C
169951290	94180	SG05S1201	KCP_94180		A/G
169951422	94312	SG05S658	KCP_94312		A/T
169951577	94467	SG05S659	KCP_94467		A/G
169951689	94579	SG05S660	KCP_94579		A/G
169951702	94592	SG05S661	KCP_94592		A/G
169951831	94721	SG05S662	KCP_94721		C/G
169951838	94728	SG05S663	KCP_94728		A/G
169951848	94738	SG05S664	KCP_94738		C/T

169951855	94745	SG05S665	KCP_94745		A/G
169952144	95034	SG05S1202	KCP_95034		A/G
169952209	95099	SG05S666	KCP_95099		A/C
169952705	95595	SG05S667	KCP_95595		A/G
169952838	95728	SG05S670	KCP_95728		A/G
169952962	95852	SG05S671	KCP_95852		A/G
169953175	96065	SG05S672	KCP_96065		C/G
169953185	96075	SG05S673	KCP_96075	rs43546	A/G
169953207	96097	SG05S674	KCP_96097	rs4374772	C/G
169953297	96187	SG05S675	KCP_96187		A/G
169953327	96217	SG05S676	KCP_96217		A/G
169953334	96224	SG05S677	KCP_96224		A/G
169953426	96316	SG05S678	KCP_96316		A/G
169953728	96618	SG05S1203	KCP_96618		C/G
169953902	96792	SG05S679	KCP_96792	rs4867987	C/T
169954134	97024	SG05S680	KCP_97024	rs4867988	C/T
169954165	97055	SG05S1204	KCP_97055	rs486798	C/T
169954260	97150	SG05S1205	KCP_97150		A/G
169954800	97690	SG05S681	KCP_97690		A/T
169954954	97844	DG00AAJIA	KCP_97844	rs222438	A/T
169955450	98340	SG05S682	KCP_98340		C/T
169956638	99528	SG05S683	KCP_99528		A/C
169956932	99822	SG05S684	KCP_99822		C/T
169957089	99979	SG05S685	KCP_99979		A/G
169957538	100428	SG05S1206	KCP_100428		G/T
169958211	101101	SG05S1207	KCP_101101	rs449521	A/G
169958651	101541	SG05S1208	KCP_101541		A/G
169958784	101674	SG05S686	KCP_101674		A/C
169959085	101975	SG05S687	KCP_101975		A/G
169959172	102062	SG05S1209	KCP_102062		A/T
169959537	102427	SG05S688	KCP_102427		A/G
169959561	102451	SG05S1210	KCP_102451		C/T
169959860	102750	SG05S1211	KCP_102750		C/T
169959992	102882	DG00AAJIB	KCP_102882		C/T
169961135	104025	SG05S689	KCP_104025	rs486799	A/G
169961268	104158	SG05S690	KCP_104158		G/T
169961404	104294	SG05S691	KCP_104294	rs4867991	A/G
169961971	104861	SG05S692	KCP_104861		A/G
169962144	105034	SG05S693	KCP_105034		A/G

169962410	105300	SG05S694	KCP_105300	rs4242159	A/T
169962429	105319	SG05S695	KCP_105319	rs4428429	C/G
169962889	105779	SG05S696	KCP_105779		A/G
169962929	105819	SG05S697	KCP_105819		C/T
169963467	106357	SG05S698	KCP_106357	rs236561	A/G
169963592	106482	SG05S699	KCP_106482		C/T
169963741	106631	SG05S700	KCP_106631		A/G
169963761	106651	SG05S701	KCP_106651		A/G
169963827	106717	SG05S702	KCP_106717		A/T
169964021	106911	SG05S703	KCP_106911	rs9587	C/G
169964087	106977	SG05S1212	KCP_106977	rs9588	C/T
169964112	107002	SG05S1213	KCP_107002	rs9589	C/T
169964368	107258	SG05S988	KCP_107258	rs95811	A/G
169964490	107380	DG00AAJIC	KCP_107380		A/G
169964862	107752	SG05S705	KCP_107752	rs95812	A/T
169964998	107888	SG05S706	KCP_107888		A/T
169965204	108094	SG05S707	KCP_108094		C/T
169965210	108100	SG05S708	KCP_108100		C/T
169965293	108183	SG05S709	KCP_108183		C/T
169965384	108274	SG05S710	KCP_108274		C/T
169965778	108668	SG05S1214	KCP_108668		C/T
169965813	108703	SG05S230	KCP_108703		G/T
169965814	108704	SG05S711	KCP_108704		A/G
169965989	108879	SG05S712	KCP_108879		A/T
169966345	109235	SG05S713	KCP_109235		C/G
169966790	109680	SG05S714	KCP_109680		A/C
169966813	109703	SG05S715	KCP_109703		A/G
169966833	109723	SG05S716	KCP_109723		A/G
169966856	109746	SG05S718	KCP_109746	rs95813	A/G
169967196	110086	SG05S719	KCP_110086		C/T
169967509	110399	SG05S720	KCP_110399		C/G
169968134	111024	SG05S721	KCP_111024		A/C
169968258	111148	SG05S722	KCP_111148		C/T
169968588	111478	SG05S723	KCP_111478	rs289191	C/G
169968602	111492	SG05S724	KCP_111492		A/G
169968614	111504	SG05S725	KCP_111504		C/G
169969010	111900	SG05S726	KCP_111900		A/G
169969185	112075	SG05S727	KCP_112075		A/G
169969769	112659	SG05S728	KCP_112659	rs4867994	C/T

169970341	113231	SG05S729	KCP_113231		A/G
169970367	113257	SG05S730	KCP_113257	rs4867616	A/G
169970440	113330	SG05S733	KCP_113330		A/G
169971048	113938	SG05S734	KCP_113938		A/G
169971464	114354	SG05S736	KCP_114354		A/G
169971531	114421	SG05S1215	KCP_114421		C/T
169971568	114458	SG05S737	KCP_114458	rs2879337	C/T
169971621	114511	SG05S738	KCP_114511		C/T
169972209	115099	SG05S740	KCP_115099	rs1553537	A/G
169972598	115488	SG05S741	KCP_115488		C/G
169973254	116144	SG05S742	KCP_116144	rs113922	C/T
169973325	116215	SG05S743	KCP_116215		A/G
169973369	116259	SG05S744	KCP_116259		A/G
169973465	116355	SG05S745	KCP_116355	rs289192	A/G
169974479	117369	SG05S746	KCP_117369	rs8719	A/T
169974926	117816	SG05S747	KCP_117816	rs1553538	C/T
169976065	118955	SG05S1216	KCP_118955		C/T
169977940	120830	SG05S748	KCP_120830	rs95819	C/T
169978197	121087	SG05S749	KCP_121087		C/T
169978247	121137	SG05S192	KCP_121137		A/G
169978339	121229	SG05S193	KCP_121229		C/T
169978427	121317	SG05S1217	KCP_121317		C/T
169980304	123194	SG05S751	KCP_123194		A/G
169980403	123293	SG05S752	KCP_123293		A/G
169980481	123371	SG05S1218	KCP_123371		A/G
169980664	123554	SG05S753	KCP_123554		C/T
169981035	123925	SG05S1219	KCP_123925		A/G
169981067	123957	SG05S754	KCP_123957		A/G
169981628	124518	SG05S755	KCP_124518		C/T
169981632	124522	SG05S756	KCP_124522		G/T
169981987	124877	SG05S194	KCP_124877	rs4146511	C/T
169982473	125363	SG05S757	KCP_125363	rs222436	A/T
169982868	125758	SG05S758	KCP_125758		C/T
169983196	126086	SG05S195	KCP_126086		A/G
169983318	126208	DG00AAJHA	KCP_126208		T/C
169983565	126455	SG05S1220	KCP_126455		C/G
169983591	126481	SG05S759	KCP_126481	rs2221441	C/G
169983692	126582	SG05S760	KCP_126582		A/G
169985824	128714	SG05S1221	KCP_128714		A/G

169985916	128806	SG05S151	KCP_128806		A/G
169985985	128875	SG05S761	KCP_128875		C/T
169986162	129052	SG05S763	KCP_129052	rs4867617	C/G
169986174	129064	SG05S762	KCP_129064		C/G
169986189	129079	SG05S764	KCP_129079	rs4867618	C/T
169986203	129093	SG05S152	KCP_129093	rs4867995	C/G
169986237	129127	SG05S480	KCP_129127	rs4867619	A/G
169986334	129224	SG05S765	KCP_129224	rs486762	G/T
169986478	129368	SG05S766	KCP_129368		C/G
169986579	129469	SG05S181	KCP_129469		A/G
169986800	129690	SG05S182	KCP_129690	rs4867996	G/T
169986957	129847	SG05S767	KCP_129847		A/G
169986984	129874	SG05S985	KCP_129874	rs4867997	A/C
169986999	129889	SG05S986	KCP_129889	rs4867999	A/G
169987419	130309	DG00AAJHB	KCP_130309		A/G
169987667	130557	SG05S196	KCP_130557	rs95822	C/G
169988155	131045	SG05S768	KCP_131045		A/G
169988354	131244	SG05S197	KCP_131244	rs95824	A/G
169988368	131258	SG05S769	KCP_131258	rs95825	C/T
169988581	131471	SG05S770	KCP_131471	rs95826	A/G
169988714	131604	SG05S1222	KCP_131604		A/G
169988812	131702	SG05S771	KCP_131702	rs95827	C/T
169988905	131795	SG05S65	KCP_131795	rs48681	C/T
169988964	131854	SG05S153	KCP_131854		G/T
169989037	131927	SG05S772	KCP_131927		A/G
169989257	132147	SG05S773	KCP_132147		C/T
169989533	132423	SG05S774	KCP_132423		A/G
169989704	132594	SG05S775	KCP_132594	rs48682	G/T
169989739	132629	SG05S776	KCP_132629		A/G
169989787	132677	SG05S154	KCP_132677		A/G
169990284	133174	SG05S777	KCP_133174		C/T
169990366	133256	SG05S1223	KCP_133256		A/G
169990548	133438	SG05S778	KCP_133438	rs4867621	A/G
169990840	133730	SG05S779	KCP_133730		C/T
169990962	133852	SG05S780	KCP_133852		A/G
169991155	134045	SG05S198	KCP_134045		C/T
169991415	134305	SG05S199	KCP_134305		C/T
169991521	134411	SG05S781	KCP_134411		C/T
169991729	134619	SG05S1224	KCP_134619		A/C

169991939	134829	SG05S782	KCP_134829		C/T
169992076	134966	SG05S783	KCP_134966		A/G
169992155	135045	SG05S784	KCP_135045		A/G
169992628	135518	SG05S200	KCP_135518	rs48683	G/T
169992821	135711	SG05S785	KCP_135711		G/T
169993032	135922	SG05S786	KCP_135922		A/G
169993096	135986	SG05S183	KCP_135986		A/G
169993146	136036	SG05S481	KCP_136036		A/C
169993585	136475	SG05S787	KCP_136475		C/T
169994082	136972	SG05S201	KCP_136972	rs48684	A/G
169994770	137660	SG05S202	KCP_137660		A/G
169995924	138814	SG05S788	KCP_138814		C/T
169997343	140233	SG05S789	KCP_140233		C/T
169997640	140530	SG05S1225	KCP_140530		A/G
169998201	141091	SG05S1226	KCP_141091		A/G
170000256	143146	SG05S1227	KCP_143146	rs95361	C/T
170000611	143501	SG05S1228	KCP_143501		C/T
170000722	143612	SG05S66	KCP_143612	rs4867622	A/G
170000869	143759	SG05S790	KCP_143759		C/T
170000983	143873	SG05S1229	KCP_143873		C/T
170001571	144461	SG05S1230	KCP_144461		C/T
170001578	144468	SG05S1299	KCP_144468	rs93185	C/T
170002070	144960	SG05S203	KCP_144960	rs2279873	C/T
170002435	145325	SG05S791	KCP_145325		C/T
170002801	145691	SG05S1231	KCP_145691		A/G
170003438	146328	SG05S792	KCP_146328		A/G
170003572	146462	SG05S793	KCP_146462		G/T
170003856	146746	SG05S482	KCP_146746		C/T
170003940	146830	SG05S1232	KCP_146830		C/T
170004075	146965	SG05S794	KCP_146965		C/T
170004199	147089	SG05S1233	KCP_147089		C/G
170004733	147623	SG05S204	KCP_147623	rs2292146	C/T
170005151	148041	SG05S795	KCP_148041		C/T
170006326	149216	SG05S205	KCP_149216		A/G
170006485	149375	SG05S796	KCP_149375	rs883848	G/T
170006645	149535	SG05S206	KCP_149535	rs883849	A/G
170006910	149800	SG05S1234	KCP_149800		A/G
170007023	149913	SG05S797	KCP_149913	rs4867623	C/T
170007516	150406	SG05S798	KCP_150406	rs48685	G/T

170007640	150530	SG05S987	KCP_150530		C/T
170007808	150698	SG05S799	KCP_150698		G/T
170007921	150811	SG05S155	KCP_150811		A/G
170008215	151105	SG05S800	KCP_151105		G/T
170008937	151827	SG05S801	KCP_151827	rs449672	A/G
170009218	152108	SG05S1235	KCP_152108		A/G
170009587	152477	SG05S802	KCP_152477		C/T
170009592	152482	SG05S803	KCP_152482		A/C
170010385	153275	SG05S1236	KCP_153275		C/T
170010518	153408	SG05S1237	KCP_153408		C/T
170010943	153833	SG05S804	KCP_153833		C/T
170011041	153931	DG00AAJHC	KCP_153931	rs2879338	A/G
170011269	154159	SG05S805	KCP_154159		A/G
170011475	154365	SG05S1238	KCP_154365		A/G
170011963	154853	SG05S806	KCP_154853		C/T
170012367	155257	SG05S807	KCP_155257		C/G
170013726	156616	SG05S808	KCP_156616		C/T
170013842	156732	SG05S207	KCP_156732	rs924876	A/T
170015154	158044	SG05S809	KCP_158044		A/G
170015582	158472	SG05S810	KCP_158472		C/T
170015603	158493	SG05S811	KCP_158493		A/G
170015680	158570	SG05S812	KCP_158570		C/T
170015727	158617	SG05S67	KCP_158617	rs236559	C/T
170016200	159090	SG05S813	KCP_159090		A/G
170016255	159145	SG05S814	KCP_159145		A/G
170016259	159149	SG05S815	KCP_159149		C/T
170016791	159681	SG05S1239	KCP_159681		A/G
170016798	159688	SG05S1240	KCP_159688		A/G
170017255	160145	SG05S208	KCP_160145		A/G
170017524	160414	SG05S816	KCP_160414		G/T
170018297	161187	SG05S817	KCP_161187		A/G
170018356	161246	SG05S818	KCP_161246		C/G
170018549	161439	SG05S819	KCP_161439		A/G
170018573	161463	SG05S820	KCP_161463		C/T
170019258	162148	SG05S821	KCP_162148		C/T
170019314	162204	SG05S1241	KCP_162204		A/C
170019379	162269	SG05S822	KCP_162269		A/T
170019414	162304	SG05S823	KCP_162304		C/G
170019958	162848	SG05S824	KCP_162848		C/G



170020197	163087	SG05S825	KCP_163087		C/G
170020606	163496	SG05S826	KCP_163496		A/G
170020870	163760	SG05S827	KCP_163760		A/G
170021444	164334	SG05S1242	KCP_164334		A/G
170022007	164897	SG05S209	KCP_164897		A/G
170022125	165015	SG05S828	KCP_165015		G/T
170022343	165233	SG05S1243	KCP_165233		C/T
170022545	165435	SG05S1244	KCP_165435		C/T
170023275	166165	SG05S829	KCP_166165		A/G
170024034	166924	SG05S1245	KCP_166924	rs4867624	C/T
170024668	167558	SG05S830	KCP_167558		A/G
170025753	168643	SG05S1246	KCP_168643		A/G
170025970	168860	SG05S1247	KCP_168860	rs222439	C/G
170026021	168911	SG05S1248	KCP_168911		A/G
170026162	169052	SG05S1249	KCP_169052		A/G
170026344	169234	SG05S156	KCP_169234		A/G
170028032	170922	SG05S1297	KCP_170922	rs48688	A/C
170028055	170945	SG05S831	KCP_170945		C/G
170028163	171053	SG05S1250	KCP_171053	rs48689	A/G
170028303	171193	SG05S1300	KCP_171193	rs48681	G/T
170028752	171642	SG05S1251	KCP_171642		G/T
170028987	171877	SG05S832	KCP_171877		A/G
170030482	173372	SG05S833	KCP_173372		A/G
170030815	173705	SG05S834	KCP_173705		C/T
170030958	173848	SG05S210	KCP_173848		A/G
170030986	173876	SG05S1252	KCP_173876		C/T
170031092	173982	SG05S157	KCP_173982		A/C
170031149	174039	SG05S835	KCP_174039		C/T
170031150	174040	SG05S836	KCP_174040		A/G
170031353	174243	DG00AAJHF	KCP_174243		A/G
170031709	174599	SG05S837	KCP_174599		C/T
170031812	174702	SG05S838	KCP_174702		C/T
170031962	174852	SG05S839	KCP_174852		A/G
170031972	174862	SG05S840	KCP_174862	rs46285	G/T
170032216	175106	SG05S158	KCP_175106	rs233995	C/G
170032280	175170	SG05S211	KCP_175170		A/G
170032361	175251	SG05S841	KCP_175251		C/T
170032362	175252	DG00AAJHG	KCP_175252		A/G
170032610	175500	SG05S842	KCP_175500		A/G

170032814	175704	SG05S843	KCP_175704		A/G
170033021	175911	SG05S844	KCP_175911		A/G
170033923	176813	SG05S845	KCP_176813		A/G
170033946	176836	DG00AAJHH	KCP_176836		A/G
170034620	177510	SG05S184	KCP_177510	rs486811	A/C
170034720	177610	SG05S1253	KCP_177610		G/T
170034980	177870	SG05S846	KCP_177870		G/T
170035009	177899	SG05S847	KCP_177899	rs486812	C/T
170036929	179819	SG05S848	KCP_179819		C/T
170037010	179900	SG05S1254	KCP_179900		G/T
170037283	180173	SG05S159	KCP_180173	rs213546	C/T
170037347	180237	SG05S212	KCP_180237	rs213547	C/G
170038967	181857	SG05S1255	KCP_181857		C/T
170039237	182127	SG05S1256	KCP_182127		C/T
170039419	182309	SG05S849	KCP_182309		A/T
170041190	184080	SG05S160	KCP_184080	rs2292147	C/G
170041385	184275	SG05S964	KCP_184275		A/G
170042689	185579	DG00AAJDX	KCP_185579		C/A
170043158	186048	SG05S213	KCP_186048		A/G
170043789	186679	SG05S161	KCP_186679		C/G
170043953	186843	SG05S850	KCP_186843		A/C
170043997	186887	SG05S965	KCP_186887		C/T
170044226	187116	DG00AAJDY	KCP_187116		A/G
170044277	187167	SG05S851	KCP_187167		C/G
170044368	187258	SG05S852	KCP_187258		G/T
170044661	187551	SG05S853	KCP_187551		A/G
170044798	187688	DG00AAJDZ	KCP_187688		T/A
170044904	187794	SG05S966	KCP_187794		C/T
170045075	187965	SG05S967	KCP_187965		C/T
170046043	188933	SG05S968	KCP_188933		C/T
170046441	189331	SG05S214	KCP_189331		A/G
170047120	190010	SG05S854	KCP_190010	rs2221442	A/G
170047129	190019	SG05S855	KCP_190019		C/G
170048070	190960	SG05S856	KCP_190960		C/G
170048074	190964	SG05S857	KCP_190964		C/T
170048090	190980	SG05S858	KCP_190980		C/G
170048315	191205	SG05S859	KCP_191205	rs486815	C/T
170048733	191623	SG05S860	KCP_191623		A/G
170049238	192128	SG05S990	KCP_192128		C/T

170049852	192742	DG00AAJEB	KCP_192742	rs1973529	T/C
170050303	193193	DG00AAJEC	KCP_193193		G/A
170051066	193956	SG05S163	KCP_193956	rs22244	C/T
170051438	194328	SG05S861	KCP_194328		A/T
170051462	194352	SG05S862	KCP_194352		A/G
170051726	194616	DG00AAJEE	KCP_194616	rs23656	T/C
170051899	194789	SG05S970	KCP_194789		C/T
170052012	194902	SG05S863	KCP_194902		A/G
170052171	195061	SG05S971	KCP_195061		G/T
170052988	195878	SG05S864	KCP_195878		C/T
170053658	196548	DG00AAJEF	KCP_196548		A/G
170053669	196559	SG05S865	KCP_196559		A/G
170053840	196730	SG05S866	KCP_196730		G/T
170053939	196829	SG05S867	KCP_196829		C/G
170054581	197471	SG05S972	KCP_197471		A/G
170054620	197510	SG05S973	KCP_197510		C/T
170054788	197678	DG00AAJEG	KCP_197678	rs96284	T/C
170054803	197693	SG05S884	KCP_197693		A/G
170054885	197775	DG00AAJEH	KCP_197775		C/T
170055781	198671	DG00AAJEI	KCP_198671		A/G
170055957	198847	SG05S974	KCP_198847		A/G
170056043	198933	DG00AAJEJ	KCP_198933		G/A
170056137	199027	SG05S975	KCP_199027		A/G
170056475	199365	DG00AAJEK	KCP_199365		A/G
170056516	199406	SG05S164	KCP_199406		A/T
170056578	199468	SG05S1257	KCP_199468		C/T
170057283	200173	SG05S165	KCP_200173		C/G
170057351	200241	DG00AAJEL	KCP_200241		A/G
170057605	200495	SG05S976	KCP_200495		A/G
170057933	200823	SG05S991	KCP_200823		A/C
170058193	201083	SG05S992	KCP_201083	rs4464713	C/T
170058699	201589	SG05S885	KCP_201589		C/T
170059095	201985	DG00AAJEM	KCP_201985		G/A
170059177	202067	DG00AAJEN	KCP_202067	rs222144	A/G
170059203	202093	SG05S977	KCP_202093		A/C
170059905	202795	DG00AAJEO	KCP_202795	rs875184	C/T
170060219	203109	SG05S1258	KCP_203109		A/G
170060292	203182	SG05S978	KCP_203182		A/G
170060393	203283	SG05S979	KCP_203283	rs95818	A/G

170061018	203908	SG05S980	KCP_203908	rs95817	C/T
170061292	204182	SG05S981	KCP_204182	rs872435	G/T
170061352	204242	SG05S166	KCP_204242		C/T
170061419	204309	SG05S982	KCP_204309		A/G
170061618	204508	SG05S983	KCP_204508	rs872436	A/G
170061670	204560	SG05S1259	KCP_204560		A/G
170061727	204617	SG05S984	KCP_204617		C/T
170061799	204689	SG05S1260	KCP_204689	rs95816	G/T
170061809	204699	SG05S1261	KCP_204699		A/T
170061845	204735	SG05S1262	KCP_204735	rs95815	C/T
170062696	205586	SG05S886	KCP_205586	rs329466	C/T
170062747	205637	SG05S887	KCP_205637		A/C
170062756	205646	SG05S888	KCP_205646	rs329467	C/T
170062777	205667	SG05S889	KCP_205667		A/G
170062940	205830	SG05S167	KCP_205830		C/T
170062950	205840	SG05S890	KCP_205840		A/G
170063305	206195	SG05S891	KCP_206195		C/G
170063313	206203	SG05S892	KCP_206203		C/T
170063377	206267	SG05S168	KCP_206267		A/G
170063732	206622	SG05S893	KCP_206622		A/G
170063817	206707	SG05S894	KCP_206707		C/T
170063983	206873	SG05S1263	KCP_206873		A/T
170064013	206903	SG05S1264	KCP_206903		C/G
170064648	207538	SG05S895	KCP_207538		C/T
170064760	207650	SG05S969	KCP_207650		A/G
170064771	207661	SG05S169	KCP_207661		C/G
170064881	207771	SG05S896	KCP_207771	rs329468	A/G
170065075	207965	SG05S170	KCP_207965		C/T
170065694	208584	SG05S171	KCP_208584		A/G
170065711	208601	SG05S232	KCP_208601	rs329469	A/C
170065715	208605	SG05S897	KCP_208605		A/G
170065740	208630	SG05S172	KCP_208630		C/T
170065834	208724	SG05S1265	KCP_208724		C/T
170066123	209013	SG05S1266	KCP_209013		C/T
170066260	209150	SG05S1267	KCP_209150		A/G
170067967	210857	SG05S898	KCP_210857	rs2194162	A/G
170068018	210908	SG05S899	KCP_210908		C/G
170068420	211310	SG05S900	KCP_211310		A/G
170068510	211400	SG05S901	KCP_211400	rs41348	A/G

170068614	211504	SG05S902	KCP_211504		A/G
170068635	211525	SG05S173	KCP_211525		A/G
170068731	211621	SG05S903	KCP_211621		A/G
170068759	211649	SG05S1268	KCP_211649		G/T
170068960	211850	SG05S185	KCP_211850	rs32947	C/T
170069885	212775	SG05S186	KCP_212775	rs434973	A/G
170070003	212893	SG05S1269	KCP_212893		G/T
170070041	212931	SG05S1270	KCP_212931	rs557	A/G
170070593	213483	SG05S904	KCP_213483		A/G
170070700	213590	SG05S1271	KCP_213590	rs12684	C/T
170070735	213625	SG05S905	KCP_213625	rs12685	C/T
170070768	213658	SG05S1272	KCP_213658	rs12686	A/G
170071584	214474	SG05S1273	KCP_214474	rs329471	C/G
170071665	214555	SG05S1274	KCP_214555	rs433936	C/T
170071715	214605	SG05S1275	KCP_214605	rs432615	C/G
170072023	214913	SG05S1276	KCP_214913		A/G
170072363	215253	SG05S906	KCP_215253	rs441562	C/T
170072373	215263	SG05S907	KCP_215263	rs172944	C/T
170072484	215374	SG05S908	KCP_215374		A/G
170072485	215375	SG05S909	KCP_215375		A/G
170072562	215452	SG05S910	KCP_215452	rs191297	A/G
170072712	215602	SG05S1277	KCP_215602	rs186646	A/C
170072813	215703	SG05S174	KCP_215703		A/C
170073179	216069	SG05S1278	KCP_216069		C/T
170073555	216445	SG05S1279	KCP_216445	rs136379	A/G
170073565	216455	SG05S1280	KCP_216455	rs329474	C/G
170074202	217092	SG05S993	KCP_217092	rs984559	A/G
170074303	217193	SG05S994	KCP_217193		C/T
170074359	217249	SG05S995	KCP_217249	rs329475	A/G
170075932	218822	SG05S996	KCP_218822		A/G
170076291	219181	SG05S997	KCP_219181		A/G
170076439	219329	SG05S998	KCP_219329	rs81987	C/G
170077257	220147	SG05S911	KCP_220147		A/T
170078779	221669	SG05S912	KCP_221669		C/G
170078881	221771	SG05S1281	KCP_221771		C/T
170078909	221799	DG00AAJHJ	KCP_221799		A/T
170078966	221856	SG05S913	KCP_221856		C/T
170079102	221992	SG05S1282	KCP_221992		C/T
170079170	222060	SG05S175	KCP_222060		C/T

170079176	222066	SG05S1283	KCP_222066		A/T
170079986	222876	SG05S1284	KCP_222876		A/G
170080026	222916	SG05S914	KCP_222916		C/T
170080378	223268	SG05S915	KCP_223268	rs486817	C/T
170080480	223370	SG05S916	KCP_223370		C/T
170080678	223568	SG05S917	KCP_223568		G/T
170080917	223807	SG05S918	KCP_223807		C/G
170081127	224017	SG05S919	KCP_224017		A/G
170081263	224153	SG05S1285	KCP_224153		G/T
170081464	224354	SG05S920	KCP_224354		C/G
170081779	224669	SG05S231	KCP_224669		A/C
170082330	225220	SG05S177	KCP_225220		A/G
170082361	225251	SG05S1286	KCP_225251		A/T
170082496	225386	SG05S922	KCP_225386		C/T
170083131	226021	SG05S1287	KCP_226021		A/C
170083226	226116	SG05S1288	KCP_226116		C/G
170083558	226448	SG05S924	KCP_226448		A/G
170083941	226831	SG05S925	KCP_226831		A/G
170084576	227466	SG05S926	KCP_227466		C/T
170084823	227713	SG05S927	KCP_227713		A/G
170084981	227871	SG05S178	KCP_227871		C/G
170085097	227987	SG05S483	KCP_227987		C/T
170085116	228006	SG05S187	KCP_228006		C/T
170085151	228041	SG05S928	KCP_228041		A/T
170085191	228081	SG05S929	KCP_228081		C/T
170085217	228107	SG05S179	KCP_228107		A/T
170085834	228724	SG05S1289	KCP_228724		A/G
170086059	228949	SG05S999	KCP_228949		C/T
170086143	229033	SG05S1000	KCP_229033		C/T
170086250	229140	SG05S1001	KCP_229140		C/T
170086709	229599	SG05S930	KCP_229599		A/C
170086826	229716	SG05S931	KCP_229716		C/T
170087721	230611	SG05S932	KCP_230611		C/G
170087734	230624	SG05S933	KCP_230624		A/G
170087780	230670	SG05S934	KCP_230670		G/T
170087950	230840	SG05S1290	KCP_230840		A/G
170088932	231822	SG05S1291	KCP_231822	rs1422978	C/T
170089182	232072	SG05S1292	KCP_232072	rs219416	C/T
170089631	232521	SG05S1293	KCP_232521	rs1592987	A/T

170090569	233459	SG05S935	KCP_233459		A/G
170090765	233655	SG05S989	KCP_233655	rs232863	A/G
170091557	234447	SG05S936	KCP_234447		A/G
170091681	234571	SG05S937	KCP_234571		C/T
170091700	234590	SG05S938	KCP_234590		A/T
170092075	234965	SG05S939	KCP_234965		C/T
170092275	235165	SG05S940	KCP_235165	rs136371	G/T
170092318	235208	SG05S941	KCP_235208	rs1363711	A/G
170092468	235358	SG05S942	KCP_235358		A/G
170093047	235937	SG05S1294	KCP_235937		A/C
170093362	236252	SG05S943	KCP_236252		A/T
170094119	237009	SG05S1295	KCP_237009		A/G
170094581	237471	SG05S944	KCP_237471	rs1422979	A/G
170094615	237505	SG05S188	KCP_237505	rs4867628	C/T
170094780	237670	SG05S1296	KCP_237670		G/T
170095344	238234	SG05S945	KCP_238234		C/T
170095662	238552	SG05S947	KCP_238552		C/T
170095701	238591	SG05S180	KCP_238591		C/T
170096774	239664	SG05S949	KCP_239664		C/G
170097477	240367	SG05S950	KCP_240367		C/G
170098637	241527	SG05S190	KCP_241527	rs1363713	G/T
170098914	241804	SG05S191	KCP_241804		C/T
170099451	242341	SG05S951	KCP_242341	rs1363714	A/G
170099467	242357	SG05S952	KCP_242357		G/T

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Table 13. The Build 33 location of SNPs and microsatellites employed for the subsequent association analysis across KChIP1.

Start (B33)	Marker	Public alias	deCODE alias	Variation
169477886	rs1895301	rs1895301	DG00AAGUZ	C/T
169500972	rs1422752	rs1422752	DG00AAESV	C/T
169518355	rs1422754	rs1422754	DG00AAESU	A/G
169653708	DG5S1173			
169661202	DG5S44			
169673518	SG05S872		SG05S872	A/G
169678484	SG05S873		SG05S873	A/G
169693772	DG5S45			
169696877	KCP_rs315773	rs315773	SG05S76, SG05S874	A/G
169702377	DG5S46			
169705505	SG05S876		SG05S876	A/G
169709735	KCP_rs952767	rs952767	SG05S79	G/T
169740666	KNB_24222		DG00AAIGE	A/G
169740703	KNB_24259		DG00AAIGF	A/G
169741172	KNB_24728		DG00AAIGG	G/T
169745438	DG5S1178			
169746339	KNB_29895		DG00AAIGH	C/T
169747941	KNB_31497		DG00AAIGI	A/G
169751683	KNB_35298		DG00AAIGZ	A/T
169751753	KNB_35370		DG00AAIHA	C/G
169751753	KNB_35399		DG00AAIHB	A/G
169753659	KCP_rs314129	rs314129	SG05S83	C/T
169782203	KCP_rs183398	rs183398	SG05S87, SG05S879	C/T
169788696	DG5S47			
169794522	DG5S1592			
169815996	rs1032856	rs1032856	SG05S96	C/G
169833941	rs2055606	rs2055606	DG00AAESP	C/T
169843903	DG5S119			
169859274	KCP_rs888934	rs888934	SG05S93	A/G
169867464	KCP_10355		SG05S229	A/T
169867555	KCP_10446		DG00AAHAR	C/G
169869845	rs933656	rs933656	DG00AAFCS	A/G
169869955	rs2339091	rs2339091	DG00AAFCI	G/T
169890856	rs1862331	rs1862331	DG00AAFCL	C/T



169895698	KCP_38589		SG05S953	A/C
169922308	KCP_65199		SG05S955	A/G
169939577	KCP_82468	rs4242158	SG05S957	A/G
169942902	KCP_85793		SG05S958	C/T
169950654	KCP_93545		SG05S64	G/T
169951970	DG5S955			
169954953	KCP_97844	rs222438	DG00AAJIA	A/T
169959991	KCP_102882		DG00AAJIB	C/T
169961410	DG5S13			
169964489	KCP_107380		DG00AAJIC	A/G
169965813	KCP_108703		SG05S230	G/T
169981986	KCP_124877	rs4146511	SG05S194	C/T
169983195	KCP_126086		SG05S195	A/G
169983317	KCP_126208		DG00AAJHA	T/C
169986202	KCP_129093	rs4867995	SG05S152	C/G
169986236	KCP_129127	rs4867619	SG05S480	A/G
169986799	KCP_129690	rs4867996	SG05S182	G/T
169987418	KCP_130309		DG00AAJHB	A/G
169987666	KCP_130557	rs95822	SG05S196	C/G
169987873	rs905823	rs905823	DG00AAFCK, DG00AAIIMM	A/C
169988353	KCP_131244	rs95824	SG05S197	A/G
169988963	KCP_131854		SG05S153	G/T
169989786	KCP_132677		SG05S154	A/G
169991154	KCP_134045		SG05S198	C/T
169992627	KCP_135518	rs48683	SG05S200	G/T
169993145	KCP_136036		SG05S481	A/C
169994769	KCP_137660		SG05S202	A/G
170000721	KCP_143612	rs4867622	SG05S66	A/G
170002069	KCP_144960	rs2279873	SG05S203	C/T
170003855	KCP_146746		SG05S482	C/T
170006325	KCP_149216		SG05S205	A/G
170006644	KCP_149535	rs883849	SG05S206	A/G
170006645	rs883849	rs883849	DG00AAFCK, DG00AAIOG	A/G
170013841	KCP_156732	rs924876	SG05S207	A/T
170015726	KCP_158617	rs236559	SG05S67	C/T
170015858	DG5S123			
170017254	KCP_160145		SG05S208	A/G
170022006	KCP_164897		SG05S209	A/G
170026343	KCP_169234		SG05S156	A/G

170030957	KCP_173848		SG05S210	A/G
170031091	KCP_173982		SG05S157	A/C
170031352	KCP_174243		DG00AAJHF	A/G
170032215	KCP_175106	rs233995	SG05S158	C/G
170032279	KCP_175170		SG05S211	A/G
170032361	KCP_175252		DG00AAJHG	A/G
170033945	KCP_176836		DG00AAJHH	A/G
170037282	KCP_180173	rs213546	SG05S159	C/T
170037283	rs2135046	rs2135046	DG00AAFCJ, DG00AAIOH	C/T
170037346	KCP_180237	rs213547	SG05S212	C/G
170041189	KCP_184080	rs2292147	SG05S160	C/G
170041996	DG5S124			
170042688	KCP_185579		DG00AAJDX	C/A
170043157	KCP_186048		SG05S213	A/G
170043788	KCP_186679		SG05S161	C/G
170044225	KCP_187116		DG00AAJDY	A/G
170044367	KCP_187258		SG05S852	G/T
170044797	KCP_187688		DG00AAJDZ	T/A
170046440	KCP_189331		SG05S214	A/G
170049851	KCP_192742	rs1973529	DG00AAJEB	T/C
170050302	KCP_193193		DG00AAJEC	G/A
170051065	KCP_193956	rs22244	SG05S163	C/T
170051725	KCP_194616	rs23656	DG00AAJEE	T/C
170053657	KCP_196548		DG00AAJEF	A/G
170054787	KCP_197678	rs96284	DG00AAJEG	T/C
170054884	KCP_197775		DG00AAJEH	C/T
170056042	KCP_198933		DG00AAJEJ	G/A
170056474	KCP_199365		DG00AAJEK	A/G
170056955	rs2339139	rs2339139	DG00AAFCR	A/G
170057350	KCP_200241		DG00AAJEL	A/G
170059094	KCP_201985		DG00AAJEM	G/A
170059176	KCP_202067	rs222144	DG00AAJEN	A/G
170059904	KCP_202795	rs875184	DG00AAJEO	C/T
170061292	rs872435	rs872435	DG00AAFCP	G/T
170061351	KCP_204242		SG05S166	C/T
170063376	KCP_206267		SG05S168	A/G
170064770	KCP_207661		SG05S169	C/G
170064881	rs329468	rs329468	DG00AAFCH	A/G
170065074	KCP_207965		SG05S170	C/T

170068634	KCP 211525		SG05S173	A/G
170068959	KCP 211850	rs32947	SG05S185	C/T
170069884	KCP 212775	rs434973	SG05S186	A/G
170070041	rs50057	rs50057	DG00AAFCF, DG00AAIOI	A/G
170073252	rs50364	rs50364	DG00AAFCF	A/G
170078908	KCP 221799		DG00AAJHJ	A/T
170080677	KCP 223568		SG05S917	G/T
170081291	KCP 1152		SG05S176	C/T
170081473	KCP 1333		SG05S921	A/G
170082329	KCP 225220		SG05S177	A/G
170082788	KCP 2649		SG05S923	C/T
170084980	KCP 227871		SG05S178	C/G
170085096	KCP 227987		SG05S483	C/T
170085115	KCP 4976		DG00AAGHK, DG00AAHUT, DG00AAINX	C/T
170085216	KCP 228107		SG05S179	A/T
170085217	KCP 5077		DG00AAINZ	A/T
170089630	KCP 232521	rs1592987	SG05S1293	A/T
170090764	KCP 233655	rs232863	SG05S989	A/G
170094614	KCP 237505	rs4867628	SG05S188	C/T
170095540	KCP 15400		SG05S946	C/T
170095700	KCP 238591		SG05S180	C/T
170096291	KCP 16152	rs486818	SG05S948	A/G
170098208	KCP 241099		SG05S189	C/T
170098209	KCP 18069	rs1363712	SG05S189	C/T
170098636	KCP 241527	rs1363713	SG05S190	G/T
170098913	KCP 241804		SG05S191	C/T
170105556	D5S625			
170167429	DG5S959			
170361737	rs1551583	rs1551583	DG00AADMS	C/G
170389497	rs1457692	rs1457692	DG00AADMR	A/G

The teachings of all publications cited herein are incorporated herein by reference in their entirety. While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein  
5 without departing from the scope of the invention encompassed by the appended claims.

## CLAIMS

What is claimed is:

5

1. A method of diagnosing a susceptibility to Type II diabetes in an individual, comprising detecting a polymorphism in a KChIP1 nucleic acid, wherein the presence of the polymorphism in the nucleic acid is indicative of a susceptibility to Type II diabetes.

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2. A method of diagnosing a susceptibility to Type II diabetes comprising detecting an alteration in the expression or composition of a polypeptide encoded by KChIP1 nucleic acid in a test sample, in comparison with the expression or composition of a polypeptide encoded by a KChIP1 nucleic acid in a control sample, wherein the presence of an alteration in expression or composition of the polypeptide in the test sample is indicative of a susceptibility to Type II diabetes.

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3. The method of Claim 1, wherein the polymorphism in the KChIP1 nucleic acid is indicated by detecting the presence of a least one of the polymorphisms indicated in Table 13.

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4. An isolated nucleic acid molecule comprising a KChIP1 nucleic acid, wherein the KChIP1 nucleic acid has a nucleotide sequence selected from the group of nucleic acid sequences as shown in Table 10, or the complements of the group of nucleic acid sequences as shown in Table 10, wherein the nucleotide sequence contains a polymorphism.

25

5. An isolated nucleic acid molecule which hybridizes under high stringency conditions to a nucleotide sequence selected from the group of nucleic acid sequences as shown in Table 10, or the complements of the group of nucleic

30

acid sequences as shown in Table 10, wherein the nucleotide sequence contains a polymorphism.

6. A method for assaying for the presence of a first nucleic acid molecule in a sample, comprising contacting said sample with a second nucleic acid molecule, where the second nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of: nucleic acid sequences as shown in Table 10 and the complement of the nucleic acid sequences as shown in Table 10, wherein the nucleotide sequence contains a polymorphism and hybridizes to the first nucleic acid under high stringency conditions.
7. A vector comprising an isolated nucleic acid molecule selected from the group consisting of:
  - a) nucleic acid sequences as shown in Table 10; and
  - b) complement of one of the nucleic acid sequences are shown in Table 10; andwherein the nucleic acid molecule contains a polymorphism and is operably linked to a regulatory sequence.
8. A recombinant host cell comprising the vector of Claim 7.
9. A method for producing a polypeptide encoded by an isolated nucleic acid molecule having a polymorphism, comprising culturing the recombinant host cell of Claim 10 under conditions suitable for expression of the nucleic acid molecule.
10. A method of assaying for the presence of a polypeptide encoded by an isolated nucleic acid molecule according to Claim 4 in a sample, the method comprising contacting the sample with an antibody which specifically binds to the encoded polypeptide.

11. A method of identifying an agent that alters expression of a KCHIP1 nucleic acid, comprising:

- 5
- a) contacting a solution containing a nucleic acid comprising the promoter region of the KCHIP1 nucleic acid operably linked to a reporter gene with an agent to be tested;
  - b) assessing the level of expression of the reporter gene; and
  - c) comparing the level of expression with a level of expression of the reporter gene in the absence of the agent; wherein if the level of expression of the reporter gene in the presence of the agent differs, by an amount that is statistically significant, from the level of expression in the absence of the agent, then the agent is an agent that alters expression of the KCHIP1 nucleic acid.
- 10

12. An agent that alters expression of the KCHIP1 nucleic acid, identifiable according to the method of Claim 11.

13. A method of identifying an agent that alters expression of a KCHIP1 nucleic acid, comprising:

- 20
- a) contacting a solution containing a nucleic acid of Claim 1 or a derivative or fragment thereof with an agent to be tested;
  - b) comparing expression with expression of the nucleic acid, derivative or fragment in the absence of the agent;
- 25
- wherein if expression of the nucleotide, derivative or fragment in the presence of the agent differs, by an amount that is statistically significant, from the expression in the absence of the agent, then the agent is an agent that alters expression of the KCHIP1 nucleic acid.
- 30

14. The method of Claim 13, wherein the expression of the nucleotide, derivative or fragment in the presence of the agent comprises expression of one or more splicing variant(s) that differ in kind or in quantity from the expression of one or more splicing variant(s) the absence of the agent.
- 5 15. An agent that alters expression of a KChIP1 nucleic acid; identifiable according to the method of Claim 14.
- 10 16. An agent that alters expression of a KChIP1 nucleic acid, selected from the group consisting of: antisense nucleic acid to a KChIP1 nucleic acid; a KChIP1 polypeptide; a KChIP1 nucleic acid receptor; a KChIP1 binding agent; a peptidomimetic; a fusion protein; a prodrug thereof; an antibody, and a ribozyme.
- 15 17. A method of altering expression of a KChIP1 nucleic acid, comprising contacting a cell containing a KChIP1 nucleic acid with an agent of Claim 16.
- 20 18. A method of identifying a polypeptide which interacts with a KChIP1 polypeptide comprising a polymorphism indicated in Table 13, comprising employing a yeast two-hybrid system using a first vector which comprises a nucleic acid encoding a DNA binding domain and a KChIP1 polypeptide, splicing variant, or a fragment or derivative thereof, and a second vector which comprises a nucleic acid encoding a transcription activation domain and a nucleic acid encoding a test polypeptide, wherein if transcriptional activation occurs in the yeast two-hybrid system, the test polypeptide is a polypeptide which interacts with a KChIP1 polypeptide.
- 25 19. A Type II diabetes therapeutic agent selected from the group consisting of: a KChIP1 nucleic acid or fragment or derivative thereof; a polypeptide encoded by a KChIP1 nucleic acid; a KChIP1 receptor; a KChIP1 nucleic acid binding agent; a peptidomimetic; a fusion protein; a prodrug; an antibody; an agent
- 30



- that alters KChIP1 nucleic acid expression; an agent that alters activity of a polypeptide encoded by a KChIP1 nucleic acid; an agent that alters posttranscriptional processing of a polypeptide encoded by a KChIP1 nucleic acid; an agent that alters interaction of a KChIP1 nucleic acid with a KChIP1 binding agent; an agent that alters transcription of splicing variants encoded by a KChIP1 nucleic acid; and a ribozyme.
20. A pharmaceutical composition comprising a Type II diabetes therapeutic agent of Claim 19.
21. The pharmaceutical composition of Claim 20, wherein the Type II diabetes therapeutic agent is an isolated nucleic acid molecule comprising a KChIP1 nucleic acid or fragment or derivative thereof.
22. The pharmaceutical composition of Claim 20, wherein the Type II diabetes therapeutic agent is a polypeptide encoded by the KChIP1 nucleic acid.
23. A method of treating a disease or condition associated with KChIP1 in an individual, comprising administering a Type II diabetes therapeutic agent to the individual, in a therapeutically effective amount.
24. The method of Claim 23, wherein the Type II diabetes therapeutic agent is a KChIP1 nucleic acid agonist.
25. The method of Claim 23 wherein the Type II diabetes therapeutic agent is a KChIP1 nucleic acid antagonist.
26. A transgenic animal comprising a nucleic acid selected from the group consisting of: an exogenous KChIP1 nucleic acid and a nucleic acid encoding a KChIP1 polypeptide.

27. A method for assaying a sample for the presence of a KChIP1 nucleic acid, comprising:

- a) contacting said sample with a nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said KChIP1 gene under conditions appropriate for hybridization, and
- b) assessing whether hybridization has occurred between a KChIP1 gene nucleic acid and said nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said KChIP1 nucleic acid;

wherein if hybridization has occurred, a KChIP1 nucleic acid is present in the nucleic acid.

28. The method of Claim 27, wherein said nucleic acid comprising a contiguous nucleotide sequence is completely complementary to a part of the sequence of said KChIP1 nucleic acid.

29. The method of Claim 27, further comprising amplification of at least part of said KChIP1 nucleic acid.

30. The method of Claim 27, wherein said contiguous nucleotide sequence is 100 or fewer nucleotides in length and is either: a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table 10; b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table 10; or c) capable of selectively hybridizing to said KChIP1 nucleic acid.

31. A reagent for assaying a sample for the presence of a KChIP1 nucleic acid, said reagent comprising a nucleic acid comprising a contiguous nucleotide

sequence which is at least partially complementary to a part of the nucleotide sequence of said KChIP1 nucleic acid.

32. The reagent of Claim 31, wherein the nucleic acid comprises a contiguous  
5 nucleotide sequence, which is completely complementary to a part of the nucleotide sequence of said KChIP1 nucleic acid.
33. A reagent kit for assaying a sample for the presence of a KChIP1 nucleic acid, comprising in separate containers:
- 10 a) one or more labeled nucleic acids comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said KChIP1 nucleic acid, and
- b) reagents for detection of said label.
- 15 34. The reagent kit of Claim 33, wherein the labeled nucleic acid comprises a contiguous nucleotide sequences which is completely complementary to a part of the nucleotide sequence of said KChIP1 nucleic acid.
- 20 35. A reagent kit for assaying a sample for the presence of a KChIP1 nucleic acid, comprising one or more nucleic acids comprising a contiguous nucleic acid sequence which is at least partially complementary to a part of the nucleic acid sequence of said KChIP1 nucleic acid, and which is capable of acting as a primer for said KChIP1 nucleic acid when maintained under conditions for  
25 primer extension.
36. The use of a nucleic acid which is 100 or fewer nucleotides in length and which is either: a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table 10; b) at  
30 least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table 10; or c) capable of

selectively hybridizing to said KChIP1 nucleic acid, for assaying a sample for the presence of a KChIP1 nucleic acid.

37. The use of a first nucleic acid which is 100 or fewer nucleotides in length and which is either:

- a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table 6;
- b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table 10;
- or
- c) capable of selectively hybridizing to said KChIP1 nucleic acid; for assaying a sample for the presence of a KChIP1 nucleic acid that has at least one nucleotide difference from the first nucleic acid.

38. The use of a nucleic acid which is 100 or fewer nucleotides in length and which is either:

- a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table 10;
- b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Table 10;
- or
- c) capable of selectively hybridizing to said KChIP1 nucleic acid; for diagnosing a susceptibility to a disease or condition associated with a KChIP1.

39. A method of diagnosing a susceptibility to Type II diabetes in an individual, comprising determining the presence or absence in the individual of a haplotype comprising a halotype shown in Table 2 or Table 5 at the 5q35 loci,

wherein the presence of the haplotype is diagnostic of susceptibility to Type II diabetes.

5 40. The method of Claim 39, wherein determining the presence or absence of the haplotype comprises enzymatic amplification of nucleic acid from the individual.

10 41. The method of claim 40, wherein determining the presence or absence of the haplotype further comprises electrophoretic analysis.

42. The method of claim 39, wherein determining the presence or absence of the haplotype further comprises restriction fragment length polymorphism analysis.

15 43. The method of claim 39, wherein determining the presence or absence of the haplotype further comprises sequence analysis.

20 44. A method of diagnosing a susceptibility to Type II diabetes in an individual, comprising:  
a) obtaining a nucleic acid sample from said individual; and  
b) analyzing the nucleic acid sample for the presence or absence of a haplotype, comprising a haplotype shown in Table 2 or Table 5 at the 5q35 loci comprising a KChIP1 gene, wherein the presence of the haplotype is diagnostic for a susceptibility to Type II diabetes.

25 45. A method of diagnosing a susceptibility to Type II diabetes in an individual, comprising determining the presence or absence in the individual of a haplotype comprising one or more markers and/or single nucleotide polymorphisms as shown in Table 13 in the locus on chromosome 5q35,  
30 wherein the presence of the haplotype is diagnostic of a susceptibility to Type II diabetes.

46. A method for the diagnosis and identification of a susceptibility to Type II diabetes in an individual, comprising: screening for an at-risk haplotype in the KChIP1 nucleic acid that is more frequently present in an individual susceptible to Type II diabetes compared to an individual who is not susceptible to Type II diabetes wherein the at-risk haplotype increases the risk significantly.
47. The method of Claim 46 wherein the significant increase is at least about 20%.
48. The method of Claim 46 wherein the significant increase is identified as an odds ratio of at least about 1.2.
49. Use of a Type II diabetes therapeutic agent for the manufacture of a medicament for the treatment of a disease or condition associated with KChIP1 in an individual.
50. The use of Claim 49, wherein the Type II diabetes therapeutic agent is a KChIP1 nucleic acid agonist.
51. The use of Claim 49, wherein the Type II diabetes therapeutic agent is a KChIP1 antagonist.

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## KchIP1 genomic DNA (Build 33 Chr5: 169716198 – 170098453)

caggagtg	gggagagag	gagggagag	ttgccctgca	ggctctctgg	169716247
atgcagaagc	cagactcgct	gcagaggcag	ctgtgctgtt	cccggagcct	169716297
GGCTTCAGGG	GTGCATCCGT	CACTCAGGGT	TCATTACCCC	AGGCAGGCTC	169716347
CAAGTTCCTG	GGGTGCACAA	GGTGGGCACT	GTCCCTTCTG	GGTGCTGACA	169716397
GCAGAGCCTG	GCTCCCCCTCC	GCCACCATGA	GCGGCTGCTC	CAAAAGATGC	169716447
AAGCTTGGGT	TCGTGAAATT	TGCCCAGACC	ATCTTTAAGC	TCATCACTGG	169716497
GACCCTCAGC	AAAGgtatgg	aaactggcct	tgacccttgc	tttctgtctt	169716547
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gaaaggctat	atgcagccag	atctcatgac	atggctcagg	tgcccgccac	169717597
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tggaggccag	aagtggggta	aacaggagg	taatgggtat	agctgtgatt	169717847
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FIG. 1.1

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ttagattcaa	ccctacatgg	atacattatg	attgcttaat	gattttctgat	169718747
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tgaggaatgt	aaagaatgtg	ttggaccagg	tacctgcttg	ttctatggca	169718897
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FIG. 1.2



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tcatcttccc	cagtcttctt	aggggttacag	aatctccctt	gggccatctc	169722747
tctcagcaga	cccagggtccc	aaatccctga	aagcctttgc	ttcccaaggg	169722797
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caggacagcc	ttgggcaagc	cattccccat	cttgagtctg	tgtccttccg	169722947
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atgggacatg	tgacaggcac	aggacctggc	tcatacaagc	tgtcagtaa	169723047
aagtcaagtt	ccccaccctt	cttttctatg	atacgacctt	ggatttgtag	169723097
ccaagagaaa	caaggctgag	cctctgtggg	tcaagtcctc	ttcccagctc	169723147
ctatccagat	gtgctgctat	ttcaaaaatta	tccccctgc	ccccagtcac	169723197
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ggagaggatg	tggaaatgag	gaaattgcac	aggcctcccg	ggccagctgg	169723847
aggaaagaaa	ggccaggact	cctgaaaaag	actcatggga	agtcatttac	169723897

FIG. 1.3

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tatcaccact	gaccacgctc	tctgtcacag	gtcttcagtc	taggggcaga	169723947
agaaagcctt	ccttctctgt	taggatgagg	ggaggaggac	catgaacaca	169723997
aagctaacct	tgggtccctc	tggctgaagc	cactgagatt	ccattttgtg	169724047
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cctcacaact	gcttgctgtc	ttaggccatc	aggctgctta	tcaacctgat	169724147
ggcctaagct	accatacaaa	gacacgggtg	cttatcaaca	acagaaatgt	169724197
atttctcaca	gttctggaag	ctggaagtct	gagatcagga	tgctagcact	169724247
gtggacttct	cgtggggact	cttcctggct	tacagacagc	atctcctgct	169724297
gtattctgac	gtggaggaaa	gagagtaagc	tagctctctg	gcctcttctt	169724347
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caaaggcccc	accttcaaat	accatcacct	caggagtggg	atttcaacat	169724447
gtgaatttgg	gggacgggag	gcacaaatat	tcagccatt	gcactaagta	169724497
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catatgggga	gcaggcccca	cagccaagac	tacagggagg	ggagaaaaaa	169725147
ggaacacacca	cccagcaaga	tttccctgtt	tatttctagt	ctggccaatt	169725197
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cagttgtggc	tttaagtaca	ttcacatgtt	gtgcaaccat	caccaccaac	169726347
catctccaga	acatttttct	tctcgcaaaa	ctgaaactct	gcactgcacc	169726397
cactaaaccc	ttccccattt	ctgtctaccc	tcaggctctg	gcagccaacca	169726447
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FIG. 1.4

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tgagtcacga	acagtatttg	tgtctggcct	atttcactta	gtgtaatatc	169726547
tttttttttt	ttttttttga	gatagggtct	cactctgtca	tccaagctgg	169726597
agtgcagtgc	tgtcatcaca	gcgcactgca	gcttctacct	cctgggctca	169726647
agcaatcctc	ccacctcagc	ctccagagta	gctgagacta	caggcgtgcg	169726697
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tctccatggt	gccccacctg	gtctcaaact	cctaggctca	agtgattggc	169726797
ccaccttggc	ctcccaaagt	gctgggattc	caggctgcca	tacctggccc	169726847
tcacttagtg	ttatgtcttt	aagggtcatt	cctgtaacag	cctgtgtcag	169726897
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aatgaatcat	atacgattat	aatccccctt	ctggaaactg	tctccagtgg	169727047
tttcttgaca	catttagaat	taaatgcaga	ctcctctcag	tggcctgtga	169727097
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gtgaccttgg	gaagtccaag	ggagtcactc	cttcgagcct	agcctccttt	169728347
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FIG. 1.5

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gctacttggtg	aggctgaggc	aggagaatcg	cttgaaccag	aatgtggagg	169729797
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caaaactccg	tctcaaaaaa	aaagaagaaa	gaaggaaaaga	aggaaaagaaa	169729897
aagaaagaaa	gaaagaaaaga	aagaaagaaa	gaaagaaaaga	aagaaagaaa	169729947
gaaagaaaaga	aagaaagaaa	ggaaagaaaag	aaagaaagga	aagaaaggaa	169729997
agaaagaaaag	aaagaaagaa	tgtgcagcac	ccagcacaaag	acctggcata	169730047
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tgtgggaata	gatgtgtatg	gaaaagtaaa	atagagaaga	aatacactga	169730747
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FIG. 1.6

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tggccaaaat	tgtaagtca	gggtacccct	agaaatgaag	caagagggga	169732647
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agagagaaca	gacatttgtg	aagcatcttt	tatgcaccgt	gctgagtact	169732847
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tgtaccagtc	tcccttctgt	tctgcttttg	catagtgacc	agttcaagga	169733697
tcgctgcaac	catggtgtgc	ctgggttcca	gttgggctg	tgatgagcta	169733747
tgggctggaa	agcatagatt	taggcagggt	ccagctggcc	tcgtggctct	169733797
gtctgtcttg	gcagtgccca	cagcagaacc	tttgtgggac	attttcagat	169733847
ccttctgctt	ggccatcacc	cccacatcta	ttgagacttc	agaggtgtgg	169733897
ccccagggag	tcaattgaga	gcctgggctc	tgtgatggaa	aggtatctgg	169733947
aagcatctaa	caagctctca	atagttgacc	ttgacctgct	tggcattttc	169733997
cactttttgat	atgggggtaaa	gacaagaaca	ggattcccag	tggttagagt	169734047
gtttttctgga	gcaataccac	ctagatttga	attccagctc	tgctatttgc	169734097
taacttctgc	cttggggcaa	gttaaatctt	ttccttgtgc	ctccattggc	169734147
tcattggtga	aatggagata	ctaataataa	cctcaaagga	tggtgttact	169734197
gttcaatgag	ctgtgcctgg	aaagatcctg	gcattcaggt	aggtgttcaa	169734247
caaagtctag	cccttattac	cgtaggaat	gatagattct	tgcacagcaa	169734297

FIG. 1.7

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gtgatcagct	aaatatatgc	ccaaatgaaa	gtggctccat	cttgctatag	169734347
tgagttattc	atccaaagag	gtgttgctgc	aggttggtcat	tgaagagAAC	169734397
tattgtagaa	agagtgtgac	tgtgttctcc	ccgacaatac	ttctgacacc	169734447
acgtaagagg	gttttcttcc	cccctactga	taccaactag	tttgacaccc	169734497
aactgggtgt	cctacaattt	aattcaattc	tgacactaac	taccagaggt	169734547
tagctcagac	cccacagggt	aagaactcag	tcccacaaga	ctgcccccat	169734597
tcaaatgcca	gccaccaata	gggtgtcctg	actatccaca	cttccacctg	169734647
actgacagaa	cattcctaca	acctccccta	cacctccaga	taggatataa	169734697
taatttacta	gagtgatcca	cagaactcaa	aagaacattt	tacttactat	169734747
tgacacttac	tattacatgt	tgattacaga	ggatataact	cagaaacagg	169734797
cagacggaag	agacacacag	ggcaagggtat	gagggatgca	gggtggagggt	169734847
gcagagtttc	cgggccctct	cccagcacct	tgacgtgttc	accaaccag	169734897
aagcccccca	aaccctatta	tttaggggggt	tttatgaaga	tttactaca	169734947
taggcatgat	tgttaaacca	ctggccattg	gtgattaaac	tcaacctcca	169734997
gcccctcttc	cctctgcaga	gggtgcccgg	tagagctgaa	ggttctaact	169735047
ctctaatacat	ggcttggtcc	ttctggcaag	cagctcccat	gccgaagcta	169735097
tttacaggcc	caccaagagt	tatctcactg	gaaaaaagac	actcctatcg	169735147
cccctaaagg	acctctgtac	caaagaccaa	atatctttct	gtgagacaac	169735197
agagagttca	agcaccaaat	ataaagtggg	gaagcactag	atgatctcta	169735247
aagtcttact	ggcacttgga	gaacaagtgt	ttgtatttga	acatgcggaa	169735297
tcaaagggga	ggtgagtaaa	aggggctcca	gaattgacac	aggaggagga	169735347
ctcagtgcag	caatctcatg	gggcgtgggg	acagaagaca	catcccaaag	169735397
cttcatgtgc	ctctcaagcc	cctgcttttg	ttttatgtgt	actggggata	169735447
ggggagggtg	gtatgggaatg	atggagatta	tgggagaaca	gagtccatct	169735497
aagccacttt	tgactctgca	actggggggag	atgcagctgg	cctgggaagg	169735547
aatcacaAAC	gtgggtccagt	actcagttta	gagttgttgg	ctttgcttcc	169735597
atataacctcc	ctttctcatc	tcccaaatcc	tttgaggaag	ttggctggtg	169735647
aaaatgtact	tatgtaagtg	gggaggggaga	gttgtgcaaa	gctaggaaga	169735697
agctgagttc	tgcatcagag	gtgacatgag	aaagaaccag	gaaagcactg	169735747
tggagaggag	gatgacccat	caactgactc	atctggggga	caggatctgg	169735797
gagccagagg	tgatggagaa	aactaaagcc	ctcctcctgg	ccccagtggt	169735847
gaatctgatg	gagcctgggtg	gagagcctca	catttctaca	gggcacgggtg	169735897
tgggaggggc	ctggaggcct	tgtctctgga	tgactagggc	tggcagttct	169735947
gaagcttttc	atcatcagga	cccttttaca	tgcttaaaaa	atattaagga	169735997
tcctaagagc	tttgggtgat	atgggttata	tctattaaca	gttaccattt	169736047
tagagattag	aactaagaat	ggtaaaaaata	tttaatttga	atttacttat	169736097
tttaaaataa	taatacatcc	attagttgct	aacaaaaata	acataatttt	169736147
ttgaaaaaca	attatgcgtg	gcaaaaagta	tattgggaga	agtgggtattg	169736197
ttttacattt	ttcacaatc	tctaattgtcc	agcttttagaa	aggcacctag	169736247
aatctcattg	ctacctcggc	attcagactg	ttttaacaat	gcatgttaca	169736297
tgacctctgg	aacattccat	tgcaactctca	taagagaatg	aaaatgaaaa	169736347
aggcaataaa	tgtcttagta	ttattatgaa	cagagttttg	actttgcaag	169736397
cctccacttt	gagaactgct	acactggact	gtagtgaatt	tctccatgtc	169736447
tctctgatct	ttctttggtc	attttctttc	ccttccatgt	gacagggcaa	169736497
tggctgggtg	ggtacaggaa	ggtggcactt	tgtcacaaca	gtgtcttctt	169736547
aaatatattca	tagaattcaa	actcccccaa	acacaagacc	aattcaaaga	169736597
atactggata	ttctcacata	acagcctgtg	ctgccaatga	acaataaaat	169736647
aaatgcagtt	tgcaatgccc	tgacccaagg	agtttaagat	aaatttttga	169736697
tgagttggtg	atttagagga	ggagctggta	tcacttcagt	aagtcacaga	169736747
aaataagatt	atattaatat	ttatattgca	ttatttttaa	tctgcataat	169736797
gctgagtcct	cactgtgaag	aaggaagccc	ctcacaatga	ttagtgaggg	169736847
gtagggaggg	agaatggcaa	gaagacacca	agttccttgc	aggcaagcaa	169736897

FIG. 1.8



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atagatacat	cataaaagt	aagtgaatt	ccagtcctct	gagatcttca	169736947
taaatagaag	aaaccctcat	ttctttcctc	ctctgggtgc	agcttggact	169736997
gatgagctga	agctctgtct	gagacctggc	actgttagga	tgtccccag	169737047
ggttctttcc	accccgagtc	tggagctcag	gtggccccct	gcctctgaat	169737097
tccaccgctt	tgtctgagtt	ctggaggacg	gcacatggga	gaaccatcca	169737147
ggtgcacctc	tccaggatg	agtcactagt	ccatgagagg	acaataataa	169737197
atgatggaag	cactagacac	tcattagcag	agtggtttat	taagaactga	169737247
tgaagggttct	ctgctcccag	gcagatatta	ttgcaaaaaa	acacgtaggc	169737297
acagggtcta	actccatcat	gcctaaattc	ccattatttc	atgcttatcc	169737347
cgtgcataaaa	gttctgtgag	cagcagacag	ttgtggcatt	tgctagaagg	169737397
ccagtccttta	ttgacaggag	gagaacatct	atctcaagca	aatgaaggtc	169737447
atcattaata	atttatggga	cagtgggggt	taggcacctc	cacatactaa	169737497
tttttctaga	ggaacatggc	cttttccctc	gcagggtattg	tttgggtatt	169737547
ctgagtttct	gtgtatttta	gtcccaaatt	cagggtgcag	gaaaccattg	169737597
acaaaataga	ccctttaaat	cagactccaa	gttgggactt	cctttcttat	169737647
ttttcttctc	tttttaactt	aaatttttga	gataattgta	gattcacatg	169737697
aagctttacg	aaataataca	gagacattcc	gtgccccctc	tacctaatgt	169737747
cccgaatgg	aatatattaat	attttgcaaa	actatagtac	aatattacaa	169737797
ttaaagactt	cttaaaagac	tcacatgagg	acctttgaga	cttccctgac	169737847
cccagaagga	aaaaattcca	gggaatgatg	agctgcctgc	ctttggaagg	169737897
aagggtccacc	aggtaagaaa	ctggaggcca	cagggtatcc	tctgggctcc	169737947
ctggctggaa	ttggcagatg	ctgggtgcaga	tgccagggcc	tcccctcaga	169737997
actccaacct	gcatgagggc	acctgggttc	cagggtatgca	acgcagctcc	169738047
ctgcctggcc	cctgtggctt	tgagtggctg	tgtccctcag	cccttcacag	169738097
ctggctctgc	ccctcagccc	ttcacagctg	gctctgcccc	tcagcccttc	169738147
acagctggct	ctgtccctca	gcccttcaca	gctggctctg	ctgagttctg	169738197
tggttgagat	gccaggtact	ggaacacaca	gctccaggct	tgagtcctag	169738247
cccctcactt	tacagatggc	cttggccagt	tacctcttac	agcctcagtt	169738297
tttcatagta	acttagatag	cacttaccat	atgtcactat	cctaggaaat	169738347
ttacataaaa	atttgtttca	tgccaaaact	ctatggaaag	atactattat	169738397
cagtttcggt	ttgcaaacga	ggaaacaggc	acagaaaggt	tattcgtcca	169738447
aagtcaccca	gcttgtgaac	agcacagctg	gaatttgaac	ccaaacagtg	169738497
cacatcccaa	gtccacatac	ttagccactg	tctctgtttg	cttctcatca	169738547
tctgtgaggg	aggttcagga	gtatctcatt	tttttttcca	aggcaaaacta	169738597
attagtagag	tgccctggc	agaataaata	agcaccata	catgccagat	169738647
aacattgtca	gtataacttc	tggaagtttc	tgagtattca	tgacttattc	169738697
tttttttttt	tttttttttt	ttttttttga	gacagagtct	tgctctgtta	169738747
cccaggctgg	agtgccgtgg	cgogatctcg	gctcactgca	agctccgcct	169738797
cccgggttca	cgccattctt	ctgcctcagc	ctcctgagca	gctgggacta	169738847
caggcggcta	ccaccaagcc	cggctatgat	tttttctatt	tttttagtaga	169738897
gacagggttt	caccgtgtta	gccaggatgg	tctcgatctc	ctgacctcgt	169738947
gatctgcccc	cctcggcctc	ccaaagtgc	gggattacag	gtgtgagcca	169738997
ccacgcccgg	ccgacttttt	cttgttacta	acaatagctc	tttttccctg	169739047
atcctctccc	tcctcctacc	tcccgcctc	caataggcct	cagtgtgtgt	169739097
tggtcccttc	tttgtgtcca	tgtgttttca	tcatttagct	cccacttata	169739147
agtgagaata	tacagtattt	agttttgtgt	ccctgtgtta	gtttgctaag	169739197
gataatattt	ggcctccagc	tccatccatg	tccctgcaaa	ggacatgatc	169739247
tccttccctt	ttatggctgc	ataatattcc	atgacgtata	cgtaccacat	169739297
tttctttaat	aatgggtact	agacttaata	cctgggtgat	gaaataatct	169739347
gcacaacaaa	ctcccttgac	acaagtgtac	ctatgtaaca	aacctgaacg	169739397
tgtaccctgc	aacttaaaat	gaaagttaag	aaaaaacac	acacacaaaa	169739447
caaacaaaaa	aaactatagt	tgccatttta	aacacctatg	atgtgtcaaa	169739497

FIG. 1.9

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cattccttca	gccctcccaa	ctatccagaa	agagtccttc	ttttatagat	169739547
gaaaaaacta	agaatcaaag	agatgaaatc	gggcagagta	gagacaggat	169739597
tcaaacccaa	gatctgcato	ttggactcac	aacactggaa	gaaacttcag	169739647
acaccagcct	aacttcacac	ccagctcagg	actggccctg	ccgaatggtc	169739697
actcacctgc	tctgaaaato	ctegcgacag	gacgctcact	tcctacaccg	169739747
gtagttctct	ggctcgaggt	gtgccacaga	atccccctacg	cattgttaga	169739797
acacagaaca	ttgctacccc	caccccgtgc	agggcttctg	gcgtgggtggg	169739847
gctgggacag	gggcctgaga	gtgtgcattt	ctcacaagct	gccacaggat	169739897
cctgatgctg	ctggcccagg	gaccacactt	ggacagtcac	cgcttctagga	169739947
aaacttcctg	gagtgggaat	ggtaaagggtg	atggcttctt	cccattttgc	169739997
cctttttcaa	tctgagatag	gcttccccag	caggctcagt	gccagagtcc	169740047
ataccctcaa	tttaaataac	aaatcctcct	ctatatcatg	acctttcctc	169740097
cagaggggtg	tttttcattt	tttggttttt	gttttttttt	tgagacggag	169740147
tcttgttcta	tcaccaggct	ggagtgcagt	ggcacaatct	cggctcactg	169740197
caagctccga	accccggtt	cacgcatc	tcctgcctca	gcctcctgag	169740247
tagctgggac	cacagggtgc	caccaccacg	cctggctaata	tttttgatt	169740297
tttagtagag	acggggtttc	accatgttag	ccaggatggg	cttgatctcc	169740347
tgacctcgtg	atccaccagc	ctcgccctcc	caaagtgtg	ggattacagg	169740397
agtgaagccg	cgcgcgcggc	ccagaggggt	ttttaagatt	gtgtgttctg	169740447
aattggcctgt	ctctgactgg	aacccaactc	cgtccccaga	cccacttcca	169740497
tctttttctg	tgagggggac	acactctttc	aactttttcca	aaatggcatc	169740547
taccatggct	tttctgatta	aaagcaaacg	aaacacaccc	ttcctataat	169740597
caaaaattta	gaaaagcagc	aaaaataaaa	aggggataag	gaagaaaaca	169740647
gaaattaacc	accatcccac	cgctaaaatt	ttgatgagtt	ctcatgtgtt	169740697
tccttgacgc	tgattgttgt	ttggcataca	tttattaata	ttggaattaa	169740747
aaatatatat	ggcactttat	atcctagaaa	atagtaatac	tgtaaatgtg	169740797
ttctagaaat	gggagctgct	gttgctctta	ttagagaatt	caaacaaaga	169740847
agggaggctc	gctggggaca	gcttctgggg	gaggatgggt	accgctttga	169740897
gacaacaggg	agaactcagg	cacagaggtg	acgatcatcg	ttctctgtgg	169740947
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aggtaataga	gagctagaac	tggctggcct	tatggcctcc	aaggcattgg	169741047
ggagccactg	tacattcttg	agcaggcaat	gacttcacaa	aaggatttct	169741097
caaagggttag	tcctgcaaca	gaagacagcg	tggattggac	tgggaagagtg	169741147
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ggcccagcca	gtcccctgtg	ccctgacaag	tggatatggca	tggatggatg	169741247
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tggcgataat	gaggaggcca	ccggtcagca	ggaaggtggg	ccagaagagg	169741347
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gctgtgtatt	tgaaatcgag	atcatgtgct	caattgccta	cagggctcat	169741997
gaaggtattg	tcagaggggtg	aagcaggcaa	agcaatgaga	tgacaggtgc	169742047
ccactgactc	ttgccttggt	gccaggaaga	attgccaggg	tgtggcaggg	169742097

FIG. 1.10



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cctgtcaata	gggagagagc	cagctgcctc	cagacaggca	gtcaccactc	169742147
cctccaggca	atggatgtca	ggccatccag	aagatctata	atagccagac	169742197
ctccaacact	ttaagagaag	ttagaaacca	gatcacacct	gtaatcctaa	169742247
cactttggga	agccgaaggg	gaaggatccc	ttgagcccag	gagttcgaga	169742297
ctagcctagg	caacatagca	agactttatc	tctacaaaaa	aagttaaaaa	169742347
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atgatctcgc	aactacactc	caggtaaggc	aacaaagcga	gatcccattt	169742497
caaaaaaaaa	aaaaaagtaa	aattattagct	aaatttataa	ttgaaaacct	169742547
ttgcagtttc	aacctgtgta	cagcaaaaca	actatgttgg	caagcgggta	169742597
tttgacactg	ggatccaaag	gaaagaaaga	atgcattgaa	aagagttttg	169742647
tgccagcaga	gcattgacaca	catttaattc	tgacgttgat	tattgttatt	169742697
aggaaacttc	tgccctgttc	agatgaggcc	agctggaaag	tgatgcaaag	169742747
cagtcataaa	gcggagtttt	atctggtttt	atctctgttc	tgagctgcaa	169742797
gtgtgggtgcc	cccactgtca	gcagaatacc	tacagggccc	ccatagccca	169742847
ggctccctacc	cactctgcat	cactgagggc	gagaccagag	aatgtgtgat	169742897
tccttctatgc	acttaatttt	gccctagtga	aatcatgtgc	aagatcaaaa	169742947
tgtgtaaaac	tgagacccaa	atggcagggtg	ttgagccaga	ttccttgacg	169742997
gcctcggcca	ctccctggat	ttatatgagg	tgccaccctg	gaagctgcct	169743047
gccctgaggg	cattcactcc	agcaacacag	aggagggttg	cactgtagtt	169743097
ctcacagcct	gggaaatgca	gatgctgcac	tcagatctag	ggccccagcc	169743147
agccagggag	tagctgaggg	tggggagacg	ctggctcctc	aggaatctgg	169743197
cattcagagc	tggttgacac	tgccagggtcc	tcagtagcat	ataatccagc	169743247
atcctgagct	gacgggtgagg	gggcctggcc	tgagtctctc	caatgcctct	169743297
gactgtgacc	ttggctaacc	tagctcctta	aatagcagtg	tggctatgga	169743347
gtcagacagg	cctgagttct	gagctgtgtg	accttgggca	ctgccacaac	169743397
ctcactgggc	cttgtaaaat	gggtttgtga	ggctacctgc	ctaggagaac	169743447
tgtcatgggg	attaaatgag	atgatgcatg	taaagcactg	agcacagaag	169743497
cccagcacac	gataagaact	caaaaaagtg	gaagatgcta	ttattaataa	169743547
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gaactcacct	gctccaggct	aagactcaca	ggaaaagctg	agggcagact	169743947
atggccccta	ccttcagagt	tggagggtgg	gatgagagtc	ttcttggccc	169743997
ttcacagtga	ttccagagga	caccagcta	gcctggagcc	ccagccactt	169744047
gaacccttat	gatggacata	ggcgggaagg	gcagctagcc	cacaaccctag	169744097
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gcagcctgct	atcagcacca	cacctgggtca	agcctggggc	gcagggggaga	169744197
ggacagcagt	ggctccagca	tgctcctcct	tcacatcctg	ctgacagttc	169744247
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ttattgaaaa	tttgtttctt	gcattgggat	aaatcaaggg	ctactgaatg	169744397
ccaacgcaga	ggcaggggtc	atgggtagga	gctgcctcca	gtgggcccctg	169744447
agacctctct	ccaccgggtg	gggcogagtc	atactagcga	tgacagaaca	169744497
cctgaccatc	ctgcactgcc	cagacccact	tctcattgac	cttcagcact	169744547
ctcaagatcc	cccagcctcc	acgccccatc	ccaggcaccc	tgcccccttc	169744597
cgtcccatca	gccatcaagt	ccggactgtc	agcatctccc	ctgctgcagg	169744647
ccacatcttg	gtcgtgagtg	cttgctgcgg	ccttggtctcc	tctgtctagt	169744697

FIG. 1.11

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aactggaccc	acacacctgt	aggctccatc	ttcccagccc	aactctgaaa	169744747
ctctgatcat	gccctaaaga	ttcccattgc	caacagcaat	aatttccaac	169744797
cttagaatca	ccttggggagc	tccatgaatg	gatctctgac	cagagattcc	169744847
accttgatat	gtctagtgtt	ggaccctagt	tttgtttttt	aagactctta	169744897
caggggttcta	atgcatagcc	aaagttgaca	tatcttgaga	catacacact	169744947
cacatttttaa	ttccatattg	tggatgatcaa	aggcctctgg	gaacagacct	169744997
tagtctgccc	tgacagcctt	ttccagctgc	atacacccca	tcatgggtca	169745047
ttttctgtag	tcagccctct	gatccctgtc	tccacctagc	ccttccctcc	169745097
gccatgcctc	gtcctatagg	catacccgtc	tctatatca	cctcattctc	169745147
tatgccttgc	atcctgcgcc	tgccctgatgt	taaaagccta	atccaagagc	169745197
ccttcttttt	tttttttttt	tttttgagat	ggagtttcac	tcttggtgcc	169745247
aggctggagt	gcaatggtgc	aatctcacca	agagcctttc	tgataccccc	169745297
atcattgtca	gctggaaaac	atccccctcc	tctaaccctc	gtaacttcc	169745347
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tgagctctct	cctcttgagt	cctacaggct	tgacacagga	ggtgctcaat	169745447
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ggaaggaagg	aaggaaggga	gggagagagg	gaggggaagg	gggaggggaa	169745547
aaaaaagaaa	agaaagaagg	aggggaagaaa	gggaaaaaag	aaggaaagaa	169745597
agaaggaagg	aagagagaca	gaatatgggc	caactgatcg	ccttaggaaa	169745647
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gccctgagtc	cctgggtttcc	tggggagtc	ccgggattcc	actttgagga	169745797
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caagcgtggc	actttatata	cagcgtctct	gacttgataa	cagctcttca	169745947
agggtgcagca	ttagcattcc	actttacaa	ggtggaaact	gaggaggtga	169745997
gaggctaagt	ggcctgccta	tgtttacaca	gccagttagc	ggcagattca	169746047
aaccacaggtc	tgtgtgactc	caacacagaa	gagctagggc	tggctcagtc	169746097
tcattccagc	tgtgagacct	ggtcaagtgg	ggtgatcttt	ctcagcctcg	169746147
gggacagggga	cagttaggaa	caggctcaca	cacctgacag	ggataaaggg	169746197
atgtgtcccc	atccctccag	ttcagtaoct	gctgggtctg	gtcccagagt	169746247
tcctccgtgt	ggtacagcac	agcccacctg	ccggcagctg	acacgttgac	169746297
ccacaggcat	gggtactggg	gcaccttctt	gcccttcagc	tcctcctggt	169746347
ccctgatgtt	ggtctcaatc	agggtggcact	tggattcctg	ggtccacacg	169746397
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cacagaacac	ccatttgaac	ccattatccc	ctgggagcct	ctagagggat	169746497
ccaggactgg	gatccctcatc	ttgtcttcag	catccagcaa	taaaggcaca	169746547
tgaccccaca	gtccccggac	acagggagga	attgtagaag	ctggatgggg	169746597
tcttagacat	tatctatatg	actggttctc	aaccttggct	actcttgcaa	169746647
caacctgggg	agcttctaaa	aagattcccg	tgtccaagct	acaccccaga	169746697
gcaagtgaat	cagaacttct	tgggtgggtt	ggcccaggcc	ctgggtgttt	169746747
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cttatccata	tcgtcttcat	tttgacagag	cagaagagaa	actcagaaag	169746847
gtcaagtga	tttgctgaga	ccttgacagga	cctgaagcta	ggtctgagt	169746897
ggttggagag	ctgtgttctt	tcccctaaaa	ggagcagatg	tagaaggggt	169746947
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cttcaccaga	ttaagagtcc	agccttgaat	cgcttcagcg	ttgtgaagag	169747047
tgaggctgca	gcaggcccg	gagaggctaa	caggttcatc	aacatattag	169747097
taaatcagtt	gtgcttcaac	tcccaggtat	cctgtgggag	accatttgcc	169747147
agtcagaagg	gggctgtcag	ctgctggaac	gtgccagag	cacaggtctg	169747197
agacttatcc	taaggacagg	ctgggggaac	tgagtgtctt	tgttccaaat	169747247
agaacacgaa	ttaggaattc	acagcttttc	cttaaaatct	caagtgggtg	169747297

FIG. 1.12

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atatgtcatg	gagcaagggc	atggaccatt	ctctgagatt	cctgagcaga	169747347
acttcaggga	agcagatgct	ggctcaatgc	agacacatca	gaaaacctca	169747397
aacatgaaat	gtatgttcag	tgaggcaagg	agctccccgt	ctcttgaggt	169747447
attcatcagg	aggctggatg	cccacctgac	agggaggcct	cagaggggag	169747497
agaattatgc	agctgagctg	taaacatctg	caattctctg	attcctcctg	169747547
ggatcaaact	tgcactggaa	cctttgctct	gattctttgc	tatttcttct	169747597
gagaagggca	tcattgtgtct	gttaccacca	cgtcctagat	catgtgtctg	169747647
ttaccaccag	gtcctagaat	ctcagaccag	tggggctcag	ttcatcctac	169747697
cttccttgca	cttgaaccct	agaacctaa	aatgagcatc	gtcttgacct	169747747
tgctgccttg	aatgagggct	aaggagaggg	gtgagtagaa	ggccaggggt	169747797
ccttacagat	gccagaccct	taggagaggg	ttgggggggtg	ggcaggcccg	169747847
gagagctcag	taccttttct	ggtagagggg	cagcacagtc	gtgaccagga	169747897
tgtagtaggt	gatgacggca	cacaccacca	tgggttacacc	caggcaaagg	169747947
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cactgggggc	agtgatcatt	tctaggtcca	cagaagcaaa	cagaagtgag	169748047
atcagcccag	ttcacagggtg	atccacagaa	agagaggaca	ggtgagaggg	169748097
gaaggtagct	aactattaat	atcactcttg	tttatatttg	gagctttgca	169748147
acttccagaa	gtcttgcttt	ttggacccca	tgtaagcctt	ccctgtgcaa	169748197
ttgagaggca	attgcagata	aaagacctac	ggctcagaga	ggtaaagtga	169748247
cttgccctag	gtcacacagt	atgtaatagg	ctcagtaatg	gccccccaag	169748297
atgtctatgt	tctagtctct	ggaagctatc	aatgttactt	tatgtggcaa	169748347
tgactttgca	gaaatgatta	agataaaggc	tcttgaaggc	caggtgcggt	169748397
ggctcatgcc	tgaaatccca	gcactttcgg	agaccgaggt	gggcggatca	169748447
tgagggtcagg	agatcaagac	catcctggct	aacatggtga	aaccccatct	169748497
ctactaaaaa	aaaaaaatac	aaaaaattag	ccgggtgtgg	tcgtgggagc	169748547
cagtagtccc	agctacaggg	gaggctgagg	caggagaatg	gcatgaacct	169748597
aggaggcgga	gcttgacagt	agcagagatg	cgccactgca	ctccagcctg	169748647
ggcaacaaag	caagactccg	tcaaaaaaaaa	aaacaaaaaa	caaaaaaaga	169748697
taaaggctct	tgaaatgggg	agacaatatt	ggattatcca	tgtagctcct	169748747
aaatgtaatc	ccaagggtcc	taataagagg	gaagtgaagg	gagattaaac	169748797
agatgagaaa	gctaagggtga	tatgaccagg	gagacagcaa	ttagagtgat	169748847
gtgaccacag	gccaaggagt	gcgtcagaag	ctggcggggg	caaggaaaca	169748897
tggctcatcc	cccacggcca	ctgcaggggg	tgcagcctgc	agacaccttg	169748947
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catgtgcac	atccatgcac	ctccttccac	ggcacttatc	tcacagggat	169749097
acttgaggta	tttctgcccc	gaaacagttc	tgtggcaggg	ctagctgggc	169749147
cgggcacagg	caggggaaagg	agaggagggc	cccagaaggc	agctgcagggt	169749197
tgtcaggaga	ggcaggagggt	ttaccatatt	ccgggtgttt	ttttttttgt	169749247
aaggaaacatt	cccctacttc	aagcaaagaa	agaagaaaga	aggcatcatg	169749297
gtggcctcag	cgactgcttt	cttattttcag	ggcttgaagc	cacctgggac	169749347
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tctttaggca	gcaactcctt	gtttttcccc	tggacattga	ctccacccca	169749447
atgcaagcaa	agattccacc	ctccccctgt	aggctcctga	tcgctcccc	169749497
aggagtgtga	gtcttgacaa	agacttcaag	aaacagcccc	tcaatctatg	169749547
ccgcctggag	ccacagagat	gcccagccat	ggcccccgcg	tgatttccca	169749597
tggttccgca	agctgtccta	gagcctctgg	taaatttatt	tgctgttggt	169749647
tttatttggt	taaagtaacc	agagtccatt	tctacaaaaa	ataccaggaa	169749697
gctatcaatg	taatcctcca	ttttagggga	aatttttaggg	gaatttaggg	169749747
gaaatttttag	ccagatatca	gggggacttt	attctccttg	ccagggtccct	169749797
aaagtaataa	acatattatg	gtttttgttt	gtttaattag	ccagtgtccg	169749847
ggtgacaggg	cttagtccaa	agagattttc	tgcaaagtgc	tctattttct	169749897

FIG. 1.13

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gctcaggcgt	ctcttaacta	ctagactggt	tcaaattatc	agagattcct	169749947
gactccctcc	ccttagccag	gctgccctca	tacccgggca	tctccgctaa	169749997
aggggaagaga	ccagggtcag	gcaccacgga	tacccatcac	accttcccag	169750047
tgagctggtc	cacctcccct	atcgatcggc	agagggtgaca	tccaatgaca	169750097
actttttctc	ctttatttgg	caccaggagg	tgagtttctc	ctgcattcta	169750147
atggagacat	tataaaagca	caagcaagca	gaaattgccc	ccgacaaaaga	169750197
gagatgtttt	attcaactct	ttttattcaa	tccttttccct	cctgttctgt	169750247
gatcttgtgg	gaatgggaga	gcccattgct	ttttctacct	ggcgtcagtt	169750297
gaacaagact	ctccatgtat	tcacaggtaa	agcaacagaa	tcacctggag	169750347
gtaagctaaa	agccccaaca	gcctgcttcc	ccaggacctg	caagggtcac	169750397
tggcacttgg	ccccaccca	gatactgtga	gacataaatc	at ttgagcc	169750447
aatgggaaat	cccatcttgg	aagcctaggg	ctgagtggcc	acaacaaagc	169750497
cattttctct	ctgggggaac	tggatcgcac	ctgtgggggc	ttcctgtggc	169750547
tccttcttgg	ctaatacagc	ccccccagcg	cccagggcca	tggcctcctc	169750597
tgctatttgg	cttctagtgc	cctctcaggg	ccctgggcac	tcctgaggct	169750647
ggtgaaggca	ggaacctggg	tttaccagtt	ttaggagctc	agaaggaaag	169750697
gaaaggagag	gcttccttgt	cacagagaag	tctggaaact	tggccttattc	169750747
aggtctgacc	cgtctctaata	ggtctgatga	gattgttgcc	tgcactgagt	169750797
gagtttatag	agtcattgata	aatcctccta	agaccatgcg	tgggggttcag	169750847
tgtagatatg	acttcagcaa	gaagttagta	ttcagcatcc	aaaggagaga	169750897
cctttggcgg	gaggaaggat	gggaactgtc	aatatcccc	aagggaacaga	169750947
aagaaaagga	agaagtgggt	ttcagctatc	ataggaggga	tttcagttag	169750997
actgtaagaa	gaacttccca	gttttgagca	tttctaaata	tctctgaagt	169751047
tccaggatat	atcttcccat	ttagaaaggt	cacttgagat	ctgggataga	169751097
ttcagagaag	atggagaagg	acaaaggaag	gcaggacttt	ggagtgtcct	169751147
gggtgacctg	atagctgggt	cgacatcctt	ttccttagaa	ggacaaggaa	169751197
tagagtacat	tgttgaacag	tttggtgggg	tgtggacagg	gcgattctga	169751247
ggtcctcaga	catggaatca	aatcctgggt	ctgccactta	cacttagcaa	169751297
ccacatgact	gtgaaacgag	aacctaggta	cctgcctcag	agagttcagc	169751347
taaagatcaa	atgccatatt	gagtatcaga	catgtatcat	agcacctagc	169751397
cccaaatacag	ccccagtaa	atattagcta	ttactactaa	cgaaggaaac	169751447
cctgaaagtt	tggagcagaa	gtctggaccc	ctcttgatga	atctattttt	169751497
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gctgcagcct	tctggccact	ctgagaactg	ggacctagag	ggccagggcg	169751597
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cctgagcaag	ttatggcacc	tctctggggc	tcagtttccct	tttttggttt	169752397
tggttttact	cccaaactta	tcgttaaatg	acctcagttt	tctcacttgt	169752447
gttactggca	tttttaaaac	ctactttgct	ttagggtagt	gatgggagtt	169752497

FIG. 1.14

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agagacgggtg	gggattttatg	gcaagggggag	agaactgact	ttttaaggac	169752547
caactgagct	gaagctggga	gtagttagag	ctccacaact	gcttccaacc	169752597
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gcaaaaaaca	tgctttttaga	tctctgcttc	ttcatctgta	aagtggaaagt	169752747
aaggattaaa	aatcagcaac	aaagggcgagg	cacagtggcc	cacgcccata	169752797
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tttgagacca	tcctgggcaa	catggcgaaa	ccccatctct	actaaaaata	169752897
caaaaattag	tcgggcatag	tggtgcatgc	ctgtggtccc	agctacttgg	169752947
gaggctgagg	caggagaatc	gcttgaacct	gggaggcgga	ggttgcagtg	169752997
agtcaagatt	gtgccactgc	actctagcct	gaacagagcg	agaccccgtc	169753047
tcaaaaaaaaa	aaaacaaata	tatatatata	tatatatatt	ttcaacaaaa	169753097
caacaaaaaac	aatcccagat	attggggctt	tcctaagtat	caggcgtggt	169753147
ggtagaaggc	agcttatctc	cacccttcac	ttgacccaag	aatcaaagaa	169753197
cctgaaactg	agacttggag	gcttgaagtc	actggtgcaa	ccctaggggc	169753247
cagaactaga	ttcgaagctg	gcccttcag	atggcacagc	ttggtctgtc	169753297
tctgatgacc	ctggggctgc	tctgagacat	taaaaatcac	ctcgatcata	169753347
cagtaagctg	ccacctgagg	ctctggaggt	caccttgagt	ttccccagcc	169753397
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gggtcttctg	ctccccctaa	atgagccaca	accaaaaggc	attgacaagc	169753997
cctgtcctcg	agggtttgtg	ggtgaaaacc	caggctcctt	gctggctgog	169754047
gggttgtgtg	tgacagatgg	ctacaggtgg	agggcaagaa	aataacaatg	169754097
ctgcaacaat	aaatattgac	ggtttgcatt	agtacggggg	gtcagagatc	169754147
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gagggagtaa	ctgagcctca	gagaggtgaa	ataaattgcc	caagcaagtt	169754297
actttgcctc	tctaagcttc	agtttgtctg	tctctaaaat	agagataatt	169754347
atacctagcc	cctcagtgtt	tttgaggaat	gagagatcac	ctaagctacc	169754397
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aatgtttcat	gcccctgcgt	tttggggtaa	tttggttatgc	agtcatagta	169754947
actggaacac	acttgcaagt	gatttcaaag	ggggactggt	acagttgctg	169754997
gtgatagtgg	taggattaaa	ccagtgagaa	ttaaaacacc	tgagattgct	169755047
atatggagtg	ttacaggaga	gtttagaaat	gctttatcta	ggtagggcat	169755097

FIG. 1.15

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ggtggctcat	gcctgtaatc	ctagcacttt	tcgagaccaa	ggcaggcggt	169755147
tcatttgagg	ccagtagttc	gagaccagcc	tggccaacat	ggcgaaaccc	169755197
cgtttctact	aaaaatacaa	aaattagctg	ggcacgatgg	caggtgccta	169755247
taatcccagc	tattctggga	agccgaggca	tgaaaatcac	ttgaatccag	169755297
gaggcgagg	tcgcagtgag	ctgagattga	gccactgtac	tccagcctgg	169755347
gcgacagagt	gagactccat	ctaaacccaa	acaaacaaac	aaaaaaagt	169755397
ctttatctac	tcttaggtca	cacactatgg	cacaaatgga	atagaagggc	169755447
agtgatattg	gagggtat	ttgtttatga	agcacctact	atgtaccagg	169755497
gaatgaccac	atagatatgc	aatacacata	catacacata	cacatggaca	169755547
ttcctctcca	caatccccca	caaaaggcct	tgttctttct	gtaaaagcac	169755597
aaggcaaagt	gattttccca	aggctcacgc	cctagcgtgt	gatgtgatgg	169755647
agcctggagt	gcacctgtgc	ccgctgactc	cacagcccg	ccctgccct	169755697
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gtaataaaaag	gcagaggaaa	taacggtggg	aggtttttta	gtagagttga	169756197
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cttcgcgatg	ctgggagcac	cgcagcctc	ttctgcagaa	cacttcctcc	169756847
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ttgggcacca	aggttgtttc	cacacctttg	ctattgtgaa	tagtgccgca	169757547
ataaatgtac	aagtgcaggt	ctctttatgg	tagaatactt	tattttcctt	169757597
tgtgtatgca	tccagcagtg	ggattgctgg	gtcaaatgat	ggttctat	169757647
				tttt	169757697

FIG. 1.16



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ttagttatttt	aagaaatctc	caaagtgcct	tccacagggg	ctaaattaat	169757747
ttatatattcc	accaacagtg	taaaagcatt	cccttttctc	tgcagccttg	169757797
ccagcatctg	ttattttttt	acttttttagt	aatagctatt	ctgactggta	169757847
cgaggtgaca	tctcattgtg	gtttaatttg	catttctctg	atgattagtg	169757897
atgctgagca	tttcaaaaac	atttttctag	aaaggctata	cagttttcta	169757947
ggttatggct	aagtogggat	agatttcac	aaagccatgt	tgtcagatat	169757997
ttaagaaggg	tacttgcttc	cctgcatgct	tgtttggtt	tagcggagg	169758047
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gactgtatct	ataagcacia	agtttgggga	ccagaacagg	tggatagaga	169758197
tggcaacatc	atagaagtgg	gagatgggtg	cagggtggca	attgctcaac	169758247
cctgtcccag	gcctgacttg	agccttagtg	agttagagag	agcaagagag	169758297
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gcaaaggtag	actcctgtgt	gaatcggtgt	ccctaggtgt	gctgcagctg	169758497
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aacatgtgtc	catggtggtt	gaattacagc	ttgattttat	aaatgttaag	169759047
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ggttcagccc	agaaaggcag	gacatctcaa	atggggatgg	attcaaagat	169759147
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gcaattgggt	gaaataatta	agttttgcct	aaagagttga	agtcaacaga	169759247
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tctatttttg	gcgtacagac	ccttctgcag	acacctgac	tcctttgggt	169759847
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FIG. 1.17

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cagccctcag	gagaccttga	gaatatgtgc	ccaaggtggt	cagggcacat	169760347
cttggtttta	tacatttttg	ggagacatca	atcaaataca	tttaagagat	169760397
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tgttctaaag	attgatacaa	atcctttcta	aaaacaaact	taggaatata	169762197
ctatacaatt	taaaatgtgt	tcttatttta	aatagaaaca	ctttcccat	169762247
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gctataaaga	tactacccaa	gactgggtaa	tttataagca	ccagaggttt	169762797
aattgactca	cagttctgca	tggctaggga	ggcctcagga	aacttacaat	169762847
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FIG. 1.18



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gacccgtgacc	ctttgaagtg	gttactgtgg	ttatccctaat	tttatagatg	169763247
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gctacttcct	gtgggcattt	acaaagacac	actgcagaga	gaggcttttt	169763797
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cccaggagtt	ctagaccagc	ctgggcaaca	tagtgagacc	ccatctctac	169764147
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cagctggcca	cggctgccac	agtgtcattc	atttacttat	tcttcattca	169765397
tgtaattcat	tatttcactc	atttttcaga	agagaacttt	gaggctcagg	169765447
aaagttaggt	gatttcactg	tcacagagca	tttaagtcac	agttcaatta	169765497

FIG. 1.19

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ttattttatta	aggggtgctg	aattaggtgc	cctcgttca	cgtacgcctg	169765547
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ggaggacagt	ggcttttgag	tgtataggtc	tccttcccaa	ggccaagtgc	169766197
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gattcctcct	actacgccgg	ctttgggtga	ggagctcttt	gaacacagtg	169766397
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gcttcccact	tcagagcctg	tggggaagaa	gcagagtggg	gctgaggacc	169766547
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ctaactctga	acacaaacat	gccagagagg	tttgaattag	aactctccag	169766697
agaggaaaat	taagcttcag	gttttagttt	ttaaaatgtg	catttattta	169766747
tcagtgtaaa	tagcttaagc	acagtcttaa	aaattggaaa	ctaataaaaa	169766797
atcatctata	attctaccat	ttaataaatg	tactatgtgc	atttataaat	169766847
ttttttccaa	gatttttttt	tccttttgta	aatgggtttt	ctgtacatag	169766897
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cctcaaaatg	tagtggcacc	agatgctcag	gattctgctg	agtgggtcct	169766997
ctgggctggg	ctaggctgat	ctcagctagg	atcactcatg	tacttgcagt	169767047
cagtcgggtcc	caggggcctc	ccttgtgtca	gggtgggtgcc	tggtatcat	169767097
gggtgacagg	ctagtgacta	tgccatgtgt	ttctcagcag	gctagacgag	169767147
cctgttctca	tgggtgacaag	atgcagaagc	agtagggaaa	gcagaagctg	169767197
caagtcctct	agaggtccaa	gcttgaaact	cacactgtca	cttacaagca	169767247
tttgattggg	ccaagcagat	catgaggcta	gcccagactc	agtggggtaa	169767297
agaaagttta	tttcttgatg	gaggaactac	aaaatattgt	ggccattttt	169767347
gcaatctatc	aggactgcgt	gaagtttttt	acctttccat	ttttaattta	169767397
ttatcgcatt	atgatttttt	ccttactaat	acaaaggatt	catgacatta	169767447
tttgatagat	agacagacta	cagttttact	aagcatctcc	caattattaa	169767497
acataaagat	gacttccggg	tctccagcac	ataaataaag	ctgcatggaa	169767547
catcttgatg	cagacaggta	tttctgtaat	tttgattggt	tccttgggat	169767597
agactcccag	aagtggattc	aaccaggcat	aaatggtttt	tgatattctg	169767647
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aaaattatgc	tgttttacct	ccagccacag	agagaaaagg	gattttcttt	169767747
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gtgggtgcaat	ctoggcatac	tgtaacctcc	gcctccagg	atcaagcgat	169767847
tctcctacct	cagcctccca	agtagctggg	actgcaggca	ccaccaccat	169767897
gcccagttaa	ttattagtat	attttaattt	tttagtagag	acagggtttc	169767947
gccagggttag	ccaggctggg	cttgaattct	tgacctcagg	tgatctgctc	169767997
accttggcct	cccaaagtgc	tgggattatc	agcctgagcc	gttgtgocca	169768047
gctgagaaga	gggattctca	gcagcagcct	ggactcaggc	atccttgca	169768097

FIG. 1.20

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ggcctcctgg	cttctcttga	ttcattttgt	tttcoctggg	cctcatgcca	169768147
ggaagctgga	atgaagcaca	actgggcaga	cccttccttg	ggcaaaagta	169768197
ttagtgctctg	tgggtcattgt	tctctgacag	tcagttctgt	ggtacataac	169768247
gattggttca	ggccctgtg	atcttcttgt	ccatgtgaga	ctggatgagg	169768297
agtctcctgg	accagtgatg	gtaacacctg	cacctgagc	tggggagcag	169768347
gtggatcac	agacgagctc	ccatcccagg	ctggctctca	cagtcccttt	169768397
ccacagctgt	gttaccagcc	cctgctcaat	catgtttcca	tgtgattctc	169768447
atggaaacct	tgtgtgattg	gcaacaccaa	gatttgtccc	acatccagat	169768497
agagactagg	ggctagaata	cctctccctt	gcccgtttct	ccgggcttga	169768547
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ttttacttcc	tcagttccct	gtttgtctaa	aacaccagct	aactgataat	169768647
tgcatttata	gttactatgt	tttctccta	gataacaagc	ttcattgaag	169768697
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agcagtgagt	tgggtgggaga	gagattgggg	gtacgtttat	ggaaaatcac	169768797
ggatccgtgg	gtctggaagt	taaaagagga	ctggcccttt	gagcaaataa	169768847
atgaagagta	agctggagag	cttgtgtgta	tagcatttga	gggcaagggc	169768897
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gtaaatgtgg	ccaagttact	tgactgctct	gtgccttgg	ttttccatct	169768997
ctaaaatgga	cataataacc	catacagggt	tattataagg	attttgacaa	169769047
gaaatggcag	gtagcaataa	ttacacctac	tgaattttaa	aagtggctca	169769097
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cagcaggggc	cagtaagctt	actagccctc	ataccagga	aagcggttta	169769197
tttctcctcc	cacatcagca	tccctctctt	cttcctatgt	cggccccaga	169769247
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gggtccttgc	acagagagga	atctgcttcc	tgcttagagc	ttggagaacc	169769347
ccaggccttc	cgcattcatg	agggtccaagg	ccaggcagga	ggcaaggcca	169769397
tggggccaaa	tctgtgccat	gagtgtcaac	agaagatccc	aaagctggag	169769447
accccaaata	aaaaccccaa	gagatgtggg	ggcatcagct	tcctcagact	169769497
caaccagca	ccattcagca	gccttcaaga	ccaagaagtc	catactgttc	169769547
tcttgctcgc	aagatactca	gcctatgaaa	tcctcagcta	atggagtcc	169769597
cagagcagca	tggagccttg	ggggtgattt	tgaggaaactg	acactgggaa	169769647
acagcctagg	gtctgtgggtg	cgcagtgggtg	gcagcagccc	ttgcctgtcc	169769697
acaccacgga	ccagctaacc	atagacgagt	taagagtga	agcatgctac	169769747
tgctagcggg	ggaagctgca	cgtgccatgg	ttaaggaccc	cagggtggg	169769797
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ttaaatgcta	tgtaaagata	gggaggtttg	aaatttttac	caacaatccc	169770047
aatccttgaa	cacaaagact	attatcata	ttgtgactgt	tgaatatattt	169770097
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ccaaccaccc	aacacgcttc	ctgagggcag	ggcaaaacttg	gacattattg	169770297
acagaacaag	tgcccaatct	gaaaatgtgt	cacattcctg	ctcaggttcc	169770347
aaacatgtca	tagcggattt	atgggtgtaa	attatactgt	ttgctcaaaa	169770397
cactacctca	tcttcagtgg	cgtagtga	gtgaccttca	aactatgggtg	169770447
gcactcttagc	tataggggtg	tccctcaaaa	agcatgggct	ttgttgaagc	169770497
acaacttact	ctgctgtgtg	acttaagtca	aatagcttaa	tctctctcag	169770547
cctcaacttt	cccacctgta	acctgggcag	gataatagtt	tttagcttct	169770597
agaacagatt	aagggtggta	atatgagtgg	accattttaga	gtagctcatg	169770647
agataaaaact	caaagtctag	ctgttgtcat	ttggctgtta	atgttatctt	169770697

FIG. 1.21

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gaaatccac	agtagtcaat	agtggatggc	attaattgga	ggaggggaatt	169770747
gttagataaa	agatgggttac	tagatgatag	aaggagattc	aaattattga	169770797
ctggcagaga	actgtttatg	gaagagttct	tggctcgtaa	gagcctcagt	169770847
tagatagagc	agggccattg	gagggagacc	agttgcttga	atgcaagctg	169770897
ttaatcctca	gggaatctcc	atggctcagc	cagatcctgg	tctgtaatct	169770947
gctctcacca	cgggctgact	gaatgagctc	attgtcatgt	aattttaatag	169770997
gagccaggtg	tctgtgattt	ccaagagcgt	gagcagaatc	atcctgcacc	169771047
ccaaactagg	agggggaaaa	acacctcgca	gaagcacact	tgtccctagc	169771097
tgctttccat	gtgtcagaca	gagaggaaat	tgtccaattc	caaattgcatt	169771147
cctatccttc	tcgggcgatg	agagaaagta	attggcatag	tttgagtga	169771197
atgaaggtgg	tggtttgggg	tatttggtat	ttcttattgg	cataaaggaa	169771247
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gccctcatgc	catctcctga	agttgaaatc	tcaaacttgg	ctgtgtcacc	169771797
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tgccctcagg	gattagacct	ggggtcacaa	tgtgtgcaat	gtgggtgtga	169771947
actcatgtgt	ccagttgctc	tcagcaagcc	aacaagttca	agtcacttct	169771997
ccatcccacg	gctttgtctc	tgtaacttgg	gaacaaacag	taccccatga	169772047
ataagttcac	agaggcaggg	ttgtgcagta	gtgacacgca	caggctcttg	169772097
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tctaagatcc	agtgtaaacta	tcaggaatcc	tgggcaaaagc	catcagagtg	169772647
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caggggcacc	tgcatgttgt	tcttgacccc	tgaaatggaa	taggaaggct	169773047
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ataaatacaa	acaatggccc	atgtctctgt	gggcaatgtg	ctctggtttg	169773247
ggaggaaggg	agaaaattaa	attataatgg	gaaaatataa	attatttgga	169773297

FIG. 1.22

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tcaggataaa	aaggaagaaa	tcagtggtgt	ctgaatgaat	ctcagtgat	169773347
ctgtcagaag	agttgtgagg	ttggctcagt	gtaggtgcac	aaagatgcct	169773397
aggaggatgg	tggaaacaggg	ccccacacag	acgcaggtga	aactccagag	169773447
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ctgagatgag	agatgattgt	atltgtcaga	ttttctatca	aagtaaata	169773547
agatgggtcac	ccaccagtg	aatgtgattt	tagcaccttc	cctggtgcag	169773597
accctcccag	gtactggagg	tttagaggga	aacagagcca	gctctatgtt	169773647
gccctcaagg	agcaccacaga	catatcatgt	ggccaagatg	attgcatcca	169773697
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tggttcaaac	ccaggggttc	gtaccttcaa	agaccaagtt	ctcatccact	169773947
gtgcagacaa	atgttctgac	agaggacagg	caggggacag	agagtgcag	169773997
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tctgtgtcaa	cctggaaggc	ttcttgagg	tggatgtgtc	tagtggaaac	169774097
ctaaaggaaa	ggtcttaaat	gctacactaa	ggaatttgga	ttttatcaac	169774147
atltttttttc	ttttttgagc	agaattcaga	catgattata	tcccccaac	169774197
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cagagaggggt	tgcagacact	taatataaga	tgtagtctct	gccctttcct	169774297
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aagtaacagt	gtcaataaac	caatgccgag	cgccaaataa	aagtgcagtga	169774397
gtaggtgagt	ggaggtcaga	agaggggggca	gtctgggctc	tgggttggtc	169774447
aaggaaggct	cccagggtag	atggagagag	agaggttgga	ggggttatgg	169774497
aagattccag	aaaggggtgca	ctttgagggc	tggggcctag	tgtttggcag	169774547
tactagttcc	cccatgctta	gcagagggcc	tgcccatagc	aagtgcaggt	169774597
gcatgctggc	tgaatgaata	aatgttggtg	ccaatgaaaa	gaaaggacaa	169774647
acggttgaga	gatgaggtcat	aacaaacgga	ctgtgggttg	cagggatgtg	169774697
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acaaacaaaa	accagcaaaa	tgccctcctg	aggctccttg	agtgcgtgtc	169775197
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cattagcttg	agcaccagag	agcagaccaa	ggcaggtcct	tggttcctgt	169775747
gccgacctgc	attgcggagg	actgcggggg	cttggttagat	gaagcctggc	169775797
ctgggtcttt	cagggccctc	tggctggggc	caggaggcac	agctgcagtg	169775847
gacactttca	aactcatcgt	gcctggcctt	ggcactcggt	gggctcattt	169775897

FIG. 1.23

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ctgggtcataa	tgacaccttt	ctaaacatag	ctacacaaaa	ttaaaatgtc	169775947
acagtgc aaa	tgctgcagct	gtgtgggtact	agaaagaaca	ctaggtcttg	169775997
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gaatgggtacc	agtagctgtg	tcacagactg	ttgtgaaggc	cgaggaatta	169776147
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ttgacctact	cagaagccac	tcactttctc	cttacatggg	gaaatcagca	169776397
aaccacaacc	atztatgaat	cctgcatgtt	cccctggctc	tgtccaactg	169776447
tatctgctac	cattcctgag	tggaagttaa	aaaaaaaaaa	aaaaaaaggc	169776497
agagcaagtt	gaagatggga	aagaggtgac	ctaaggtgac	aaagagtcaa	169776547
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tggagtgtca	ggagccctgc	cttaggaaga	actctgagac	tggctccaga	169776647
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caggcaaggg	agaagaaact	atgggtctgta	tgtcatatct	aatattctcc	169776747
cttatatcta	aggtaccctc	tgctgtgaga	catgcaatca	acccgatgaa	169776797
gcttttttagg	aaaaagtcta	ttgtttacatc	aagtttaacg	taaagctgcc	169776847
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agggcaaatg	ctgagctata	accaaccacg	ctgtttctgt	ccctcacttc	169777047
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tgaagttttt	cttttatcac	tctattaatg	ctagatgttg	actattgaat	169777247
ggatccaagt	ttcaggaact	tacaaaatgt	gtgtgtgttt	gaaagaagga	169777297
aatcattact	tgctatccct	tctctatcaa	aatctacttg	agcttttcaa	169777347
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tttttctctc	tttttctgtg	agtagacgcc	atgataatca	atcgggataa	169777697
cccacgagga	cgttggtttca	ttctttctga	gtgaggggat	ggggctgata	169777747
gaggaagccg	gggaggggtt	tgccctgctga	tttcttccctg	cttttgtgtt	169777797
tgtgtttgcc	gtctgcctgt	ccctcacatt	tcctcagtg	tgttcctatc	169777847
cttggatccc	taatcctaca	gccacaggact	ttctacaacg	gtactactga	169777897
cattttggat	gggataattc	tttgctgtgg	ggggactctc	ctgtgtgctg	169777947
tgacatttag	caatatccct	ggcctctacc	tactggatac	cagaggcacc	169777997
ccccaccccc	agccgtgaca	actaaaaatg	tctcaagaca	caccacccag	169778047
gtgagaacca	ctgcttagcc	tccccgggga	acatggctgg	ttccttcttt	169778097
ctgaacagtt	tcagaaggaa	catcaagtct	gcaacaagtc	ttctgacttc	169778147
atgggtccaca	ccagtgtcag	gccaccgcgc	ctatcaaccc	tcagggtca	169778197
tgtctccaag	gagctctctg	atcattccct	gggtgtctctc	tcgtttgctg	169778247
tctgccccctc	tcccctgggc	tatgagcgcc	acaggagtgt	tttctatttt	169778297
gattatctct	ctatccctgg	ggcccagaag	tccttggcac	tcaatagggt	169778347
ctccagtggga	ttaaagggtgag	gacgaggtga	ctggggggagc	ctccctgtgg	169778397
agtgcagctct	ccatgccatg	aaattgccag	ccctgggaag	tcatgaggaa	169778447
gaacactcca	ggcagagggc	acagtcaccg	cacagctctc	aggcaggaac	169778497

FIG. 1.24

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aggtttgcct	tgtggaaggc	tgctggggag	gagaggggag	cgggattgga	169778547
gaaggggtgct	ccaagagcca	gaaaagctag	tcaggaggcc	acagtgaggg	169778597
gtgcaaaactc	agttccagga	gtgacaacaa	gccctctgga	aacctcccag	169778647
atgtcccaag	gtccacccct	ggcccaactct	cactctcctc	tctccttgct	169778697
gccagcctc	actctgggaa	ggctggggag	gattcctaaa	tctggtctga	169778747
actcctgagg	ctgaagccag	agctgggtgtg	gcccccaagt	catatctcag	169778797
gggtgggagag	agtccttcca	tcaaggaggc	aacgctatga	gggcagctca	169778847
gtgctcagcc	cacccctcta	accctcatgg	gcgggccctc	aatcagaaac	169778897
cacaaattcc	aggtcagtc	agggaaggcc	tggatcctcc	acttcoggct	169778947
cctcccgga	gtcagcttaa	agaaatgatg	cggaggaatg	atcactgaag	169778997
agactcgtca	ttcctgggtca	aacctatgctg	gaggtcaggg	gtttgttaac	169779047
tcagccttgt	cacaggggcc	ttcccttcca	cctcaatgct	acgacagagc	169779097
tgggtgttgaa	ggctcttgac	gaaaaagcta	catttctgca	tttaaaatgg	169779147
agaagatcag	gccactcagt	atctccggtg	taagaagaca	tttggcaata	169779197
gtaacagcta	atTTTTTTT	atacttaccg	taactcattt	taccatttcc	169779247
ctgcctagaa	aaaaaaaaaag	tgcagctcac	tgccagcact	catttcttgg	169779297
ggcaaacagg	aaataagtta	atcttaacaa	caacctgtga	aggtgcatag	169779347
ttttattatc	atccccattt	tacagatggg	gaaactgagg	cagtgaagtt	169779397
tagtaatttt	cccagattca	ctaaaatttc	taagatatgt	ttaacaaaga	169779447
aatccaccct	ttaactctta	aataatatcc	tcttttttaa	attaatgcta	169779497
gaatatgggtg	caatatcttt	ttaattgagt	gtatcttttg	ccccagcaat	169779547
tctaccacta	ggaactgagc	ctaaggaggt	ataaatattt	agttagaagg	169779597
atgcagtatt	atntagtatg	tggaaactcaa	tgagaatctc	cactaagagg	169779647
ggttatTTTaa	ataaaactgtg	atgcctccat	ataaatgtag	ctggtcaaaa	169779697
tgacatctgt	ttgtatgtac	caacataaaa	agacatctaa	atcatatatt	169779747
ttaacagaaa	agtcagaaat	aatcacattt	ttgtaagcag	tcatttttgct	169779797
tgaggactgg	gatttctatt	gacttttaaat	ttcttatTTT	cacgtgtcta	169779847
tagtctctaa	tttttctaca	atgaacatgt	actacattta	taataagaaa	169779897
gaaactcaat	aaaagttatt	gagtaaaaga	ataagcagcc	agaaatctgt	169779947
ctcttctggg	gaattagtga	gcctcttcc	ccttgagagt	agacgctatg	169779997
gctgctttgc	tggaaaccttc	catttgtccc	aaatgctcca	ctctctgcca	169780047
atgggagacg	gggtctatat	tcacctgggtc	ccttctgcgt	gaggccacct	169780097
tggcagaagt	cactgcccc	cccaaggcat	ctgacctgct	aaaacctct	169780147
tgctgtctgg	gttctggtaa	actccccatt	ccttgTTTT	tttgtgggta	169780197
tacagatagt	aaaagctctg	ctgcctgggc	cctggTTTTa	aatgccccct	169780247
ggtgttttct	ctatacgcca	ctgacacctt	gatcatgagt	caaataccct	169780297
gaacatagag	tagcatctgc	ttcctgttga	gaatccaacg	aatacattta	169780347
cctgattttgc	tctctcttct	tttcctaagt	cctaacttcc	taaaataaaa	169780397
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cttgcccaact	agacgtcttc	gtttgggcaa	ccacacagct	tataagcctc	169780497
ctgatgccca	ccacaggagt	cttatTTTgt	gctgccacgt	taaattctct	169780547
cttccatgag	caccactctt	tcactttcca	cccaactcaa	acctgaaaat	169780597
cacctttctc	cacccctcct	ttaatTTTT	acatctcatc	agtgcccaaa	169780647
acttctgaaa	tcaacctcag	taatgtttcc	ttcaaataac	cccttcccgg	169780697
ctgggcgag	tggctcatgc	ctgtaatccc	agcatttggg	gaggccaagg	169780747
tgggtggatc	acttgaggtc	aggagttaa	gaccagcctg	accaacatgg	169780797
agaaacccca	tctctactaa	aaatacaaaa	tttagctggg	cagggtggca	169780847
tgcacctgta	atcccagcta	ctggggaggc	tgaggcagga	aaattgcttg	169780897
aaccaggag	gtggagggtg	cagagctgag	actgcaccac	tgcgctccag	169780947
cctgggctac	aaagtgagac	tctgtctcaa	aaaaacaaaa	caaataccct	169780997
cttcccatca	tttctccagc	ccttgccctc	tcaagtctc	ctgactgggt	169781047
tcccttgggt	ccctgcttcc	ccctcagctc	gttatgtgtg	acttctgggt	169781097

FIG. 1.25



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aaaggttctt	aaaatacaat	tcagatccta	tccagtcctc	tactcaaaac	169781147
tgtgcccatt	ggatcaaaac	caaactctgc	aacattccat	tcagagcttt	169781197
aagagtactt	ttcagcctga	ggtctcctcc	tcaccactaa	cacccttccc	169781247
tccaatcaaa	ctgatccatt	gtacctacaa	aaagcccgtc	ccacctocta	169781297
gcctttgttc	acactgggtt	ctctgctgga	tcaccatccc	tccacatttc	169781347
caggtgtccc	tcaagactac	tcagcagcag	ctatccatac	aagttcctca	169781397
accctggctt	tcttgccctc	aagtaaccag	ttcatcctcc	ccagtcatat	169781447
agccctctat	ttacatttct	tttctggaag	ctatcatttt	tcacgtgcca	169781497
tttgagttag	tgtcctcgct	aagacgatat	tttctttgag	ggcagtaacc	169781547
tttcttatat	gtctctgtat	cccatgaact	tagcaaaaaa	caagggacag	169781597
aacaggtgca	aagtctacgt	ggttagtgaa	tttaacagat	cttcctaacg	169781647
tgtaaacgtc	ggtgtccagg	tgaatggaag	aagttagctg	agatagaggg	169781697
gacagacaga	gtcagtgctc	agtgtcgacc	tctgaaatgg	aaaaacatgg	169781747
ccagtcctta	ggaggctgca	gaggccaaga	ccccagtgag	gtttgggggt	169781797
tccacagcag	aggaggagct	gtggaccaca	gcaggacccc	gatgccatca	169781847
gcaggggagg	aagtaatcag	agaggtggag	gaaggaagcc	aagggaagtc	169781897
aagtaaacac	caaataattcc	ctcccgggtc	aatgctgtga	cctgcataag	169781947
ccaccactcc	cccagtcctag	actctaccca	tgggaagaagg	aagaagatag	169781997
aactctggat	ttgaatataa	ttctaaaata	accaaattta	tctgaaaatg	169782047
actaggctga	gttttctgct	tcaaccagaa	atggagcttg	gagtcagaaa	169782097
ttatgtgaaa	ttatagaaga	gaaagtcacc	atcttccatc	tctgagtcgt	169782147
atgatcattt	tagacataaa	attgtgcact	tacgatgtac	caagtgcctta	169782197
atatacgtga	tctcatttca	ccaggggaaac	tgtataattc	attgctttta	169782247
ctgacaaaat	tctgcaactg	aagaaggtgc	tgttaataat	tgcattggga	169782297
cgcaggcctg	agcaggccat	gatttgtggc	tgtcctacat	ctgaccctca	169782347
cagtatccat	gggagaaggc	agcatgttta	tgccccctga	cagctgggga	169782397
aaccaacact	taaagtgatt	aagtcacaag	tccaaaataa	atgacagagc	169782447
tgcagttcaa	gcccagggtg	tcatthacca	aaggccatgc	tcttttccat	169782497
ttgcatggga	ctgtgaccgc	tggctctacc	cagcttccca	gtgcgacct	169782547
tccccgcccc	ctgtttctct	tctctggcca	acggaaacac	aatgagacca	169782597
catatgtaac	attacatttt	ttcatagcca	cattgaaaag	aaaaaggaac	169782647
caggtaaaat	ccattttta	atgatatttt	atttaaccca	atacagttga	169782697
ggcttgaaca	acacagggtt	gaactgtgtg	ggtccgctta	cacatggctt	169782747
ttgttcagtc	tctgccaccc	ctgagacagc	agggccagcc	cctcctcttc	169782797
cgcctcctcc	tcagcccact	ctacatgaaa	acaaagagga	tgatgatctt	169782847
tttgatgata	cactttcact	taataaatag	caaataatag	ttctcttctt	169782897
tatgatttct	cgtaataaca	ttttcttttc	tctagcctca	tttactgtaa	169782947
gaatacagca	tattcccagc	tactcaggaa	gctgaggcag	gagaatcact	169782997
tgaacctggg	aggcccgagt	tgcagtgagc	caaaatcgca	ccattgcact	169783047
ccagcctggg	caacaagagc	gaaactccaa	ctcaaaaaaa	aaaaaaataa	169783097
aaagaataca	gcgtataatg	catgtaacat	ataaaatag	tgttaatcaa	169783147
ctgtctatgt	tatgggtaag	tcttccagtc	aacagcaggc	tattaggagt	169783197
taagtttctg	gggaatcaaa	ggttatacac	aggattttga	cggcatgggt	169783247
gttggcactc	ctaactccca	catcgttcag	ggtcaactgt	atattcaaaa	169783297
tagtattcaa	aatgtaatca	ataggaaata	gtcattcatg	aaatactgcg	169783347
tcttcttctt	ctccccccca	acccacttcc	tttgatttca	gtcttcgaag	169783397
tcagtgggta	ttttaacctt	acagcatatc	tcaattcaga	ttactcacac	169783447
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ctgccatctg	gtggacagat	gttccttgct	tgaaaaacca	cctcgaagga	169783597
aagtatcagc	atcagggaca	atagcacagt	gggcctcagg	atcagctccc	169783647
cggaaagagc	ttgggggttg	aggggggtgt	gttgctgagg	atgtccccag	169783697

FIG. 1.26



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agaagatgta	cagccatgga	gcaaactcaa	gtcacttatg	atgtcggcaa	169783747
accttggccg	tggtgcactc	ttgtttcctg	gttgcaaaag	gatttagcag	169783797
aaaatggtaa	ctctttttca	gaaggcatat	ttaaagcagc	tctttaaaaa	169783847
gcaggagttt	ctttcacacc	cagtttcgcc	atgtggttgt	gtgaagggct	169783897
tctccccaga	aatcatgtgg	tctctctttt	aattcacagt	aaaaaccttt	169783947
cttctgtctt	ggcccattat	ggctgctata	acaaaataac	ataagctggc	169783997
cttatatacc	atagaaatgt	atttctcaca	tttctgaagg	ctgggaaatc	169784047
catgattaag	agttggtgtc	tggtgggagc	ctgctttctg	gttcactgat	169784097
ggcgtcttct	tgctgtgtct	tcaccgaggg	gtagggacaa	ggcagctctc	169784147
tgcagcctct	tttctaaggg	cactagacct	atltgccatg	gttccagcct	169784197
catgaactaa	tcatttccca	aagtccccac	ctcccaacac	catcatcttc	169784247
atgattagat	ttcaatatat	gaatttgagg	gaggatagaa	acattgagac	169784297
catagcatct	gccaaagtgt	gtcttcctca	ctcaaattgg	gtaggtgtgg	169784347
ttattccaga	gtttcagtga	accaagacgt	atltttccaa	tgtgaataat	169784397
taattaagaa	cacttgatta	gggtcaatgt	tattctggac	ttctgaatca	169784447
ctccacacatt	tgaaggggag	ttttaaacac	aactttgtgt	gaataaaatg	169784497
atgtgtctgc	atctctccag	gaagcagtgt	ttggagctga	gatgacttgg	169784547
cagggagaag	aatccactgg	gacattcaat	aacttggcat	tgagagtgtt	169784597
ttcagcacca	tgctgtcctc	agaatagtgt	tagaatttat	ataaacacag	169784647
atgtgacttg	tgccctgaag	gagaatacag	tcttcccagg	agagacatgc	169784697
aaaaccatca	tagacaaaca	gcaagaaaac	agcatcaagg	atgtacatgc	169784747
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gaaaggaact	tggttctggg	ctcaactctg	ccaccacacag	ctgcgtgact	169784847
atgtctctgt	cacactgctt	ctcaggtctt	caactttatc	gtctcatact	169784897
gagcaagaga	cagtctggac	aatttatgct	tctagaatgg	ggagacaaga	169784947
agaaaagaaa	gatagatacc	caaggacttc	agtgactggc	tcaggaagaa	169784997
ttactcagca	gtgagggggc	cagcatgagc	ccaggggcaa	gaagccggga	169785047
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cgttaatagg	caaaaattgt	tgctttaaag	aacctagaat	ctaaaggggt	169785197
ctttgacata	atacagaata	acaggtccca	gagattatlt	tacagaatgt	169785247
tagtacctca	tgatattaat	agatatataa	caaaacagac	ttctttgcc	169785297
caagacttct	cagtaccttt	aacattttat	gattttccca	aaggacaaag	169785347
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catgacgaaa	ccctacctct	accaaaaatc	caaaactcag	ctgagcatgg	169785497
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gcttgagccc	aggaggtgga	agctgcagtg	agctatgttc	acaccactcc	169785597
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ctagtcttga	cttttttatag	ataggggaaac	tgaaaagcta	agaggcaagt	169785747
ccaaattttca	caaagatagt	ggcagagcca	agattggatt	tttgggtcttt	169785797
tgactctaata	accagtgtaa	tttctttttc	tttcttgttt	tttttttttc	169785847
aattcctatt	atacactatt	taagacacac	aaacagataa	aaagactaat	169785897
acaagatatc	catgcaccac	cacctagtgt	aagaaataaa	acatcaccaa	169785947
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cccatatcct	gaatttgagg	atataataca	tgaaaattct	ggtggaattt	169786047
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tctaagttgt	ttcaaaaaca	aaccaaatac	cccacttggc	ccagaagagc	169786147
aaagattaaa	agccagcctc	gaggatcccc	agcttggcta	cctgcagctc	169786197
acagcatatt	ggaaaaattt	tatgaatcgg	tgaacttttt	cattctcaaa	169786247
tgggctcttc	agatgggtta	ttaattctgt	tagatgcggg	ggtgcgtctg	169786297

FIG. 1.27

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gctttattct	gtgtggaatt	tttggatgaa	ttcactgcct	cacccccctcc	169786347
cctccacagg	ccagatgggg	agccgggtgc	tgtataaatg	tttaattgtg	169786397
gctcagtaaa	aatatttgct	ttcagtagct	ggaagctacc	aaacggaggt	169786447
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aaggctgatt	aaatcaaatt	ccccatagt	tagaaccact	taaataaatg	169786547
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ccattaggct	ggacataaat	cattcatcgc	catcactgcc	gtcaaagcag	169786647
cactggctct	ttttcttctg	ctgctgacat	ttccattact	agggagcttc	169786697
tcagacatgc	tcttgggttc	cctgtcctta	cccaagtgcg	gggtagcagg	169786747
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tgaggcctat	ggaaatgaag	tgagctgccc	ccagagtagg	gaatacagcc	169786947
tgtatgtgaa	ctcaggtgtg	tctgagcctt	ggcaactcac	acaaggctgc	169786997
ccgagaacaa	aggggtgcac	ccaccccag	gctccacaca	cctcaggcct	169787047
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aaggatttgg	actccttttc	ctagtccaaa	tccccatcgt	ctctcccctg	169787197
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atccatcatt	cacccagtag	cctgagcgat	ctttttaaag	tagaagtcag	169787297
attatgtcat	tctcctgctc	aaaagcctcc	aatggcatcc	caccactcct	169787347
agaataaagc	ccaacctccc	accatggccc	tcaaggcctt	ttatgatatg	169787397
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agcttcaacc	tgtcattcag	acctcagctc	caagtcactt	cctcagaaag	169787597
gccctccctg	taccctggat	tgaaaacagc	cctcccctgc	acacgctcca	169787647
caccatagct	ctgtttcatt	tactttacag	cactgaacac	tgtctctatt	169787697
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gtagtaagt	ttcaataact	attacttaaa	taaatgaatt	aacttgtctc	169787847
attcttttcc	cctgcattcca	agttgggtga	acctgacct	ggccccttga	169787897
aagagacaat	ttgattctga	aaaccaattc	ttacctccag	gctcaggccc	169787947
catgcaggag	tctttctcca	ggtggcctgg	ccatgcagg	gatggcagtc	169787997
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gttcttgaat	tggctgcaac	tccaccctcc	ctcctgcaag	tgctcttcc	169788247
tctgccacgg	aagcctctgt	gccatgaaga	agaccaccag	acctctccag	169788297
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gttccttgca	gtaagtcctt	tcttctctga	accactgact	gatgcagagc	169788697
tcctccatgg	tagggactgg	ttctcttagg	cccctgtatc	ctcaggccca	169788747
gcatgcttgg	gaaaatgttt	gctaattgct	tgtgactcaa	aaggaatcac	169788797
acacacacac	acacacacac	acaaacacac	acacacagtt	tttaatatata	169788847
tcagtcatat	cagccccctg	aggcagctgc	tctgttccag	acaaaccctg	169788897

FIG. 1.28

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ttaataacat	tottatcctc	tttgtttcat	tttccagctc	aatttggaag	169788947
cctgaccttg	tcttgctttg	cctcctactg	agagttaata	ctgggacata	169788997
ctgaaggcg	aaggcttgag	tcacaaagtc	acagggataa	atcctagatc	169789047
cagcagttac	tgtctacatg	acactaagca	gattagttgc	cactgggact	169789097
cagttttacc	agtctgcaaa	atggagctat	cagccgcata	tagcactagg	169789147
ggcgctgtga	gcattggagg	cagtctgcac	acagaggctt	aacacagtgc	169789197
ctgagcttgc	aggtgcttgg	taaattggcaa	ttgctgtcag	cattgtctga	169789247
tttacctgaa	ggaacagttc	acactccacc	cagattttca	ctgcagcagc	169789297
caagaaagaa	cttctgggaa	agcatctgct	tccacccaac	tcccaagagg	169789347
ggttcgtaga	gggtggagct	gagagcccg	ctcccctacc	agcctgcaga	169789397
aagaaagcca	tgttttggcc	tcaggggagga	gaaacccaga	taaaaaccac	169789447
cccatgtgca	gcctttgctg	ggccacagga	ccagctccac	agggagaggg	169789497
aagaggcgcg	gccgcaggac	cagctccaca	gggagagggg	agaggcctcc	169789547
tttcaggggt	ggggagctga	gggcaagaca	gaccttttct	gactcagccc	169789597
aaggaggggt	ggagcagggg	ctgcaggttc	cctgctttct	gctacaacac	169789647
agggtagggg	agagtcattg	cctcccagag	cctctgcagg	ttcacctgcc	169789697
aaatggaaat	aatagcatcc	tcctctgcaa	gtcacagcct	taaagagggtg	169789747
ctgagagtca	ctagttagac	ccaagccagc	tgtttctggt	gcattaggac	169789797
tatcgaccag	aacccttgca	ttcccagccc	ctcctgcggc	ctccaacgac	169789847
caggagagaa	aggcgtaagg	tgtaagactc	tgggcccagg	tctggcagct	169789897
tatggccact	cttttcttgt	gtctggacag	gagcattata	gctacaacca	169789947
tctcatctaa	tctcactgct	tgccctatga	ggcgggcatt	cttatttccc	169789997
cagttttgag	ataggcacag	aaaggggaag	cgacttccca	ggttcacatt	169790047
gccagtaagt	ggtaggacta	ggccctgaaa	agcacagcct	gccatgggga	169790097
agagaattca	tcccagctg	agaaccactg	tatcctcacc	caggggttcc	169790147
cagccaatgc	aaacagggac	gtgaccagtc	tccactggtc	ccctgtacca	169790197
ggtctccacc	ttgcccggct	gctgctgggc	cccaggactg	ctcccaggct	169790247
gcacctgtgg	ggtctgccc	ctcctccact	tccttttgag	aagctgctcc	169790297
cacccttctg	ccttcatctc	aaaggaaagt	gtgctgccag	gcagctggag	169790347
ccagctggcc	cagagacaac	tcttcccact	acacttcctg	cagcatctga	169790397
gtccaacccc	caactccaga	gctggcaagc	tgcccagagc	ctcccagagg	169790447
aggcctatgg	gttaacttca	catttagtat	tttcagcata	tggtagaaag	169790497
aaaatagtgt	tggttagatgt	acaagtgtga	tttccccttt	ccagaatgcc	169790547
ttcctctctc	ctccacgtgg	tgagctccta	ttcatacttc	aaaaccatgc	169790597
tcaactattc	cctgcccacc	tgtttccttc	cactcctccc	cttctaattgt	169790647
gggtgtgtcc	caggggacaac	atctgtgttc	ctcagtgaag	ttgagagaag	169790697
cctaaatttg	ctctacataa	gaaaaaagaa	taaggaggta	aactggaaac	169790747
gggaggaggc	tgggaaacgc	agggttggtg	gaaggacttg	tggggatgtc	169790797
gtggcagcca	cctgagggtg	aggaacgtga	cagccagagc	agctatgctt	169790847
aaggggcttt	gccacagtgc	gaaagatagg	atacaaggct	ctcttcagtc	169790897
tctccatgaa	aaccacagtc	aaagtacaca	ttactcacc	atgctttgga	169790947
gctagatttg	ggcttaattg	tgtctttttt	tttttttatt	aaaacaatat	169790997
tccaggctga	tggaaattta	caacaaggaa	cataatatct	gacacaaaca	169791047
tagcctaagc	cttgatattt	atcatcttat	atagcaagag	atcagggtgt	169791097
tgagaacttt	agagcagctc	cgttatgtcc	aggctctggg	cggtttctgg	169791147
gattctgtct	gctgtcccat	cagtactcac	gggggtggctg	tgtctgctac	169791197
agacatcata	gcctcacgaa	accacctaca	ctaaagccaa	taggaagaaa	169791247
ggtgtgtgtc	accttcacct	tcccaccctt	tatggggggag	gaaaatatatt	169791297
gccaaagtgc	ccacctttcc	cttctcaatg	cccctttgat	caaagcctgg	169791347
ttctatgtcc	ctgccagctc	gcgggtgggtg	ctaggaaaga	aggtatctgg	169791397
ggtttgacag	tctgctgtga	gggctaaata	aaaagggcgt	gagaggtctg	169791447
ccctctgctt	gtactcctct	gctgaggggag	aacttgctgc	ttctggatac	169791497

FIG. 1.29

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caccctttcc	catcgtatga	tagcctgaag	tggtcagaac	ttttccatt	169791547
aatcacttg	aaccgggag	gcagaggtg	cggtgagccg	agatcgccg	169791597
actgcactgc	agcctgggca	acagactgag	actctgtctc	aaaaaacaac	169791647
aaacaaaatt	gactttctcc	cactgagccc	aaggtgcttt	cctggtaact	169791697
tctctttgac	ccagtcctgc	ctcctgcac	ttccttcagc	aaccctgttc	169791747
tccacatcag	ccaccagagg	gaacatctta	aaacacaggg	ctagactggg	169791797
catgccgttg	tctctgctaa	accctcact	gagtcaccag	tgtctacagg	169791847
ataaaatcca	agcttcacgg	cattggaggc	tcaccacagt	cctacttcag	169791897
cctagtctct	cttccttatt	cttcccctac	atatatatgt	atatatatat	169791947
atattctcat	actgtaggtg	aagcaactga	aatgcttttt	attcccctga	169791997
cactttttgt	ttttcaaatt	cttggtgtac	aaatttatgg	gggacatctg	169792047
cagttttgtc	acatgcatag	attttgtagt	agtgaagtca	gggcttttag	169792097
ggatccgtc	cccacaatga	cgtatatatt	acccatcaac	taattttctca	169792147
tcatccactc	ctccccaca	ccctcaccc	tccaagcctc	cattgtctat	169792197
tatcccaactc	tctacatcca	tgtatacagg	ttattttatct	cccattttatg	169792247
gggtgggaaca	tgtgatattt	gactttcttc	acctggcttg	tttcacttaa	169792297
gataatgaat	tccagtttca	ttccagttgc	tgcaaaagac	gcctcacaga	169792347
attttaaatg	cttatatata	tacatacacc	ccctttgtat	ttgcctacac	169792397
aaaactaaca	aacctttgtg	aaatgtaacc	tacaggaaat	atgatcatgt	169792447
ctaagtctgg	acatgaagca	gatgcaatac	acaaatccat	gaggtagacc	169792497
caggtatttc	agatcctgac	cttgatctca	ggtttactta	ttagaccaca	169792547
gaccaaagac	tcccactgat	gtccccacag	atttcaccac	ttattcctct	169792597
tgtcccacac	actctactcc	aaagtcaccc	tcctctagag	gatagtcacc	169792647
tgagatactt	cagcgaccct	gctcaccttg	gaaaatcagg	tgacaggaat	169792697
catcagttaa	gcctgtggac	agtaagcatc	tggttggtctg	gatgggtgtgg	169792747
tgggcggaag	gtaggaccca	ataggggctt	ttcatgggtc	cagcccaaaa	169792797
cctctgacca	tgccagtgc	tgctgaaggg	ccccattcca	tttatgggtcg	169792847
gggcccacatg	atttacattt	actgtctcag	gttcttcttg	taacactgtc	169792897
ttctccaatt	tttgataagc	caatgccctt	gacacttcta	tgttttgttc	169792947
aaattgttct	acttgcccag	cattctcttc	caccttctcc	agctgtcaaa	169792997
ctcctacaca	cccttcaaag	cccagctcat	gggtcctctc	cctgacaatg	169793047
attccagctg	aaggagatga	cattgctact	tccttggttc	ctatcatacc	169793097
cgggtatggct	agtgtagcac	ttaacattgc	ttgggtgctt	gtgacattcc	169793147
caaacgttca	tctgtcctca	aggatgggaa	cgtcctcatt	tcccatcatt	169793197
taggaagtgc	ttgctaacc	aaagactcag	ccctcatca	ggaaccagt	169793247
aaggacagag	ctgggaaaga	gttgtcatgg	gcatggggac	tatgtgaggt	169793297
catacgagct	tcctgggtca	cagaggtgac	ccacgaatgg	tagctgcagc	169793347
gttgattgtt	gcccctaact	ttactgtgtt	attactgatc	tcagcccttc	169793397
tcttaagtga	ccccttccact	agtctcatag	atgagcggcc	agcctgcctc	169793447
ctggatccca	gaatttgctc	actgtccacg	acttctgtc	atggctggga	169793497
acattcaggg	aggatctggg	cccactcgta	ggaggggaag	acaaagagt	169793547
ccatccctcc	aggccctccc	ctcctgcagg	acagatcatc	ctgcctcact	169793597
ccatctgcag	atgctggcaa	agcacattcc	agccctcgcc	tctgaggcag	169793647
agaaacagat	tccaattaag	ggacttgccg	aaagtggctt	cattttacaa	169793697
gcaattgggt	tgtgaattga	agcgggcatt	aaagtttaca	agctaggctg	169793747
gcggaggagc	cagaaggcct	tgctgccact	gcctgtcagg	agacatcttc	169793797
tccagttact	caacaattgt	gtggagtgag	tgaggagtgc	gcacgaatcc	169793847
tgccctccat	ggctgatggg	ggaagaaatg	tccattcatt	cgtcttctta	169793897
aaaccaagga	tcaggctgct	ggagggcaca	ggatcatctc	tctcctgata	169793947
ggctttcccc	ttctctagcc	ttatgtgaga	atctggggga	ttttaggtgg	169793997
tggtgagaaa	atggggaaag	aaatcacatt	cgttgacctc	tgcttacagc	169794047
tgggatcccc	acgcagctga	gaaattttcca	ggaaattacc	tgggttcaat	169794097

FIG. 1.30

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ggaggaactt	aacacttcaa	gctgtcacct	ggtgggaaag	ggtggtggca	169794147
agaagtaaca	agatctccca	aatggatcca	accagagaga	aggcctcctc	169794197
atttccttct	cagccaagcc	cacggggggc	ctggaagaca	gaggttgccg	169794247
gggcatccag	ggtctacacg	ggctgagctc	cccagacctg	gtgcaagggg	169794297
gccaggcatt	cccgccaaag	ctctgccacc	taccagcag	gacccatgag	169794347
ctcagcacct	ttctggactt	gaggagatgg	gtctgggttt	ggccttttcc	169794397
ctccagactt	ccttctgtct	ctgcctctcc	actgacacct	gcctctgctg	169794447
tccccagga	cattccactc	tcttctctaa	ggctcaggcc	tgaggggttg	169794497
ctggtgggca	gattccatct	catggttgag	ctgtttggcc	tcaatggcat	169794547
tttatctctc	tctctctctg	tgtctctctc	tttctctttt	tttttttttc	169794597
acattgagcc	atcttcttac	agctgaggtt	ttcatataaa	aaagcaagtt	169794647
gctggtttct	ctttaaaagt	agggcaatct	ggcagttctg	ggcttggtga	169794697
aaaacaattc	ggtagagcta	aaaacagggg	cttctgataa	agcctgagct	169794747
cccagcagcc	aaaggactta	tcacccca	aaaaaatccc	ttcctgcact	169794797
catttatatc	aaccctgcc	cctgcagaca	cgtattgtag	gttttaacta	169794847
gaaacaagag	gattagcttt	atttaaacag	caaaactgct	taaatgagat	169794897
aatatatgta	ttgggaatgg	tgctggcac	ctaacctaat	ccttagttaa	169794947
ttaatattta	ttgagcaaat	catcttgatt	attaaaaaga	caggccagct	169794997
ggacacaata	agaatgctag	ctcagagctg	gcacttgagg	gttcggtaga	169795047
atattcatgg	cttggagggtg	ggggctatga	tacgagccca	tataatcaga	169795097
gaagttcaga	tgggaaatga	gaaccacttg	gtagcctaaa	ttcagagaaa	169795147
ctaaagccag	cctaacgctc	tgaagctggc	aagtgttcat	ttttggaaat	169795197
cagaaagtga	tgatgtgtta	tccaagaga	ctcctgggac	aagatgcagt	169795247
gagcagccat	tcacaaagac	taccttgaa	cgggctcttt	ccctacattt	169795297
tggtattata	tcctcgctac	aaccttctga	ggtggaaatt	aatatcccca	169795347
ttttacagat	gcataaactg	tctagtggag	gtgacagata	gtattgacat	169795397
gaccagaaga	ataaatataa	atgagataaa	ttctctctga	aggaaaggaa	169795447
tagggattta	caatggtgta	aaacaaagga	agtggggcct	ggtctaagcg	169795497
atcagggaat	gtctctttta	agaagtgaca	tttaagctga	ggtctaaagg	169795547
attagatgag	tgttaaatag	gaggagactg	ggcaggaggg	aaatcttctc	169795597
catggctctc	aatccagaca	cacaatttga	accacctgag	gttcacaaac	169795647
acaaagaaag	tatcgtgacc	tgatacagtc	ccagtcta	taaatcagta	169795697
gaaccaggt	gccgatgttt	ttgtttcttt	ttattttatt	tattactatt	169795747
ttttgagatg	gagtctcgct	ctgtcaccca	ggctggagta	cagtggcaca	169795797
atcttggtct	actgaacccc	ctgcctcctg	ggctcgggcg	attctcctgc	169795847
ctcagtcctc	tgagttagctg	ggattacagg	cgcccaacat	cacacctggc	169795897
taattattct	attttttagta	gagatgggat	ttcaccatgt	tggtcaggct	169795947
ggtctcggac	ccctgacctc	agatgatccg	cccgcctcgg	caccccaaag	169795997
tgctgggatt	ataggcatga	gccactgtac	ctggctggta	ccaatgtttt	169796047
taaaagcttt	atgggtgaac	cactgaaatg	aaacaaaaag	taaatccaaa	169796097
gctcatatac	tctagccaaa	caatagccat	taatagctat	taagtaaata	169796147
gaggagatgc	tcagtgataa	tgagcaggta	gatcatcagc	atccttgtca	169796197
tcaccactac	atctgcctcc	tccagatcat	ttggtagcca	agtccaatgt	169796247
caaaggaata	aaggaaatct	gcctctgttg	agggcttgct	gtatgtcacg	169796297
cactatgcta	aattcttcac	tgtttcattt	aacgtttacc	gaaaccctta	169796347
ttatttttaca	aatgaggacg	ttgaggctca	gaacaaggca	ccaatttacc	169796397
caggatttca	cagctcatcg	gggcagtggg	ggaccctctt	ccaggccccc	169796447
ctggctgtag	agaccacact	ctttcctgtc	tccatgcaga	ggggcctcct	169796497
gctcacttta	gctcccattt	cccagcctga	ctgccttgat	tgggcgcgat	169796547
ttctttgttc	tgacctcaaa	aagagttttg	tagatttgtg	cccacttttc	169796597
tcatcacgct	taagaaaagt	gaccaaagct	gaaccaagct	atctagggtc	169796647
aaatgctgct	tactggctat	cgggccccaa	actatctgtg	gaacttcttt	169796697

FIG. 1.31.

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gagcctcaat	tttttgtttt	ctataacatg	ggaataatat	cagtacctcc	169796747
ctcataagtt	tcttatgaag	attaagtatg	tatgtgttaa	gattcatatt	169796797
aagtgagaat	tacgcatgta	cgcataatac	tacaagatta	agtatgtatg	169796847
taagcatata	tatatacaca	cacatttaga	atagagcatg	aaatatagcc	169796897
agtgttcagt	taatgtcaag	tattgttaat	attatcctat	gggctggagt	169796947
gagaggcctc	ctgggggtgt	tgctttccag	cccccaatcg	ggtggcatcc	169796997
tggatagggg	atcatcatac	ctctccccag	gagatcagga	tagggaattg	169797047
taagagcact	cagggtggag	gtaggatgtg	caccaggga	gctcaggcag	169797097
gaagctgctg	tctttcctgg	tctctgcaga	ctaggagcag	cagccaggga	169797147
cctgggttga	ctgggggacg	ggtcgggtgg	tgggggtgaga	tgactatcac	169797197
acctcctcta	aaaacaagat	ggggcctggg	gcgctggctc	atgtctgtaa	169797247
tcccagcact	ttggggaggcc	gaggcggatg	gatcagttga	ggtcaggagt	169797297
ttgagaccag	cctgggtcaac	atgggtgaaac	cccatctcta	cttaaaatac	169797347
aaaaatcagc	cgggcggtgg	ggcacgagcc	tgtaatccca	gctactcggg	169797397
aggctgaggc	aggagaatca	cttgaaccca	ggaaggggag	gttgcagtga	169797447
gccaagggtcg	tgccactgaa	ctccagcctg	ggcgacagag	cgagactcca	169797497
tctcaatcca	tctatcagta	aaatacagga	tgggaaggga	cgcccagctc	169797547
tcagtcaact	gccagcccac	ggccttggac	gccactgatg	tgagcctgtc	169797597
tgggctgggg	cagaaggggc	cagcgtcagg	tcctcagaca	atttcctcct	169797647
ggtagcctgg	cctgaggccc	acccaaccca	gggagccggc	cctggccagt	169797697
tgagccaggt	accacctggg	gccagcaga	gggcagcaca	ggccacaggc	169797747
tggctttttc	taggtgaaat	tttgctacaa	cgtgtagcct	cttgggttcg	169797797
gtgtctcccc	tgtacttctt	tgaggccggg	agaagtcccg	gacattatca	169797847
cagacacctt	gcctcatccc	cagcttctga	ggtctttctg	gactctgtta	169797897
gcatatttca	gaggttcaact	gcaaaccaga	aacgggactt	tgagcttgtg	169797947
ttccaggggca	gagggcccca	gcgcctgtag	gtgcagacag	cgcaccccca	169797997
acacccccga	gtttccgcct	cctcatctgg	agagcggggc	tggacaggat	169798047
ggtttttggg	gcttttttgc	aagctcaccg	gggccaagtg	agctatttcc	169798097
ccttgccatt	ctctcccagg	aggagaaggc	ataagatgat	gctgaaggca	169798147
caggctctgg	aagaggacag	ggccatgctt	attcctgcct	tgttatgtga	169798197
ttatggacaa	gccttcactg	acccttggag	tgatggataa	aatccgtacc	169798247
ccacagggtt	acaggagaag	taagttaggg	accacgtgca	cggagcccag	169798297
caagggtgctc	aggaaacaat	gctattgttt	ttcagggttac	atcttgggga	169798347
gaccacccag	aggaccttct	ttcaaggaca	ggtacctgga	atttctctcc	169798397
ctttcctaca	tcatcttctt	gttttcatgc	gcaggggaggc	caccactacc	169798447
tgagccagac	cactcccttc	ttaagccagg	gcctgcaa	tgctgcagca	169798497
ctgccccctc	gatctcaatc	agacaccac	attcctgccc	accatgcccc	169798547
aagcccttca	ttgaccaaga	ccctggcctc	gtcccaatcc	tctgtaaagt	169798597
acacatgogt	cttcaatcca	ccctacagga	ctgtggagcc	gagaagatgt	169798647
ggggctgagc	atttaccttt	ccataagttc	tccagggggt	tctgaggccc	169798697
acagaatcaa	agagccactg	ctctaggcaa	tgagatagta	ttctaaaaca	169798747
attaatgaag	gcccattgatg	gggacaggag	agccattatg	caaattccgg	169798797
ccattcgagg	ttattaattt	gcaggagaga	ctgtagacgc	tgggtaaaga	169798847
atgccacaaa	tattaggcag	tcaggaggct	accctgcagg	gcctgttcct	169798897
gctccgcctg	gtgagcagaa	aggtctcagg	gaccagcttt	aaaggatgac	169798947
aggcctccca	ctgggtcaca	gggcacagct	gccaggactg	aggccagaat	169798997
gaaggcgatc	gcccattcgg	ctcagtgggt	ctcagtcttg	ggtcagcact	169799047
ggaatcccca	ggagggaaca	cggaaccccc	gagagctggc	tccgccccta	169799097
gagctgacct	cagtaaatct	gagatgaggc	cagagaaatt	gcatttcgac	169799147
aagttcccag	gtgttgcagc	gcagggtgtg	gcatgcatgc	atgcatgtgt	169799197
acttgtgtct	gtgcccgtgc	atgtgtgtgt	tcccctgttt	tctgctttct	169799247
gcagtgtttt	agctcagact	tcctgattgg	ggtcccatcc	ttgaccagag	169799297

FIG. 1.32



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gcccagtcta	gacctagaag	aatactaata	catgcccagc	tgttttagagc	169799347
ccacaagccc	tctcatggcc	cttgtttcca	ggccccataa	cagccccata	169799397
agtttgtttt	aaaagtgcac	ctgtagggga	gaaaagattt	ctttcctcat	169799447
ccatcactag	gttcatggct	gaggcacctg	taacaaaaga	cagactcaca	169799497
agagaaaagc	aaccaagtaa	tttaagtttt	gtgtgacatg	ggagccttga	169799547
gaaatgaaga	cccaaagaaa	cagggacatc	tatgtgattt	tttgccaagt	169799597
ttgatgaaga	agcagataat	tgtggagaag	tataatcgga	aaatgggggt	169799647
atgatttgat	ggtaatgacc	taagtggcat	ttggaaggcc	tgtttcttca	169799697
gattctttctc	tgcgtctctg	catcttcata	gagaaggact	ttccttccct	169799747
gtgggtctag	ggaaggcacc	tcttaaataa	aggtttcatg	accacttga	169799797
gaataaattc	aggaaattct	tttatggcct	gcttcagggg	agaagggcag	169799847
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tcctccaaac	aaaccttcaa	atctctgctc	accccatatt	gagagaccag	169800047
agatgagcca	agagacatga	agcaaccttc	ccaagggagc	agagccaaga	169800097
tttgaaccag	ggctgttggg	ccagtgaaga	agggcttgaa	atccagtga	169800147
gcacagggtat	cttctcagc	aggctcagag	acaggagggtg	gaccggccgg	169800197
agcagaacgg	accctcccct	tcaaagcggg	actctgccct	tgagccctga	169800247
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agcttttctc	gtcagcccct	tgggtcactg	cagacaaggc	tctagtgttc	169800847
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tcgtgtgggg	acagcagggc	acactggaga	ggtgaggagg	gtctcctgtc	169800947
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cactcgccca	gcccaccagc	ctcaccacac	tcccatagac	ttccccactc	169801197
ttgggtgggg	gtgggagggc	tacacgaagc	tctaaagtca	gcccgtgctc	169801247
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ccctgtatct	gacttcgaca	tgtttcttcc	tccaggaagc	cctccctgat	169801347
gccccattcc	ccctccaagg	actgcccagc	atctggagca	ccctgtaccg	169801397
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ggacactgca	tgtgggcctg	tccatacgcc	accagaccc	ctcgggtacc	169801497
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gtggtagggt	ggagggtctac	aatcaactg	acaatggaca	gattcacagg	169801647
agaaaaaac	aatcagttgt	actcacatgc	ctggggaaga	ctgaacagct	169801697
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gttagggctg	ctgtggaggc	ccaggaatca	atcagaagcc	ttcagctttc	169801797
acctcccatc	ccccgttccc	tgaccccatg	ccaccagatg	caaataagaa	169801847
ggaaacttta	attccacaaa	ttgaagcatt	tatgaagctc	agcaggcaac	169801897

FIG. 1.33

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ctggcaggca	ggcaggcaca	agtgaggaac	aagggccccc	ggctgggctg	169801947
ccttccaggc	aggtcccctc	gacacaggcc	actgcagctc	tctcctgcaa	169801997
tgtgtcagga	gagcctggca	caatgtgggg	gacgggggcg	gggggggtgcg	169802047
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tggatgcctg	ctggggcaga	aggcggaatc	cagcctgacc	acttagtggg	169802147
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caaggccaca	caacaacttg	gaggaaacac	ggaactgaag	gaaattgatt	169803047
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cagaaattta	tagcacctac	ctccaggggag	agttgggggt	taactgagat	169803347
cacgatgtac	aaacctgtaa	gctgtaaggc	aatggaaaag	tggagggtat	169803397
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ggctgggctg	ctggctcaca	ggtgttctct	ccccctggcc	caatgccctg	169803497
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cacagatctg	tctaaaatct	aactagtagg	aagcagttag	aacttggtgc	169803847
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ctgaggcagg	agaatggcgt	gaacccagga	ggccgagctt	gcagtgagcc	169804447
aagatcgtgc	cactgcactc	cagcctgggt	gacagagcga	gactccatct	169804497

FIG. 1.34



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caaaaaaaaaa	aaaaaaaaaaaa	aaaaagaatg	aacaactgct	gactactgtt	169804547
tactacaata	agcatagctg	atactctatc	caggaagagg	aagccaccac	169804597
tcagtgcctc	agccaagatt	gttctcaagc	ttttgtccgt	cccaaaccct	169804647
tatgaagcat	cctcaccac	tgacatgtgc	agtacttaag	acgggtgcacc	169804697
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agacagcggt	gcaaagaccc	cagggggccga	gtaagcagag	gcctttcaga	169804797
gatcagagaa	aaggccacat	agctgggagc	ctttgtgaaa	ctggagaggt	169804847
catcggggcc	agatcctcag	gggcccagtg	gccctggaaa	ggaatctggt	169804897
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gtcctattct	gagcttcagt	tttcttgtct	gcaaagggct	ctggaccaaa	169804997
ccatctagga	tccaccctga	ccctgggcct	tcatgtcagg	ttaaggagag	169805047
acagggcctc	gttctgctgt	caggatgagt	ttctccaggg	aaaggccctc	169805097
tagctccgcc	ctgccctgtc	tggctctggg	gaccacgcag	gactctcaag	169805147
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tattgtcagt	gtagacatgt	ttcacacaga	ggagaactca	ggacagggga	169805347
caggaatgga	ggcaggaact	cgatctatta	gaacaagttt	tctgatgtgg	169805397
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tggaaaccaa	atcaaccttg	ggaaaaggag	gtgcagaggg	caaggtcaaa	169805947
accaattcat	ggaagtggga	agaaagcagg	gctggcctca	accttttcac	169805997
tattagagag	atggccatgt	aaagttagtg	gcctcctgtg	gaaggcatat	169806047
gcaagaacag	gtagaatgat	tatttcttag	gggttttgta	gaaaggattc	169806097
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gaaaacttgt	tgtaatagat	tgagtctcct	ccaccactcc	tgtcctcgtc	169806197
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gaaatgggca	ggaagtggaa	ggaagagaaa	gggagtcagg	cccagggcag	169806447
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cctcccaggt	gggtgtaaat	ttgcaaacc	aaatgggtta	gaagatatat	169806547
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ctgtgaccct	ctgccatgca	aggtaacata	ctcacaggca	tagggatgag	169807097

FIG. 1.35

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gatgcggatg	tcttttagagg	gccactgttt	tgcctaccac	agcttccatt	169807147
tggattccttg	tcccaacccc	tacaaaagtg	aggcatataa	tttgttgaat	169807197
tctgaataaa	atgctaccag	tgtctacaaa	ttatatTTTT	tcttttttta	169807247
aaaaaaaaaa	aaaaccttct	tccccaagtc	tggtttcctt	tagacctcag	169807297
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tattgattga	gcagctaccc	tgtgccagtg	aggttggaaa	cacaaggggtg	169807647
atgaacaagg	tacatgtgcc	tggccgtcac	tggccagctc	tgtcactgca	169807697
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tcocatctgta	gagatctcct	tggatctaaa	ttatcagggc	ctaaagccag	169808347
gccatactac	cgagggttaa	gaagggtgaa	gggctgcatt	gggcaacatt	169808397
gttccttcaa	tcctaactct	ttaatcctaa	ttcatcactg	cacactctgc	169808447
tccttccctt	gggtgaagac	agtttgattt	gccagtatc	cagaaagttt	169808497
gtgctaagac	aagggaaatt	gccacatggc	tctctgtttc	attcagtcct	169808547
tcataagcat	gcagcctgac	ctggagaaa	tgacagtgtg	aaatgcatgg	169808597
agcagctcct	gtccctctct	ttcctaccct	tgagcactct	ctaagcagta	169808647
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catcttctta	ttcatctgaa	tattcctcat	gcctggcatc	acgcctcact	169809647
catagagtag	gaattcaaâa	acatcccagt	aggagctggg	aaagctccta	169809697

FIG. 1.36

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ctgcatgtct	tgtacatctg	ctgtatgcca	gctgggaaaag	ctcctactgc	169809747
aagagagagg	caaaccacaa	aggggactaa	ggggaagaat	tgggaggggg	169809797
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cttacaatatg	agaccttgac	tgagacaagt	tgtcttgagt	ttccagttga	169810397
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gcattcctgac	cctggatttt	actgtttatt	tctgtgtttc	ctcactattc	169810647
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tgaactctct	taggccagag	tgatcccca	ctatcactgc	ctggcagcat	169810797
ggagcagctt	cagtttttgg	actcagggca	attgcctgt	tccaggaaac	169810847
cccaaaatag	agttgcctca	tttcacttct	accagcatgt	cttgtagatc	169810897
tgctgtagc	caggccccgt	gtcctcttac	gccacatcc	cagatcctgc	169810947
aggtagaagt	gtcacattg	ctgtgctccc	ttttctctga	ccagccatgg	169810997
aggccctggg	ggcttgagg	agtggctgct	tactccctgg	gggaagtgtg	169811047
ggctgcaagc	cccttgagt	ggcaggttgc	catggtgatg	ctaattggaga	169811097
gacttgccctg	aggaatactg	accacccaaa	ggaacaatta	ccagagaagg	169811147
cccatttctt	tagcaatttt	caagaatggg	caagataaaa	agccacaagt	169811197
gaaaaggcat	tgcaaacaaa	taatagtgtg	tgagctggtc	tggacccaac	169811247
aaggcctgtt	tcccacccct	ctttccctct	ggttgtagtg	aataaagcca	169811297
tacttttcag	tgattttataa	ctgttcaaaa	atgactcgtt	tccatatctt	169811347
ctttcatcta	cccagcaccc	attatgtacc	aaatgcctaa	cagacactta	169811397
aaatatactc	tataattatg	aaaacaacc	tacaaggtaa	ttgttcccgt	169811447
attacagatg	agaacactga	ggctcaggga	gtgtaaggga	cccgtctagg	169811497
gtaacgcagc	tgggaagcac	atgcagcact	ctacttcatg	cttaattcaa	169811547
ggaagcgaat	tctccttggtg	ggtaaacatc	atcacagtgg	caattccagt	169811597
gcctccataa	gaaagtgtcc	ttggaaatga	gacactagcc	ctctcctgtc	169811647
tcatctgcac	aatatcctat	tgccatctat	ttagaagaga	ggtagtgagt	169811697
tggttcattc	attcattctc	catttggttca	ttcatacaca	tttattacac	169811747
tcaaacttct	agggcaaaaac	cagcaagccc	cgtactggac	acttcagact	169811797
caaagatagc	aacttgctaa	gttacaggag	cttcctcata	attgctgagc	169811847
ttctaagctc	tttgtcccaa	ctcctgaaaa	gtagccctca	acttccaaac	169811897
tgtgcttcgg	gcactgacat	tccctgagct	ccacacaccc	ttggaccaca	169811947
gttttctgag	gcccagatga	gcacaatgtg	cagggcagag	cctggcactt	169811997
ccagggctcc	aaggagtcca	gaggaataac	gggcagggtc	tgaatcaggc	169812047
tgctgtaggt	tgaactcctg	ccccacttag	cagctggatg	atgtgcaaat	169812097
tgctcagcct	ctctgtgctt	cagtttctct	acctataacc	tagggctaaa	169812147
aattagaagc	acctactcca	tacagctatt	gtgctgatac	aatacaataa	169812197
tccacataag	gaacttagaa	cagaacagtg	ccggcggtgt	atgttaaatg	169812247
ctgagtggac	accagttggg	attagaagta	gcagcattgc	caggtactcc	169812297

FIG. 1.37

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tgagcaatgg	gtcagctaata	tccactctac	cctcagaccc	caccctcctt	169812347
tgcagttcct	tctcctgctt	tgataactag	aagcagtcac	atagggcctg	169812397
gggtctctac	ttgtaggagt	tcagtcaggg	tggtaggaaa	aattataaaa	169812447
attatagaaa	gactcaaacc	ttcttggaag	gccgggaggt	tttgcaaaag	169812497
ttttgggaaa	ggatttggtt	gaaggcagct	gaattttctc	agagtaaata	169812547
acaaggaagt	gtaagggaat	taatctagat	aagttagttt	acttaggcct	169812597
tgaaacatgg	cctttaataca	tccatgctca	ggactgctct	cttgggggaa	169812647
aggatcgccc	gacccccccac	cccaccctca	ccccaccccc	tgccaccatg	169812697
ttaattaccc	acaagtgtgt	tgactcaaag	cctttgtcat	taaattctgta	169812747
ctgaatatat	gccacacagca	ccagcttgct	aaggctgcag	ctgctgactc	169812797
tttacagcac	cctcctcggt	gcctgtgagt	ggcccagtc	cttagccgtg	169812847
cagccaggca	aaaaatctgt	gtctgcatac	attttttcat	ccatcactca	169812897
gccagggtct	gcggttgga	ccccgcattc	actcacaat	caagatgttc	169812947
agttccgcc	ccccccctg	tctgtcttcc	tttctcacag	tcactctgta	169812997
ggtgtatcct	gaaaatgtaa	atcagaccac	agcattccct	agctgaaaac	169813047
ccttccgtgg	ctccctatta	ctcaccatag	gctaaattcc	gccagactc	169813097
ctctgaaggg	cttgcaaggc	ctcctgtgtt	ctagctcctg	cctgctatcc	169813147
accacacccc	ctcattcctg	cccctgtaaa	cccctgttag	ctctcacatc	169813197
tcaagaatta	aagatttgac	ccagttgctc	cgaccacctc	cgccccgatc	169813247
cccagaaaca	gtttccccct	tctctttctc	tgcccaactt	ctatcggttt	169813297
tcagaatgtc	tcccctggcc	acgcaggatc	ccttccattt	tgaggctgat	169813347
aaaatcctgc	ggatcgcaag	ctgagcgctc	atcacacccc	atcgtgatta	169813397
tctcccctgc	aaggccaggg	gctttgagag	ggtgggactg	tggttgacac	169813447
gttcagtgct	ccagtcctat	cacctgacac	ttgccataga	gaagggtgctt	169813497
agtatttaga	agagtgtgtg	cgattaccga	gagcatggat	atgaagaagg	169813547
ggatcacaac	cttgaaaaag	ttgtttgctg	agaaagaggc	aagcagcccc	169813597
aactgacggg	agctggcctg	gtcctcacag	tttgtctcct	gttgaacaat	169813647
ttcacagaac	attgacatca	gacaaggcta	ttctgactgt	gttggagcaa	169813697
gacaaaatcg	agagcacttc	gtagtcatgt	ctaaacgcag	ataaaacaag	169813747
aacattgtct	aaaccacaaa	aatgaccaga	catcccgcct	ttttgggcta	169813797
atgggagtaa	ctgtttacca	atgtttataa	tggtggccct	gcactagtcc	169813847
ttctacctta	tagataagat	tataggtacc	caattataga	atgattccta	169813897
ctgcctgatg	gcatccaatt	gaaccctccc	tagtcactta	acacaagccc	169813947
ccatcccttt	gtaagttctt	cgtaacaccc	tctcacaag	acccctcact	169813997
gttccccaca	gtgcacaatc	tccttgctgc	aatgagccaa	taaaccagc	169814047
tccgttcaac	tgcaggtgtg	ttcctggctc	ttggctaaaag	ggcattgaca	169814097
ccaccatttt	cccagaaaacc	tgaacttgca	aaaaaaaaaa	aatacctaata	169814147
taaacaattt	ctgcaagcta	attgatagt	agaaatgtat	ttctgatagg	169814197
gagcatcagc	tggagtagac	aactttgtac	atactatatg	ttttccggac	169814247
agttgcttca	gcttctcctg	cattgtgtgt	gtgtgtgtgt	gtgtgtgtgt	169814297
ctgtgtgtgt	gtgtgtgtgt	ttgcaggggg	aagatgcaag	ccttgctgtc	169814347
ctgggtgtcc	gtgactgggc	atgtctcatc	tggaaagaga	tcagctaata	169814397
ttccttgaga	aaaagaatgt	tatcactgga	tgattacatc	tgcttccaga	169814447
gaggtaagag	catgcagcat	ggagcagaca	ctctctatcc	caggagctgc	169814497
cctgcccagg	cctgggctgg	tggctattgt	catggagtgg	taactgtaag	169814547
gccatcctca	taagtctctg	tgatatcact	ccaatccatg	gacacccctg	169814597
tgactccgtc	tccattcctc	aggcctgctt	cccattggaaa	gacccagagg	169814647
gaaacgtggg	tgggtggcatt	ggggactgag	aacagaacaa	aattcaggct	169814697
ttgagtgtgg	attagagacg	cactgtgtgg	tgcttgcatc	acctctgaca	169814747
gtggttgggt	aatgggctga	atcacccaat	ggagacagaa	tgccaacaga	169814797
tggttagttga	ggaggatgat	taatctcctt	cttcgaaaac	tcagagaatc	169814847
tttattggca	acgttgaagt	caagataggg	cttctcctta	gcaaccggaa	169814897

FIG. 1.38

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agcgcctag	gtgcatggct	acagaattca	atatgaaact	cagatgatga	169814947
aggtagccat	gggcacctct	gattgcccac	tgtaaatttc	tgcctggaat	169814997
ggggctggg	gcctcataaa	tgtcaacaaa	agctggtgat	gggtccagag	169815047
agggatgta	ggccagcctt	gatggatgag	gaagtttcat	ttaggggctc	169815097
ctgtcacttc	ccatcttcag	gccaaagtga	catccatggc	tgtaaaattg	169815147
tcacccctct	cctttgcctc	tcaggaaagc	aaaacttctt	tacgacactt	169815197
ttaatcaaat	ctgtcttttg	ccacttctct	ccccacctg	ctccctctgc	169815247
ctttatcctg	acaaagaagc	gaactgttac	tctctgtcag	ttattttgtct	169815297
gagtaatttc	ttgatgaaat	tgcaactata	attgaatttt	ctgaaaacca	169815347
ggaattcaaa	tgaggcgaca	acagaggaaa	cagcgtgatt	aaggaattgt	169815397
tattcactcg	ttgtacatca	ttaccaccca	gaattcatcg	ctggatcggt	169815447
cacagatgga	gttgctgaac	tatgattata	ttttagaaaa	tgaaggggga	169815497
aaaatctaaa	aaggcaataa	aacatattag	aagccttctt	gaggaacagg	169815547
attattactg	attaagtata	ttttgcatga	aaaatgtgct	agcactttgg	169815597
cagtttaaat	tatacgtccg	tgcaagtcaac	atttttgtctg	gtctcaaaat	169815647
tctttgttag	tttggtcttc	taatcacatt	cctcttcacc	ctccaaattg	169815697
acgacttgaa	agaacattag	aaatgatcat	tcctgaagga	gcatttgctc	169815747
tcaaaatgca	tttacgtcga	gcagccatta	aaaggatatc	atccagtcac	169815797
ttagtttctc	aatttaactt	taaaggaaaag	ttgccttatt	agagaagtgg	169815847
cctctatttc	aatgtaatgg	tctttgtcac	atcttccaat	gtgctggctt	169815897
agtgtgaag	gatgggggaa	ggcagttttc	acatattgca	gccaccatac	169815947
caccaaagaa	aacaggtgca	cttccaggca	tcatttagcg	gggtaccaca	169815997
ttcctgggtc	cagttttcctt	tttagaaaaat	ctgaaagtaa	ctttggggca	169816047
tatcttttaa	ggagtactcc	aacacgacta	gtggacagac	cctaaattaa	169816097
ttgccaatca	gctctgcctt	ctgggtattta	cacctttatg	taataacctc	169816147
cacttgaagg	tagatgagat	ctgtgacttg	cttctaacca	gtggaatatg	169816197
goggaggtgg	tgggacgtta	ctcctgtgat	tacattacat	catgtggctc	169816247
ctttatgatg	gaagattcat	gctagagatt	ctccttgctg	acttgacaaa	169816297
gtatgtaacc	atgatgaaga	cttccacgtg	gcaaggagct	gtgggaagcc	169816347
cagggtgctga	gactggcatc	cagcaaacac	ccagcaagaa	acagacgtcc	169816397
ttgggttctac	acatacagga	aatgaattct	gccaacatcc	tgagtaaggc	169816447
tggaaactaga	ttctcccca	gttgagcctg	acaagtaaaa	tacagaccag	169816497
ccaacacctt	gattgcagtc	ttgtgagacc	tggggaaaag	gacacagctg	169816547
aaccgtgtcc	attcttctga	cccacagaaa	ctgtcacatc	ataaaggtat	169816597
gttagttggt	acacagttta	gaaaactatt	acagctgctc	aagaaggtta	169816647
gctagctcca	gatttcaatc	cattcacagg	aaagcaagct	ttattcctag	169816697
agaataaatt	catgctttgc	aaaaagagga	aaacgtcctg	cagttttaga	169816747
aggctttttc	tttctcaaca	cacccaaatt	tctttaaaat	cctcaagaag	169816797
tgcatttggt	ttcatgggtg	actcgaagaa	gtgagtataa	ttaaactaca	169816847
aaaggtggga	ggaagggaca	aattaaattt	tggtatgcat	acaggtagct	169816897
tcttccaagt	gataatgagc	aatgtgaaac	aaagagattg	gcattaaatg	169816947
taatgaagga	ctagaggagt	gtacctaacc	ctgaaacaaa	ttccaagaag	169816997
tggccttgac	ctaaaatggt	tgcactcctg	cagagaccct	tacttataag	169817047
tcaggagata	cctgatgccc	aggagaactg	gtttttgtac	tctgtcttac	169817097
acagactaag	aattaagaat	gcaggtgaga	agtttagaaa	acttcctgat	169817147
gatcatatga	aaagacatta	aactttacct	ggtaaaacta	tgaaatgttg	169817197
cctgtagatt	tctaagaaaa	atgagtagga	agttggaaat	atttcagaat	169817247
taagaatggt	tttatataat	tagaactctt	taagctatgt	aattctgaaa	169817297
tctgtgtgac	agacttctgt	gtaaacataa	agaactagtt	atttttacag	169817347
attatctagt	ctgtgtattc	atttgatggt	tctattactt	ttaccctcac	169817397
tacaaagtcc	aatgaagggt	aaaaaaatat	tggtcttaaa	aaaagaagag	169817447
ataaacctgg	agtagctatt	tcaatgttag	acaaaatgga	ttttaaaaca	169817497

FIG. 1.39

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aaaatgttaa	tacagataga	aagggacatt	ttataataat	aaaagtatca	169817547
aaatatcagg	aagataccac	aattataaac	aaatatgctc	ctaaaaatag	169817597
aatctcaaaa	tacataaaac	aaaaactgac	aaagttgaag	ggataaataa	169817647
ataggcagct	cagcaatatt	tagaaacttc	aatacctcac	tttcaataat	169817697
ggatagaaca	actagacata	agatcaacaa	gaaaatagaa	tattttaaca	169817747
aagctataca	ccaactaggc	ctaattggata	tctatagaat	aatccaccca	169817797
acaacagaag	tcttcctcct	cctactttctc	ctcctcctcc	ccttcccctt	169817847
ccccttcccc	ttctttcttct	tccttcttct	ctttctcctt	ctccttcttc	169817897
ttcttcttca	acaggatcct	actctgttgc	ccaggctaga	gtgcagtggg	169817947
gtgatcatgg	ctcactgcag	cctcaacttc	ccaggctcag	gtgatacatg	169817997
ggcctcagct	tcccaaagtg	ctgggattat	aggcacaagc	cacatgcctg	169818047
gcccacatat	tcttctttaag	tacacatcaa	acattctgta	gaatagacca	169818097
tatgctaggc	cacaaaacaa	gcttcgataa	tttaaaagga	ctgaaattat	169818147
acacaatctg	ttccttggcc	acaaagaata	aaattagaaa	gaacttttgg	169818197
aaactcacaa	ctatatagaa	attaacatac	ccataagtaa	ccaattgggt	169818247
gaagaagaaa	tcacaaaata	aatgagaaaa	tactttgaga	tgaatgaaaa	169818297
ttaagacaca	acataataaa	atttatgcaa	tatagctaaa	gcaatgctta	169818347
gagggaatt	tatagctcca	catacctaca	ttaaaaatgg	agaaagttac	169818397
actgttgggtg	ggactgtaaa	ttagtccaac	cactgtggaa	gacaatatgg	169818447
cgattcctca	aggatctaga	accagaaata	ccatttgacc	cagcaatccc	169818497
attactgggt	atacacccaa	aggattataa	atcattctac	tataaagaca	169818547
catgcataca	tatatattat	gaggcactat	ttccaatggc	aaagacttgg	169818597
aaccaaccca	aatgcccac	aatgatagac	tggacaaaaga	aaatgtggca	169818647
catatacacc	atggaatact	atgcagccat	aaaaaagaat	gagtttatgt	169818697
cctttgcagg	gacatagatg	aagctggaag	ccatcattct	cagcaaactg	169818747
acacaggaac	agataaaacaa	acaccacata	ttctcactca	taagtgggag	169818797
ttgaacaatg	agtacacatg	gacacagggg	ggggaacatc	acacaccggg	169818847
gcctgtcgga	gggtgggggg	caagtggagg	gagagcatta	ggacaaatac	169818897
ctcatgcata	tgggggttta	aacctagatg	acagggtgat	aggtgcagca	169818947
aaccaccatg	gcacatgtat	acctgtgtaa	caaacctgca	cattctgcac	169818997
atgtatcccc	aaacttagag	taaaattttt	ttaaaaaaag	aaaaaacatc	169819047
tcatatcaat	aagctagact	tctatcttaa	gacgctaggg	gaaaagcagc	169819097
aaactaatcc	taaagcaagc	agaaggaaga	caataatgaa	agtggaaatt	169819147
aatgaaattg	aggacagaaa	aacaatagag	aatatcactg	aaacccaaaa	169819197
gtggttcttg	ttttctttct	ttctctttct	ttctttctct	ctctctctct	169819247
ttttctttct	ttctttcttt	ctttcttgtt	tcttttgaga	caaggtctag	169819297
ctctgtcact	caggctggag	tgcagtgggt	caatcacagc	tactgcagc	169819347
ctcgatctcc	tggacttaag	tgatcctcct	acctcagact	ctcgagtgc	169819397
tgaaccaca	ggagtgcacc	accatgtcca	gctaattgtt	tcaatttttt	169819447
gtagagatga	ggtttcccta	tgttgcccag	gctggtctca	aattcctagg	169819497
ctcaagcgat	cctcctgcct	cagcctctca	aaatgctgag	ccaccacacc	169819547
cagctgggta	tttcaaaaga	tgagcaaaaag	tgacaagctt	ttagctaaac	169819597
tgaccaagaa	aaaaagaata	cttaaattac	cataatcagg	aaagaatgag	169819647
agaacattac	taccaacctc	atagatacaa	aaagtataga	ggaatacaac	169819697
aagccaattg	atatgccaac	aaattaaatt	acaaatgaaa	tggacaaatt	169819747
cttagaaaaga	cacaaactac	aaaaactgac	tcaagtagaa	atagaaaatc	169819797
taaataggta	tttaaaaaag	attattaaac	tgagagctga	agacagggca	169819847
gcaaaactgc	agggggccacc	accaccacca	ccacatgtca	ggaagagtac	169819897
ggagaggccc	tggaggggca	taacgactgc	aggaataaat	taggagagcc	169819947
aagagaaccc	acagaccctc	tgaaggaagt	ggattgctcc	tgcaggacct	169819997
gggagacacc	tcaataactg	tgctggtatc	tgtggctgag	aaacccacag	169820047
atgggttgca	tcacaggact	ctgtacagac	aacccccagt	accagcctgg	169820097

FIG. 1.40



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aacctggtag	acatcctggg	tggctagatc	cagaagagag	ataacaatca	169820147
ctacagctcg	gctctcagga	agccacatcc	ctaggaaaag	ggggagagta	169820197
atacatcaag	ggaacacccc	atgggacaaa	agaatctgaa	caacagcctc	169820247
gagccctagg	ccttccatct	gacagacact	acacaaatga	ggaggaacca	169820297
gaaacccaac	tctagtaata	tgacaaaaca	aggttcctta	atacccccca	169820347
aaaaatcaca	ctaggtcacc	agcaatggat	gcaaaccaag	aagaaatccc	169820397
tgtttcacct	gaaaaagaat	tcagaagggtt	agttattaag	ctaatacagga	169820447
aggcaccagt	gaaaggcaaa	gtccaactta	aggaaatcaa	aaaaatgata	169820497
caacagggtga	agggagagat	tttcaatgaa	atagatagca	taaataaaaa	169820547
acaatcaaaa	cttcaggaaa	caatggacac	agttatagaa	atgcaaaagg	169820597
ctctggaaac	tctcagcaat	agaattgaac	acgctgaaga	aagaacttca	169820647
gagctcaaag	acaagggtttt	agaatgaacc	caatccaaaa	aagacaaagg	169820697
aaaaattata	agaaaatatg	aacaaagcct	ccaataagtc	tgggattata	169820747
ttaaattggcc	aaacctaaga	ataattggca	ttcctgagga	agaagagaaa	169820797
tctaaaagtt	tggaaaacat	attcggggga	ataatcaagg	aaaactcccc	169820847
cagccttgct	agagccctag	acatccaaat	acaagaggct	caaagaacac	169820897
ctgggaaatt	cattgcaaaa	agatcattac	ttagacacat	tgtcatcagg	169820947
ttatctaaag	ttaagatgaa	ggaaagaatc	ttaagagctg	tgaggcaaaa	169820997
gcaccaggta	atctataaag	ggaaacctat	cagattaaca	gcagatttct	169821047
cagccaaaac	cctacaagct	agaagggatt	ggggccctat	cttcagcctc	169821097
cttaaacaaa	acaattatca	gccaaagaatt	ttgtagccag	tgaaactaag	169821147
ctttataaat	gaaggaaaga	tacagtcttt	ttcagataaa	caaatagctga	169821197
gagaattcac	cactaccaag	tcagcactac	aagaactact	aaaaggagct	169821247
ctaaaccttc	aatcaaatcc	tggaaacaca	tcaaaacaga	acgtctttta	169821297
ggcataaatc	tcacagaaac	tataaaacaa	aaatacaatt	aagacaacaa	169821347
caaaaaacaa	ggtatacgga	caacaaatag	catgaagaat	gtaatggtac	169821397
ctcacacctc	aatactaaca	ttgaatgtaa	atggcctaca	tgctccactt	169821447
aaaagataca	gaattgcaga	atggcctaaga	attcaccaac	cagctatctg	169821497
ctgccttcaa	gagactcacc	taacacataa	ggacacaaat	aaacttaagg	169821547
taaaggggtg	gaaaagacat	tctatgcaaa	tggagtaact	attcttatat	169821597
cagacaaaac	aaattttaga	gcaacagcag	ttaaaaaaga	caaagaggga	169821647
cattatataa	tgataaaaag	ccttgaccac	caagaaaata	tcacaatcct	169821697
aaatatatat	gcacctaaca	ctgaagctcc	ttaattttata	aaacaattac	169821747
taatagacct	aagaaatgag	atagacggca	acacagtaac	agagggggac	169821797
ttcaatactc	cactgacagc	actagacagg	tcacaaagac	agaaagtcaa	169821847
caaagaacaa	tggattttaa	gtatatcctg	gaacaaatgg	acttaacaga	169821897
tatttataga	acattctatc	aaacaactgt	ggaatatata	ttctattcaa	169821947
ctgcatatgg	aactttctcc	aagatagacc	atatgatagg	tcacaaaatg	169821997
agccttgata	aattttaagaa	aattgaaatt	atatcaagca	ctctgttaga	169822047
ccacagtggg	ataaaaactgg	aaattaaggc	caaaaggact	ttctaaatca	169822097
tgcaaatata	tggaaatttaa	ataacctgct	cctgaatatc	actgggtcaa	169822147
aaatgaaatc	aaaatgcaaa	tttaaaaatt	attcaaactg	aatgacagta	169822197
ctgacacaa	ctatcaaaac	ctctggggtc	cagcaaaggg	gatgctaaga	169822247
ggaaagtcca	tagccctaaa	ggcctacatt	gaaaagtctg	aaagagcaca	169822297
aatagataat	ctaaagtcac	acctcaagga	actagagaaa	caagaacaaa	169822347
ccaaacccaa	attcagcaga	agaaaggaaa	taaccaagat	cagagcagaa	169822397
ctaaatgaaa	ttgaaacaaa	aaaattacaa	aagataaatg	aaacaaatag	169822447
ctgattcttt	gaaaagataa	atacgattga	tagaccatta	gcaagattaa	169822497
ccaagatagg	aagagagaaa	atccaaataa	gctcaattag	aaatgaaatg	169822547
ggagacattg	caactgaaaa	ccacagaaat	acaagagAAC	attcaaggct	169822597
actctgaaca	cctttatgtg	cataaacttg	aaaacctaaa	ggagatggat	169822647
aaattcctgg	atagatacaa	ccctccttgc	ttaaatcagg	gagaattcga	169822697

FIG. 1.41

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taccatgaac	agaccaataa	caagcagtg	gattgaaatg	gtaattaaaa	169822747
aattaccaat	aaaaaagtcc	aggaccaggt	ggattcatac	cagaattcta	169822797
ccagacattc	aaagaagaaa	tggtaccaat	cctactgaca	ctattccaca	169822847
agatagagaa	agaaggaaac	ctccctaata	catoctagga	agccagtgtc	169822897
atcctaatac	caaaaccagg	aaaggacaca	accaaaaaag	aaaactacag	169822947
accaatatcc	ctgatgaaca	tagatgcaaa	aaatccttaa	caaaatgcta	169822997
gctaaccgaa	tccaacaaca	tatcaaaaag	ataatccacc	atgatcaagt	169823047
gagtttaata	ccagggatgc	agggagggtt	taacatatgc	aaagtcaata	169823097
aatgtgatag	ccacataaaa	cataattaaa	aacaaaaatc	acaggatcat	169823147
ctcaatagat	gcagaaaaag	cattcaacaa	aatccagcac	gcttctatga	169823197
ttaaaactct	cagcaaaatt	ggcacacaag	ggacatacct	cagtgtataa	169823247
aaagtcattc	atgacaaaac	cacagcctac	ataatactga	gaactggaac	169823297
aaagatgccc	agtctcacca	ctcttcttca	acctagtaat	ggaagtccca	169823347
gccagagcaa	taagacaaga	gaaagaaata	aaaggcatcc	aaatcagtaa	169823397
agaggaagtc	aaactgtcac	tgtttgctga	tgatattatt	gtttacctag	169823447
aaaaacctaa	agatgcctcc	agaaagctcc	tagaactgat	caaagaattc	169823497
agcaaagttt	tgaatacaaa	attaatgtac	acaaatcagt	agctcttcta	169823547
tccaccaact	gcaaccaagc	tgagaatcaa	atcaagaact	caacctcttt	169823597
tacaatagct	gcaaaaaaaaa	taaaataaaa	tacttaggaa	tatacctaac	169823647
caaggagatg	aaagacctct	acaaggaaga	ctacaaaaca	ctgctgaaag	169823697
aatcataga	tgacacagac	aatggaaac	acatccaatg	ctcatgtatg	169823747
ggtagattaa	atattgtgaa	aatgacaata	ctaccaaag	caatctacaa	169823797
attcagtgca	attccatcaa	aatactacta	tcattcttca	cagaattaga	169823847
aaaaaacagt	cttaaaattc	acatggaagc	aaaaaagagc	ccacatagcc	169823897
aaagcaagac	taagcaaaaa	gaacaaatct	ggaggcatca	cattacctga	169823947
tttcaaacta	tactataagg	ccatagtcc	ccaaacagca	tggtactggt	169823997
ataaaaaatag	gcacataggg	ttgggtgag	tggtccacac	ctgtaatccc	169824047
agcactttgg	gagaccgagg	caggcggatc	acaaagtcag	gagattgaga	169824097
ccatcctggc	taacatggta	aaactccgtc	tctaactaaa	atacaaaaaa	169824147
ttagccagggt	gtggtggcag	acgcctgtac	tcccagctac	tccggagggt	169824197
gaggcaggag	aatggcatga	acccgggagg	cagagcttgc	agttagctga	169824247
gatagagcca	ctgcactcca	gcccgggcca	caaaacgaga	ctccatctca	169824297
aaaaaaaaaa	aaggcaaata	gaccaatgga	acagaagaga	gaacgcagaa	169824347
ataaaaccga	acgcttacag	caaactgatc	tttgacaaag	caaacaaaaa	169824397
catatagtgg	ggaaaggaca	cctcattcaa	ggaatagtgc	tgggataatt	169824447
ggcaagccac	atgtaggaga	atgaaactgg	atcctcatct	ctcaccttat	169824497
acaaaaatca	actcaagatg	gatcaagggc	ttaaactctaa	gacctgaaac	169824547
tataaaaaatt	ctagaagata	acattggaaa	accccttcta	gacattcgct	169824597
taggcaagga	tttcataacc	aagaaccaaa	agcaaatgca	ataaaaaaca	169824647
agataaatag	ctgggactta	attaaaactaa	agagcttttg	cacagcaaaa	169824697
tgaacagtca	gcagagtaaa	cagacaaccc	agagagtggg	agaaaatcct	169824747
cacaatctat	acatctgacc	aaggactaat	atccagaatc	tacaacaaac	169824797
tcaaacaaat	tagcaaaaaa	aaaaaaaaaa	aaaaactacc	aaaaaaaaatc	169824847
atcaaaaatt	gggctaagga	catgaataga	caattctcaa	aagaagatat	169824897
acaaatggcc	aagaaaaata	tgaaaaaatg	ttcaacatca	ctaatgatca	169824947
gggaaatgaa	aatcaaaacc	acaatgtgat	accacctcac	tcttgcaagg	169824997
atggccataa	taaaaaaatc	aaaaaataat	agacactggc	atggatgtgg	169825047
tgaacaggga	acacttctac	actgctggtg	aaaatgtaaa	actagtacaa	169825097
ccactatgga	aaacagtgtg	gagattcctt	aaagtactaa	aagtagaact	169825147
accattttgat	ccagcaatcc	cactactggg	tgtctaccca	gaggaaaaaga	169825197
agtcattata	cgaaaaagat	acttgcacac	acatattttac	agcagcacaa	169825247
ttcgcaattg	taaaaacgtg	gaaccagccc	aaatgcacat	aaagcaacga	169825297

FIG. 1.42



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gtggatatat	atatatatata	atggaatact	actcagccaa	aaaaaggaat	169825347
gaattagtg	cattcacagc	aacctggatg	agattggaga	ctattattct	169825397
aagtgaagta	actcagcaat	ggaaaatcaa	tcatcatatg	ttctcattca	169825447
taagtgggag	ctaaactatg	aggatgcaaa	ggcataagag	tgacacagtg	169825497
gactttgggg	actcaggggg	agaggggtggg	gagtggatga	gggataaaag	169825547
accacaaata	tgggtgcagta	tatactgctc	gggtgatggg	tgcacaaaaa	169825597
tctcacaaat	caccacaaaa	ggactcactc	atgtaacaaa	acatcacctg	169825647
ttccccaata	acctatgaaa	ataaaaaaaa	taaaaataaa	attttaaaac	169825697
taccaaataa	caaagaaatt	gaatttgtca	ttttaaaact	tcccacaaag	169825747
aacagcttaa	gcccagacag	cttcactggg	gaattataca	gaatatttaa	169825797
attaaagaat	taatgtcaat	tcttcacaaa	gtcttctaaa	atgtagaaga	169825847
agagggggaca	ttttccattt	cattttgtga	ggccagtatt	atcccattac	169825897
caaaccatac	aaagccacta	caaagaaaac	tacagaccaa	tactgcttat	169825947
gaatataaac	ataaaaatcc	tcaacaaaat	actagtaaac	tgaatccagc	169825997
agtctgttaa	aaagactaac	accatgacca	aataggattt	atcaaaggaa	169826047
tgcaaagttg	gtttaacatt	tgaaaattaa	ttaatataat	acataattca	169826097
atagaaaaga	gaaaaaaaca	catgatcatc	ttatttagaca	cagaaaaatc	169826147
atttaacaaa	atccaaactg	acgtcatgat	aaaaacactc	aacaaactag	169826197
aaatagagtg	gaactttctc	aatgtgataa	aggacatcta	ccaaaaatcc	169826247
acagctaata	tgataaataa	tggtaaaaga	ctgaatgttt	ttcctctaag	169826297
atcaggaaaa	atacaaggat	gtctgctctc	agcactttta	ttaaatattg	169826347
tactggaagt	tctagccaga	acaattaggc	aaggaaatga	aataaaatga	169826397
actcaaattg	gaaaggaaga	aataaaaacta	tttcoggatg	ataccacctt	169826447
atatagagac	aatccataat	aatccattat	tagaattatc	agaactaatt	169826497
aacaagatca	gcaagggttac	aggatataaa	attaaaattc	ctatacacta	169826547
gtaatgaata	atccaaaaat	aaaattcaaa	aaacaatccc	acttacaata	169826597
gcatcaagaa	aataaaaatcc	ttatgaataa	atttaacaga	agtctaaaac	169826647
ttatatatac	tctaaacacg	acaaaatatc	attgaaataa	attaaagatg	169826697
gaaataaatg	caaagacatc	catgttcatg	atcagaagac	ttatattggt	169826747
aagatggcaa	tacttaatat	tataaagtga	tttacaatt	gatttatagg	169826797
ttcaaagtga	ttcgatgcaa	tctctgtcaa	agtttcatag	cattttttgc	169826847
agttatttat	actgcaaagt	gattttacaga	tttaatgcaa	cccgtgtcaa	169826897
aatccccatg	ccatttttgc	agaaatggaa	aagctattgc	tgggaattcat	169826947
atggattgca	agtgaaccca	aatagccaaa	acaatcctga	taaagaacaa	169826997
agctagacaa	agtcocatct	gcacttctctg	atttogaatc	ttacttcaaa	169827047
gctatggcag	tgaaaacatt	gaactgagta	cggtaatatt	tatcatctca	169827097
aaacctcaca	acaatgcagt	caagtggaaac	cactgtctca	gtatttcaga	169827147
tgacagagccc	aggctcaaag	aaatatgggg	aattgcttga	ggtcagagag	169827197
ctgggtaacc	acaaatgcgg	gtccacattc	agatctgccc	taagtataaa	169827247
gacattgcat	cctctcagcc	actacctaca	ccactcttga	gtttcttcga	169827297
cacaggacct	gtgaacagac	agcccaagac	gcttggggaat	catggaattc	169827347
taacccccaa	agcctggctt	agggacctca	tccagcgacc	agacagggcg	169827397
tggttgctcct	catccacatt	tctgaaagtg	tccactcagt	ggacagcctg	169827447
ctttctagtc	tctgccctac	tggcttgagt	gtggatgccc	agacggttag	169827497
gaggcaagct	ccagagctcc	catatgatca	cttccactgt	cacctgtgtg	169827547
ccacaagtgc	tctctgtaca	catgctccac	ctgttctgat	gatctttcag	169827597
tctttcaact	tccaagccat	gtgagggatc	cttcagggaac	atgagcactg	169827647
ggacatgctg	gacgctggag	agagatgcag	acaccagag	ctggctgagc	169827697
taacatgcta	cagtttgtga	ggaggagaca	caaaatttca	tacagatgat	169827747
aaaatttttc	tgtacaacaa	accttttgcta	tagatcctac	aatatatcca	169827797
ttattctcac	tagaatgtga	acatgattct	gcaaattcct	aggagaaaaa	169827847
cccagcctgc	cccttatcag	aggctataaa	ccacctgttt	ttctttccat	169827897

FIG. 1.43

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cctccttccc	ttgcttccct	ctcacacatc	agtccttttag	agaaaactga	169827947
gcttttccaa	gctgttattg	ctcaaagaaa	tgtcttcato	caagggaacc	169827997
aagggatgtg	aagggcactg	gcctccgaag	catttgccat	tgtcaacttt	169828047
tattgagcac	ctactatgta	ccaagtactg	tgctaggttc	tgacgacact	169828097
gaagaaacaa	aaaaatagat	acttcctaata	ctcaaggggac	agtcactctgg	169828147
tggagtcaga	ccttcatcac	gcacacacac	aaacacaaag	agagagacag	169828197
aaagagagag	agagagagtg	agagagaaat	acatgtattc	agatactgct	169828247
ctgaacctta	tctgggtccg	gagggcagag	aaggcttctt	gaactaggac	169828297
ctaagaaatg	ggaagaaatt	tgctagttaa	gcagggtgtg	ggggaagggtc	169828347
ctcagaagaa	cattctagaa	caagtgcgaag	gtcccaagag	ggagggagat	169828397
ggtccattcc	tgcaactgaa	agaagaccaa	tgtttctgaa	ccacatggag	169828447
caggaggaag	cagcaggaga	atccaacagg	gggagggtca	gaaagcccat	169828497
gtttgttaact	aaccggaacg	atgaatgtgg	tttggaagac	aagtgagagg	169828547
atgtgtacca	cgggccagat	gtgggagacc	aaggagggga	ctagtgcatt	169828597
ttccagtaaa	agaaataata	gtgcttgggg	ctagggaggc	tcaaattgag	169828647
aagaagacaa	gtggggagggt	ttaagagaga	tttctaaatt	aaaatgtaca	169828697
gggaatagtg	acagatgatg	catggggtag	agagagagaa	ggcaatgtca	169828747
agagtgactc	ccaaatctgg	cttgcaaaaca	gaatgaacgg	tggtgtcatt	169828797
cactgagaaa	ggacacccaa	gaggaggatg	tgattagcag	gggagagagc	169828847
aggagttcaa	gctgatatgt	agatccacat	taatatgtct	agtcagaatg	169828897
tggatacgta	ggtttggggc	ttagaagaaa	ggtctggggg	gaagatctaa	169828947
ccctagcagt	catctgcaaa	gagatggtaa	taaaataaat	acaattttta	169828997
aatggatgga	atttccaggg	aaaaagcaga	gggtgaaatg	agtaaaggat	169829047
ctagggccaa	ggctaaaaga	aatccattat	tagaaacaga	aaagggtgtct	169829097
tagtgcattc	aggctgctat	aacaaagtac	catagcctga	gtggcttata	169829147
aaccacagaa	attcatttct	cacagttctg	gaggctggga	agtctaggat	169829197
caagggtgcaa	gtgagagtct	gccttctggc	tcatagatgc	tgcttctctgg	169829247
ctatgttctc	acatggtaga	ggatgtacgg	aagctctctg	cgacttcatt	169829297
tatgaggacg	ctaattcccat	tcatgaagac	tccaccctca	tgacttaatc	169829347
acctccccaa	atccccacct	cctagtacca	tcaccttgag	ggttaagatt	169829397
tcagtatatg	aacttttaggg	gtcacaagta	ttcagtctat	agcaggagga	169829447
atagccaaga	aggatgaatg	aaaatcatac	aaggatgatt	tcatggaagg	169829497
caagggagta	caatgtctca	aataaaacaa	gtcctgagtc	aaacattact	169829547
gagaatgtga	gtgtaataaa	accgagactc	aaaagtaggc	attggatgtg	169829597
atgacatgac	tatcactggg	taccttaggg	agagaagtgt	tggcggaggt	169829647
gacaagcaca	gtcagatgga	atgtgctggc	ggatggcaaa	gatggggaaa	169829697
tgaagatacc	cagtgtagac	agcttctgaa	agcagctggc	cgtgagtcag	169829747
aggtagacag	gaaagtgact	aatacagtgc	agaggctcgac	gttttttagct	169829797
ttattgtatt	taagagagag	acctgagcac	atttaaaatg	ctgatgtgac	169829847
attgtccaag	ctgagaggaa	acaattagat	ctatatgaga	gaaaagaatg	169829897
atgaatatca	ggcaagtatg	gcaaagacca	ccattacttt	tgaccaacc	169829947
caataagaaa	ggttgaggat	cttcacaaaa	caaagggtgg	tttggcctga	169829997
gtggggagga	ggaacagctt	ctttactacc	agtggaaaga	aggagaggct	169830047
ggtgcagggg	caggagaggta	gcaggggagca	gaggggaggcc	ccatccacgc	169830097
tcagggttctt	agaatgagga	agatgacatt	ggcaggacca	taggtgagca	169830147
tcttctaacc	caaggaagat	ttagaactaa	gtataggctg	ggcgcggtgg	169830197
ctcacgcctg	taatcccagg	gcttcgagag	gccgaggcgg	gtggatcacc	169830247
tgagggtcagg	agttagagac	cagcctgatc	aacatggcaa	aaacccatct	169830297
ctactaaaaa	tacaaaaaatt	agccagggtgt	gttggcgctt	gtctgtagtc	169830347
ccagctactc	aggaggctga	ggcaggagaa	tgccttgaac	ccaggagggtg	169830397
gaggttgtag	tgagctgaga	tcacgccatt	gcactccagc	ctgggcaaca	169830447
aagtcagatt	ccatctcaaa	aaaaaaaaaa	aaaaaaaaag	gaaactaagt	169830497

FIG. 1.44

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atagaagtat	ggaatagaac	tatatctctt	ctattaagat	atttgtgctt	169830547
tgaaataagc	tatgtttaca	cacttgtaat	gtttaagaat	ctgtggcctt	169830597
tcagagtcac	atatgaactt	ttccttctaa	tataaaatgt	ttaacgggagc	169830647
aattgacttt	gacatcagat	tctaagttga	aatcttaactg	tattttaaata	169830697
agatttgga	cctgtaaaaag	aattttaagcc	ttgccgtctt	tagaagttta	169830747
atgaattaga	tttataacaa	ttacttaaat	atctgagaag	gtttgttaga	169830797
caattgaagt	acttaaaaag	gaattaaaat	atattaagcc	tataaatgca	169830847
gtttacaatg	tttagagcaa	tttaattaaa	aacatttgta	aatgagacga	169830897
aacatttctc	aaaggctactc	ttaaatgtga	ttgttaaaaat	ttgctagacc	169830947
tataaataaa	taataagatt	cgtaagctga	atttcaaagc	ttatggagga	169830997
acttggttcc	atatgaattt	gttactttta	taaattgaat	gttaattttg	169831047
aaaaacaaag	aaacctttca	tcaatatttt	tggcgccctaa	gagctgctct	169831097
tgagggcatc	taattaatag	tttttttatt	attttaaaaaa	tatcattagg	169831147
ccaggtgcag	tggctctctc	ctgtaatctc	agcactttgg	gaggccgagg	169831197
tgggtggata	gcttgagccc	aggagtttga	ggccagccctg	ggcaacatgg	169831247
agaaacctta	tctctactaa	aaaaaaaaacc	acacaaaaat	tagctggatg	169831297
tgggtggcaca	ccgctactta	ggagactgag	atgggaggat	cacctgagcc	169831347
caggaggtgg	agggtgcagt	gagccgagat	cgccccccta	ccctccagcc	169831397
tggaagacac	agtgagaccc	tgtctcaaac	aaaatttttt	taatggctat	169831447
aatgaaaaaa	aaaaatcaac	cagtatgtaa	ggaaaaagct	gaagcccttt	169831497
gccccatttc	ccagaggtaa	ccatcattac	aagttccttg	tgtttctgcc	169831547
cagaaatggt	atttgcataa	gcatagaatc	tctccccagc	cccatTTTTa	169831597
aacaaagaga	tatatctctgc	atctaacatt	ctgtactgct	tttgtgctta	169831647
acaagataac	ttgagccggg	tgtggtggtt	catgcctgta	atcctcaagc	169831697
tttgggagct	gagacaagag	gattccttga	ggccagaagt	tcaagatcag	169831747
cctgggcaac	atagtgcagc	ccgatctgca	aaaaaacatg	taaaatttagc	169831797
tgagcatggt	ggtgtacacc	tgtagtccca	gctatttagg	aggatgaagc	169831847
aggaggatca	cttgagccca	ggaattcaag	gctatagtga	accatgatca	169831897
cgccctgcac	tcctgcctgg	gcaacagagg	gagaccctgc	ctcaaaacaa	169831947
acaaacaaac	aaaaaacaat	atatctttaa	aacatgttca	tgtttcccat	169831997
aagaataaag	attaacatcc	ctctctccct	tcctcatcgc	ctttgggggtg	169832047
tggcctcatg	cctccctctc	gggttgtgcc	caaacttctc	tcaagagtgg	169832097
atcctctcac	tgtctctact	tcctgcctcc	ccagctactg	actgtaccaa	169832147
gactgtgctt	tctgagggca	ccaatgcctc	ccaccttacc	aaacccgcta	169832197
gaggcttctc	agttctcata	tctcttactc	tcgggctttc	aacacgtgag	169832247
ccatcttttc	cttgctgcat	tgcaaagcca	ccttttatcta	gcaatgaatt	169832297
cccatTTgt	tctgggtcta	tttctggcct	ttccattctc	ttccattgat	169832347
ctctctgtcc	ttgggtgcaa	gttttctgat	gacctgactt	gattcatgga	169832397
taaaacctat	actcttgagc	aatgaatgtc	cttcaactcaa	tcctccataa	169832447
ataacaattc	tttcaataga	gcttttctct	ctttcttaat	aagagatagg	169832497
gacagcagag	gttcacgtat	ttcctggcaa	ggcccagaat	gccgttatcc	169832547
ttgattgagg	gcagagttat	cagccaggca	gatagtggaa	ttgatatccc	169832597
tgtgtgaaaa	tggaagagcc	aatctgagct	gtcgccccat	tcctacagaa	169832647
ctagctgccc	gtctttgaat	tcocagtgct	cattcaggcc	tctgcacttt	169832697
cacttgagca	catctggccc	ccactttctc	ctttcctcct	ctcttctact	169832747
aaatagtaaa	agagctcttc	ttcacatctc	agctcagggtg	tccccttgcc	169832797
caggaaacct	ttcctgaggg	tcctccctat	gccccacatt	agccactctg	169832847
ggcttccctc	tgccccagcc	cttaacacaa	cagaatcaac	atgcctgtaa	169832897
cagaattgcc	ctatgcccc	tctcccttag	accaccgtga	gctccccaag	169832947
ggcaggacct	gtctctcagc	agacttttac	tcttgttacc	gaactgatct	169832997
tgggtctgcc	caccgggcac	agtgcagcca	aacactgata	ttgggattgc	169833047
agccagagaa	agtgaggcat	ttattgcagg	gcgccaagca	agcagaattg	169833097

FIG. 1.45

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ggcagctcat	gcttaagatc	agaactccct	gatggcttac	aggtaagggt	169833147
ttttaaggt	agagggggag	aggttacagg	caaaatcata	aattaatata	169833197
tggagactat	gtgttgggtt	ggcctaaaaa	ggcaaagcat	cttgaagcgg	169833247
aagtttggga	gtgtggcaag	tgaaagggtg	attcaaagat	ttttcagtgt	169833297
tgtgatgggt	taaggagggt	aagttttgtc	taaaattttg	gtgtaggcag	169833347
aaaagaacgt	tagctcttgc	cogtgggcat	gatctcttcc	aggccctca	169833397
gcaagaaact	taggagaaag	catggtgggt	ggagttcggt	cctcagcttc	169833447
cccttatcca	aggctctctgt	gcctgcagat	ggcactttcc	atattggtgga	169833497
ggtctgggtt	tctgaaacac	aactcagggg	cgtaggttga	gatgttatct	169833547
ttagtctcta	caggaaacca	aatatcctat	gactctaatt	tccttggcta	169833597
ttgtcttaag	ctactattac	cttcttgcct	gtcaagttgc	gcatttactt	169833647
ttcaaggctt	gctacgtgcc	tgggaatttct	agatttttcc	ttatttccat	169833697
gcttggggag	aggagtgcct	ggcaggctcc	taagaggggt	ctgtgctcca	169833747
tctcgccccc	tatcttgaac	tatcggttgg	gtgctctaga	atctgtatgg	169833797
ggtggaagt	ttcattcatt	ttctgtacaa	aagcaatcaa	tgcttattgt	169833847
ggaaaaccca	aataagagag	ttgctctaaa	caacaccctc	cccagtccca	169833897
ataccttgtc	cagaagaaac	cactgtttgg	tgagtatatt	agtcaatgtc	169833947
tgacagaccg	atcggtatgac	caagttttcc	ataaatggat	ggccatccac	169833997
ttcccttcaa	gggcgagggt	agtttgttct	gatccatctc	ccttttcaca	169834047
gctcagggag	ggaggaagac	ccaggaagga	gagctgccac	agttactagt	169834097
ggcccagctg	ggattttaag	tccgccgtga	ctgaagcttg	gctccacatg	169834147
ccagtctgca	aggccctgag	tgccctcagc	agtaattcca	agcaaagcag	169834197
ggaagcagcg	ggccagggtgc	tgaactgaac	tgctgctcag	ggctcctgag	169834247
cctccccctg	cctcctccct	ctcttctcca	ccctggggcc	tctctctctg	169834297
tcctacttcc	ctcctttaga	tctcttttcc	cctgaaccca	ctcattttatc	169834347
accttttgat	gagttccacc	aggcagacca	tgtcagggaa	tttcttgggtg	169834397
ttcatttttaa	taaaacttaa	ttattaagac	agcctcacia	gtcatgatac	169834447
atttactggt	tcatttttca	catctccgtc	agaggcctcc	tggcagccac	169834497
gtgggaggca	tgaaggctat	ggggtggaag	tgtcagagcc	ttttctggcc	169834547
tctgcagga	gctgggtttg	gggaagcagt	tcctgaccct	tcctctgccg	169834597
gcccaccccc	gttattctcc	agacgctgag	gatgggatgg	aatgagcacc	169834647
aaacatggag	tcaggagacc	tgggactcaa	tcctcctcct	gctgcagact	169834697
atgctcagac	cctgctgaag	gaaggcatcc	tctctgggcc	tcagctgtct	169834747
catgtacaag	atgggaatca	tctcagtcca	aaccagacag	agccactgtg	169834797
agattcagaa	gaaagctctc	gcaatgagag	gcctccccag	gcagatggag	169834847
gcaaaactgc	aagggtggat	tgacgctggg	gcggcgccctg	ccccacagtc	169834897
ctgtaggtcc	gcccgcctgg	gtaaggggat	gggtgaaatt	gggggtctct	169834947
gatgatcaca	gtaataactg	acttttttaa	aaattttatt	tttccatagg	169834997
ttattgggtg	acagggtggtg	tttgggttaca	tgagtaagtt	ctttagtggg	169835047
gatttgtgag	atatttgggtg	accatcacc	caagcagtat	acactgcact	169835097
ccatttgcaa	tcttttatcc	ctcgccccc	tcccaccctc	ccccccaagt	169835147
cccaaagtc	cattgtatca	gttttatgcc	tttgctcct	catagcttag	169835197
ctccacaca	tcagtgagaa	catacgacgt	ttgggtttcc	attcctgagt	169835247
tacttcactt	agaataatag	tctccaatct	catccaggtc	actacaaatg	169835297
ctgataattc	attccttttt	atagctgagt	agtattccat	tgtatctaca	169835347
tataccacag	tttcttttatc	cactcgttga	ttgatggaca	tttgggtcgg	169835397
ttccacgatt	ttgcaattgc	gaattgtgct	gctataaaca	tgtgtgtgca	169835447
agtatctttt	tcatataaag	acttcttttc	ctctgggtag	ataccagta	169835497
gtgggattgc	tggatcaaat	ggtagttcta	cctctagtac	tttaaggaat	169835547
ctccacactg	ttttccatcg	tggctgttct	agctgacatt	ccaacgagca	169835597
gtgtagaagt	gttccctgtt	cactgcatcc	acacctacat	ctactgtttt	169835647
ttgatttttt	attatggcca	ttcttacagg	agtgaggtgg	tgtcgattg	169835697

FIG. 1.46

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tggttttgat	ttgcattttcc	cttatcatta	gtgatgttga	gcatttttttc	169835747
atatgtttct	tagccatttg	tatatctttt	tctgagaatt	gtttataaatt	169835797
gacattttatt	aagtgccttg	cagacgctgt	gccaaaggatg	tcatgtttgtc	169835847
atatgtatta	gctggctaaa	tctcacagtt	gctgtacttg	ttactaatat	169835897
tgtaaaatgt	gtaccagtgt	tatgccctatt	ttatagttga	gaaaactgag	169835947
gcataggggag	gcaaaagcaa	cgtgcccga	gttacaaagc	cagtcaatgg	169835997
tggaaaccaga	attagaactc	tggccaactc	cagagtctac	cttcttacca	169836047
ataaagtcac	cacccctgag	aaatcagggg	ggggccagga	gttttttaata	169836097
atcaaagcaa	cctcacaccg	aagtctaagg	gaaagcagag	gttcggctga	169836147
gcaccagggc	ccctggcagc	tcagcatggg	ggccgtcagt	gacacctgca	169836197
ctcatgatata	cccacacctg	tggtcttcca	aggggacaga	ctgaactctt	169836247
gccacttcat	ccacaaagcc	cccctctatt	tcctcctttc	cctcgactgc	169836297
acttccttga	taacagaccc	aattttgttc	agcaattcac	ccccagggaa	169836347
gctgaccac	aaatcccatg	atgccaacag	ggccccagta	tctttgccag	169836397
ttctctgacc	cagcctcaca	ccaggggtgtg	gcatgagcaa	cgagacaggg	169836447
tagtggttggt	gcaggtgaca	caggggctagg	atatggcaca	ggaatttaga	169836497
aaataattag	actgcgttgg	gcgtcaggac	acaccactcc	aaaatatgac	169836547
tgtaggcgac	caggaatctg	ccacagcaaa	atctactttg	gcattttttca	169836597
agctagttat	tatgagaaac	tgcagacaca	ggagtagctc	tgaaaagctg	169836647
tcctttttgta	aaagaaattt	acatctataa	aggaaatcca	cattagtaaa	169836697
acaatctgta	tcaggaagag	ggctgctcag	agacagcttc	tattacccga	169836747
gaggcttttt	atctttataa	cgagacaacc	tttacttata	atacattttcc	169836797
tccccttacc	ctccaagaac	tccaccatct	ccgagaaacc	caaagcacc	169836847
ctattccttt	ctgtagctca	ggatgctaca	ttagcttcaa	tcactctggcc	169836897
ctactttgag	tctcatgtat	tgtgggaacc	cccggccccc	atacctatgc	169836947
aagtaattat	aaatgttttt	gcttctgcta	atctgtctta	tgtaaaattta	169836997
atttatagct	cagtcaaaga	acctagaagt	gtgggggtta	accaccgttc	169837047
cctcccctgc	aagaggattg	gtctatgaga	gaagtcagct	tccattttatc	169837097
gagcacctag	taagcaccag	gccccagacc	ttaagcttta	catgtgttat	169837147
ttctgattcc	catagactcc	tctagcttca	gtggtattac	ttgcatttttg	169837197
ctgatgaata	aacggagggt	cagagagggg	aagtgcattg	tccaaggtca	169837247
cacaaccagg	aaacagcaat	gctgcgagtg	gaaccaggt	gttgtgtccg	169837297
tgggtctgtg	gtctcgctga	cttcaagaat	gaagccacca	gaccttcacg	169837347
gggagtgtga	cagccctcaa	agggtggcaag	gacccaaaga	gtgagcagca	169837397
gcaagatttt	ttgtgaagag	caacagaaca	aacccccac	cgcgtagaag	169837447
gggacccac	tgggttgccg	ccgctgggtca	gggtagccag	ctttttatttc	169837497
cttatttgct	cctgcccatg	tcctgctgat	tggtccattt	tacagagtgc	169837547
caattgggtcc	atttttacaaa	gtgctgattg	gtccacttta	cagagtgtctg	169837597
attggctctat	tttacaaacc	tctagctagc	tacagagtgc	tgattgggtgc	169837647
attttgacag	agcactgatt	ggtacatttc	acaaacctct	agctagctac	169837697
agagtgtctga	ttgggtgcatt	ttacaatccc	cttgtaagac	agaaaagttc	169837747
ttcaagtccc	cacccgaccc	agaagtccag	ctggcttcac	ctctcagtgt	169837797
gaccaacctc	caagcttttt	tatttcattg	cttggtctcc	ctctctacca	169837847
tgtccatttc	tgcacattta	tttcagcctc	acattgacca	gctcctgcgt	169837897
gccaggcatg	gcctaagtgt	tattcgaaca	aagcttcgga	agctagtcca	169837947
cttgcttctg	tctagaagag	gagggcggtg	ctgggaggaa	cctccctgac	169837997
tcctgctgca	gacccactga	gaggtgactc	ccacacggct	gtcctggaac	169838047
aagacagcag	cttttcttag	gttggttctaa	gttaagggtc	ctcactgctg	169838097
gtaagacagg	gaaatagagg	agataaaaaat	aacaaaacaa	aaggagaagt	169838147
cacaaagtta	caggaaatct	caatatatct	ttctgttctg	gatgctgtctc	169838197
caaacacaa	tgcagcaggg	cctctttgtg	gggggttctt	atgtgagagc	169838247
cacaaaggac	ctcaaagcca	aaacagactg	attatctagc	ccacctccat	169838297

FIG. 1.47

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gtcctccct	ccttccccct	acttccttac	taacagaccc	aattttgttc	169838347
aggaatccac	cccctgccga	gaagaaactg	atcctattcc	cagctcagag	169838397
ccaaatcctg	aatcatccaa	tattaccccc	ttgtcaggag	taggttgagg	169838447
ggtgacaagt	ggcccatgct	ttttctgggg	tcaggagaaa	gaaatgatta	169838497
ttagaacaat	tttggtttaa	actttttttt	tttttttgaa	acagggtctc	169838547
actctgtcac	ccaggctgga	atgcagtggg	gcgatctcag	ctcactgcag	169838597
cctcaacctc	tgcagcctca	agtgattctc	ccacctcagc	ctcctgacta	169838647
gctgtgacta	caggcctgtg	ccaccatgcc	tcgctaattt	ttgtattttt	169838697
tgtagagaca	gtgttttgcc	atgttgcccc	ggatgggtctt	tcacttctga	169838747
gctcaagcaa	tccatcagcc	ttggcctccc	aaagtgcctgg	gattacaggc	169838797
atgagctact	gcaccagccc	taaacttggt	tctaatttagc	agttccaaat	169838847
ttttagatgc	tcatactctc	gactaattac	aataacagat	gatgaaatat	169838897
cgaagtgttg	aactgtcctc	tcaattccag	ccggaacaaa	cagattctgt	169838947
tttctctaca	ttttgactga	actgtcttgg	tgtcatacat	tagatggtaa	169838997
acttctcctc	tgttccaatc	tcccccttct	tcatggctaa	ttagttaaaa	169839047
gcacactggt	gataaacaca	atatgaatag	aaaaattttt	gtttagcctt	169839097
aaaaaatagc	agtatgacaa	tttgtcttga	attttgacct	ttcagtgggtg	169839147
gcttgatatca	aagttacggg	cttgggatag	tgtcatgacc	cgctgaaatg	169839197
gctgcggggc	tgaaattttg	atcgtaaggc	aaatttttgt	acagaaaatc	169839247
gcctgtttct	gctgacttct	gcttttagaca	tcactctta	aggaaaagca	169839297
ttgttatccc	accagctaac	acatcactct	ctaccatata	tcaaagagtc	169839347
tcaagatcct	tctattcatg	aaaaatgaaa	atattctcac	cacatcctcg	169839397
cagtaatggt	caacataaat	taccaagcac	agagacagtt	tgggaatgta	169839447
cattataaat	ggccttccct	acaagactaa	gagtgaatcc	taatgtaaac	169839497
tatagacttt	gggtggtaat	aatgtgttaa	tgtcgggtga	cagattgtaa	169839547
taaatgcacc	gctgtaatgt	ggaatgttga	agtgagggaa	gctgtaagtg	169839597
tatggagaca	gataaatggg	aattctctgt	actttctgct	caattttact	169839647
gtgaacctaa	gactgctcaa	aaaagtagaa	gtaagtaaata	acataagtca	169839697
gtaaataaat	ggccttttct	tgggctgaga	aatgaagaca	tttcctatat	169839747
gttacttgga	cctgtaaatt	cactctgggg	agatatatat	atatatcaga	169839797
aagtatatgt	tacttggacc	tgtaaattca	ctctggggat	gtgtgtgtat	169839847
atatatatatac	acatatatat	tacatatata	tataacaca	tatatattag	169839897
aaagtaaata	tttcttggtta	aaatctgaga	tataactgcc	ctctaaaggt	169839947
gtttattttcc	tgggttggt	tttttggttt	gttttggttt	gtttatttgt	169839997
ttttgaggca	gagtctcggt	ctgtagccca	ggctggagtg	cggtggcaca	169840047
gtctccactc	actgcaacct	ccacctcctg	ggctccagtt	caagcaattc	169840097
tcctgcctca	gcctcccaag	tagctgggat	tacaggcaca	tgccaccatg	169840147
ctcagctaat	ttttgtattt	tttagtagag	acacagtttc	accgtgtggg	169840197
ccaggctggt	cttgaactcc	tgaccttggt	atctgcctgc	ctcggcctcc	169840247
caaagtgcctg	ggattagagg	tgtgagtga	agcacctggc	cgggttggt	169840297
cttatctatt	tacttgatag	ccagggttgg	agtcattagt	ggctgttgct	169840347
tactccttga	acaaacattt	ttgagtgttg	tgtgtacag	gccactggat	169840397
agatagcgat	gaatcccaca	cagtctgtgc	ctcagagccc	acatcttcat	169840447
agatctataa	attaatat	gcagtagagt	atgacaaaaa	aactccaata	169840497
gaagtgcctc	cagggaagat	ggtaccaatt	gaactgggtg	ctggggaggt	169840547
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gtcaaatgat	agaaggcctg	gggcggggaag	gggcaggtaa	agatttgggg	169840747
ctttatccaa	atggacttta	ttgtagttgt	attcatttga	taccttttgt	169840797
aagttccttg	tttagttatt	acatgattat	cataaagttt	gggagcataa	169840847
tggtagaaa	gatatcacag	acttaggaaa	aggatgcatg	ttcctttaat	169840897

FIG. 1.48



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ttggctcttt	taatggactg	agagactatg	caacgctcat	ggctggagga	169840947
caagcttccc	cggccttcca	gtcccataag	gacacctgct	gttaatggca	169840997
gtcctgatgg	agtgtagatc	cctcgggctg	ccatcctcac	aaaggtgtgt	169841047
tactttctgg	ctggcagctc	cagatggccc	tagggactct	gaactcagcc	169841097
tgtgtccgaa	ggcttactgc	aagactgtgc	gactccacca	tggtcagttt	169841147
ccccggggaa	ccatctctct	accaagccca	gttttccatt	gcaagaacaa	169841197
ttgccaagat	gtctaagttt	ctatgtgaga	atthttggcat	cttgggttcc	169841247
ttttaaatag	gacacacttg	tatgctctaa	agaaaaaaag	aaaaggtttc	169841297
tcatgaagca	ttagctttca	agattacagt	tcggtaggat	gttcaagatg	169841347
cttagggtga	ataaaaaatga	cagacagctg	aacacttcct	ataaatgaaa	169841397
caccaatata	gatctaagtt	tcatgcatga	ctctcaatgt	ggttaatgaa	169841447
aaggaagata	aaaaaaaaaaa	agggttgcca	tatttgcagg	gcatttgctc	169841497
ccaaatgttt	caatcctggt	ttcttttagac	tttgaaaagg	gggattgcac	169841547
gttatctgtc	aagaaggcat	caaagcagag	aaatccacaa	atgtgtagtg	169841597
tcagatagaa	ttcaagcctt	cagaaaggac	tccactcctt	tggttactaa	169841647
gagaactagg	ggcttgtatt	tctaagatgt	cactagctgg	aggcgctgag	169841697
caggtaatgg	tctatgtttt	cctagactat	aaaatcctga	ttatatgggt	169841747
taataaaaata	agaatctcag	agttctgtatg	gaaaacaagt	aaacttcagg	169841797
tcttagcagg	cactagcaga	aagcaccaga	gaaaactggg	ggagagggtta	169841847
ggactcctgt	cccaaagatc	cccctcaatt	atcctgccat	gttatcagtt	169841897
ccctctttac	atgtttacca	acatgactac	taattttctat	ttttttccaa	169841947
gactattaga	tgtattcaaa	attcactcct	cttacaagga	tagagaaaaag	169841997
tgcctatcga	tgccttaataa	cccaacatat	atttaataga	agaattaaat	169842047
caccttctgc	aaaggaccaa	gaaaagctcc	atttgatcaa	ttcctttaag	169842097
acatgaagac	ttctcctttt	ctaagaatcg	ccatagtaaa	atgcaagctc	169842147
agcatgacat	accccaagga	aaaatgtatc	tgtcccttct	gcttttacta	169842197
cagttccata	agggttaatac	cgagttgttt	tgcccacatg	ggggctctgg	169842247
aatcttggct	gtgatgcatt	ggtaggatat	ttgtcaccaa	aactgactca	169842297
gcaatcagtt	aaatatataa	caaagcactg	attagtgttc	ctgattcata	169842347
tttgtgcttt	gtttaacatt	taacttccga	attttataca	tctattaaac	169842397
aatattcctc	ttgacattcg	aacactatct	gcacaattaa	taaatcaaaa	169842447
acttattaaa	aattgaaaca	attaaaaatt	cccaaaactta	taaaccattg	169842497
tttacaaaat	tatttaacca	cactctccaa	cacttttaaa	taaaaccata	169842547
agtttaatat	gtcagaccct	tttaaatgtt	tcaaacacct	aaaaagtcag	169842597
caaaaatgca	cacaaaacgt	catactgatt	gaaaaatata	tatgcacact	169842647
tacctttaca	ctgggttaca	aggcatgaag	atttatgggtta	tatatgggtt	169842697
ttaaaaagta	ctttttatact	tattcttata	ttttctctgt	tactttctta	169842747
gagtcaatgc	gatcgtttcc	taggattaga	gtatgaagtg	atacagtttc	169842797
tcctaagaat	acaaatttct	ttcagaacca	aaagaaaaat	aatctcaggc	169842847
cagccagctc	tggggttact	gattccttatt	tgaaactgat	aaagtgtctc	169842897
ccaacattat	tgcacttgag	cttaaatgtg	gcctaagaat	ataaaaagtc	169842947
gtgccttcac	attggtatcc	ttttctgaga	ccagagtgtt	tcctaaagtg	169842997
cgcttcacat	cctaggagac	tagggatttt	tttttttttt	ttttgagaca	169843047
aagtctcgct	ctatcaccca	ggctagagtg	cagtgttggtg	atctcggctc	169843097
actgcagcct	ctgcctcctg	ggttcaagag	attctcatgc	caccacgcct	169843147
ggttaatttt	ttgtattttt	tgtatttgag	atgggggtctc	tccatatttc	169843197
acaggctggg	ctcaaaactcc	caggatcaag	tgatccaccc	acctcaacct	169843247
cccaaactgc	tgggattaca	ggcgtgaggc	actgcacccg	gccaagacga	169843297
ggaattttaa	ccttgcagtt	tgctgtcctt	acgagcacat	ttggccaatt	169843347
atccttccat	gttatcagtt	ccctctttac	atgtttacca	gcatgactac	169843397
taattttctat	ttttttccag	gactattagt	tgtattcaaa	attcactcct	169843447
tccttcttac	aaggatagag	aaaagtgctt	atcgatgctt	aataacccaa	169843497

FIG. 1.49

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catatatatta	atagaagaaa	taatatcacc	catatatataa	tctgccatta	169843547
aaaataatat	gaaataaaaac	cctatcgcat	ttgccattta	catcaacttt	169843597
tctcttcata	gcttcattag	gaacttacag	ctcttcacag	actccatgtg	169843647
ttttaattga	ttatagccat	caatcttatt	tgatattcaa	aatctcagag	169843697
cttgaccaga	ggaaacctct	ttaatctagc	ttcttagtcc	ttccagaacc	169843747
accctgtgat	attctagaaa	gcaccccttg	tttctgggta	caaaagaaac	169843797
ttccaggctt	aaaccatttg	ttttacccta	ctcaggacaa	cccttcctaa	169843847
gagccctgt	ttctttaagt	ggagaaaact	ggttagagaca	aagtctggcc	169843897
atttaggggt	acaggagagt	tgtgggtggg	attagtacta	ctcctgctgc	169843947
tgctgtgct	gctgctgctg	tgtccactgt	agtgacaga	agtgaggaaa	169843997
tatttaagtt	gagttcacat	tagtgttccc	agtttagcgt	gagcattgct	169844047
ccattatggt	gttctaattgt	aaaaatgtca	aacacatttt	tctcaatgag	169844097
atacttaaca	ttttaaccct	tcatccaagc	tatatgttac	acctcacttt	169844147
tctatagtgt	tatatattaga	aaataaatat	ttatgaaata	cttgatattt	169844197
ctcatcaatc	cttgggtcact	caattgaagg	gtgtagaagt	aagggtcagg	169844247
tcaccttagt	gaggggcctg	catctaacc	tatctgaagg	ggcttatgaa	169844297
tttgggattt	attaccttga	cagaaagaaa	tattgagaat	gaccccaacc	169844347
atgctttata	gcaatcgctc	tttatagttt	atttcatagt	gacaagaagg	169844397
aactcatcca	tgggtgggttt	ttccctgagt	gggtctgtatg	gtcatatcag	169844447
aactgaaatc	atcccttctt	gcttctgagc	ccccgtttcc	aagtcttggt	169844497
ctttgtttct	gtaggtagta	aagtgaattc	tttaaatccc	tgccctccat	169844547
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ctgtgggttac	gggatgcttt	gcagtctatg	tcttaaacca	agccagccat	169844647
gttagcattt	cctctagtgg	tgggtgtttta	ggccaattga	gaatgtgggt	169844697
gatattaata	ttttccaacc	agctgataac	aggaaagaca	cttctgcttg	169844747
gagtcactt	tgagaagaga	tttattattt	aggcagcaca	ggacacctcc	169844797
attaatcttc	ccccagcagt	gcccatctac	catcaagtcc	atatactttc	169844847
cccagggttc	aaagaagggt	ataatttttag	ccagcgatta	gtcaatattt	169844897
atcaataaga	ataataacag	taaaattaca	atggccaatg	tttgaatccc	169844947
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aacccttaca	acagccccc	gaaattttgca	ccatgatttg	cttcattttta	169845047
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acagatgagc	ggtggcagag	cctggaatta	gatataatctg	atgttagtgt	169845147
tttgaggaat	cactctccc	aaaagccata	gctcccagac	attcttatgt	169845197
aatttgtctt	tgctgaggct	tgggtattga	tgatttaaaa	gtccccagag	169845247
accagatttc	atctgggtatg	ctgtgggagt	caagtaacgt	ccaaggccaa	169845297
gcctgtctga	gagagggttt	tattagctcc	aaaattataa	taacttccac	169845347
agccttcttc	caccaattct	gccttccact	gaaacagcgc	tgggtgatgtt	169845397
tagaggtagt	agtttgggac	aattatcagg	agaagcattt	tgggtgctatt	169845447
gtcccacccc	ttctgtcctg	agagggtttta	tctgggtcttt	cagtatttca	169845497
aataggtcat	gactagattc	catgcatccc	tagaaaacat	agcctaaatt	169845547
ttaaattaaa	gtatgagggtg	gaagaaacag	cctttcttcc	cttttgtttc	169845597
caaggacaga	tggagtcaaa	agtggaaactg	gggcccgcag	agccggatag	169845647
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tggagctcac	tcgccctgcc	tctcatccag	gcctgaaaat	cataggtaac	169845747
tatgaggcaa	gaggaaccca	gggtgggtggg	aacaccctag	ggtgatccca	169845797
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ctccatttta	agaccacatc	tcctgtctgc	tacagccctt	ctcgcttctt	169845997
tttctttaag	gatattctggc	tgggtgtatt	gggttaacat	gcaagaagag	169846047
agtaccaatc	actccataac	ttgggtaatg	catgtcaatg	gtgatctgtg	169846097

FIG. 1.50



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tggggccgca	aggttccaga	tggttgggac	aactctacaa	tcagtcacat	169846147
ttgggttggg	taaatcccc	actcatcttt	acagctgtat	cctgcaagtt	169846197
agtggctgcc	tgtctctgaa	cttcaccttc	cttatggttg	tcaaaaatac	169846247
ctccatggga	taaaaacgca	gcatctgtag	attcccaaat	agggtgcaagt	169846297
agattcccaa	atagggtgcaa	ataggttcat	tcgttggttc	attctgcagt	169846347
cagggagctt	tcagttctact	ggcatgcaag	acgcaatgat	aatgagaata	169846397
cttcacaatg	agtgtgacgt	gatgactgat	gaatgtgaca	aaggagaagt	169846447
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gagagtgtcc	attctccacc	tcatcacttt	gctgccaaaga	gaaacaggaa	169846547
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cgcacgttgg	ggaagctgga	aagagcctgg	tggctgccgg	gcctccctct	169847047
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ccttctctct	accogtttcc	ccctccctct	ctctctctcc	tccctctttc	169847247
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ccctttgcct	ctcaaaccct	cctccacctt	tccaccctct	ctctgcgttc	169847347
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gctcagagct	gggtctttct	tttttttggt	ttttcttttt	tctttttttt	169847497
tttttttgag	atggagtttc	actcttgttg	cccaggctgg	agtgcagtgg	169847547
cgcaatctcc	actcactgca	atctctgcct	cctagtttca	agcaattctc	169847597
ttgcctcagc	ctcctgagta	gctgcgatta	cagtcatgcy	ccaccacgcc	169847647
cggctaattt	tgtattttta	gtagagacgg	gatttctcca	tggttggtcag	169847697
gctagtctca	agctcccagc	ctcagggtgat	ctgcctgcct	cggcctctca	169847747
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aagtgcctcc	aggaatcatc	aaggagagta	gggcagctct	gagtctccac	169848147
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cctccaggct	gcctctgggc	ctggcacagg	aaggaggagg	agaaaatagg	169848297
gagcccaagg	aaagatcaac	ccagcccagc	ccaaggaccc	ccagccccag	169848347
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gcttttgccc	ttcctctagA	CTCAGCATCA	TCAAGACTGG	AGGGACAGAG	169848447
CATTTGAATC	ATCAGACGCT	GGGCCAGACG	TCACCCACG	CGTTTCTCA	169848497
TTTTATCGTC	CTAAGAGGCC	CAGAAGgtgc	gtaaaatggc	ctgtcccaaa	169848547
cagatgagga	cattaccttt	ctcctcttcc	tcctcctcct	tcttcttctt	169848597
cttctttttg	cttcattttt	ctttcatttt	ttcccccaga	tggtgcattt	169848647
cagagaggct	gagcgtgttg	actaagggtca	cacagctaca	aacatcaggg	169848697

FIG. 1.51

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acctgcgaaa	aagctctgtt	ccctgggtgac	aggtgttctg	tgatcctaac	169848747
acagccggag	gtggggacaa	cgtccttgca	gtaacaaagg	ccctgttgct	169848797
caactcagtg	gacatcaggc	cctgttttca	ttcattagca	ggtcagggat	169848847
tccagtgtca	cctgtgccat	gtattccagc	tgatctacct	gcaagcctct	169848897
actccccatt	ttcccagcag	cagccgcaga	caccacccaa	ctggcagaaa	169848947
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ggactcacat	gtgaccaatc	acattgtctt	tcctgagatc	ctgcattttg	169849047
accagaggaa	tcaagaacaa	aaagtgggtg	caactgattt	atccttaaga	169849097
aatccaagta	atgagttcct	gctgccaaaga	tttctgggat	ttccctggct	169849147
cctgccagtt	tctggatttg	gttcttaagc	atcttctggg	tgtgtgagcc	169849197
ccataccctt	ctcatagctt	cttcagccag	agtcagtttc	tggtttttgc	169849247
aatcaaaaat	aacccaacta	agatttgcta	tcctgcaggc	aagagagggc	169849297
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tatacacatt	attatatatt	acacacatgc	acacacacag	acatatctat	169849597
atatctagag	agagaaagag	atcttcttta	aggaattggc	ctacatgatt	169849647
gtaggggctg	gcaaattcaa	aatcggcagg	gcaagtagtc	aagggaattt	169849697
caaaattggc	agggcaagaa	gcctagggaa	aagttgcagg	cagaattggt	169849747
tcttctggg	agagacctca	gtctttttcc	ctgaaggcct	tcagctgact	169849797
caatgaagtt	tacctatatt	atggagagta	atccactttc	ttcaaagact	169849847
cctgctttaa	atgttaattt	ctttgaaaaa	attgccttca	cagcaacatc	169849897
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cacgcaaaaat	taaccgacac	aattcacata	cogtagcata	aaatgaaccc	169849997
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caaggatatcc	acctaccctg	gcctcccaaa	gtgctgggat	tacaggcatg	169850347
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aaacctgac	tcctcccagc	tcctggcaac	caataaacac	attgggtctgc	169850447
atgttggttca	tgttggttca	ccttccctct	tgcctccctt	tgactgcctc	169850497
ataaattttcc	actcattcct	caagagttag	cccttctgaa	atatcttctt	169850547
tgatcccacc	tactagaagc	acctgtccc	acctcaaact	gagtcaatca	169850597
ctttatttttc	tgtgaacccc	caatataagc	tgatgggtgc	tcctggaata	169850647
gccttttagca	aaagatatta	aaattgccta	atcaacttgc	ttctctttct	169850697
caccaaacca	gcagttctta	aattatgatt	tcagggtctc	ttgacactta	169850747
ccccatattt	ttaccatttg	atgtgcttgt	gtttccggga	agagagttca	169850797
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gagtagtcac	atgtaggaaa	agtgtccttc	cttcaagggg	tttccatcat	169850997
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gctcccagca	gcgggtgttc	agagctccga	gaagcaagca	ggcaccacat	169851197
gttggtctca	gaaggtagag	agagactgta	aagtaaacca	aggaaggctc	169851247
cctgggggag	aggccgcatg	acatgagcga	agccaagagc	aaggactggg	169851297

FIG. 1.52

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actcagccag	atggaacaga	gccccggggaa	gggtgtcttg	agtgtgtgtg	169851347
ctggggggag	catccacgtg	agcaaagtgc	aggcctgcag	aggacccaga	169851397
gaaggggagag	aattttacaca	cccacagtcc	ctgaagcctg	gagaggactt	169851447
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agtgaggtgt	ggggtgtaat	taccaagcca	gagtgcagag	ctgagccaag	169851547
caggtaagag	tactgacccc	gagcccactc	gggctctgag	cagaagggaag	169851597
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agggcaggag	accagccagg	cggggaggct	gacccaatgg	ccccggaatg	169851697
gtgatggagc	agcctgggag	gctgcaggca	ctgaagggaag	aggtagggga	169851747
cgatgactcc	atctgtcacc	tcggcactta	ccccaaaaga	tggaggactg	169851797
ctggcagaaa	cagacagaaa	tttcccttga	gaaggagaaa	gccatgctat	169851847
aggcaatcaa	gattttgcaca	ttgtcagcag	agaagggaatg	agactgtctg	169851897
gttgccgcta	gactttggcc	agggtgttcc	tgcaggtaag	ggcctcgtgc	169851947
aggaggcccc	tgggcaaggg	ccggcccttc	tcctctccct	cagtgtcctg	169851997
gaaaggcccc	agggtgtccc	caacccttga	cctctctcct	tctttctcca	169852047
tattgtctaga	cccccttctc	ttgggtccct	gcctcctccc	actggtgtgc	169852097
acccacacct	tcagacagtt	ctgagcagac	cacgcaaaat	acaactgtga	169852147
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ttgaaaggta	gcaatcactc	atactcctct	cccatgaaca	atcttgagaaa	169852247
aatggaggc	tcagggcaga	agttaccccc	tttacaactg	acgggagcta	169852297
tcctggggaa	tgaagcctga	ggctaaaacc	tatgccctat	ttccagcctc	169852347
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gggtctcccc	cagggtctgcc	ctccaactgc	cccaagcccc	acatgcctgc	169852447
aggcgccct	gggatattctg	ccatgtgcag	ggaataatga	gcctggcagc	169852497
tgcaagaagg	agatgagctc	caggggttga	gggttaagga	cattcaccag	169852547
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gctcaagggtg	ggggcaacag	gttctctcca	ttaccttcca	gccaatacct	169852647
gcatgtacat	tgagatactc	agtaagccat	gagaagcgct	gtgtgaccat	169852697
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gcattcaaaa	tcactctgtat	tcattggtgaa	cctaactttgt	tctaaggcct	169852797
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gatgaatgaa	tgaatgaatg	aagaatgaat	gaagaatgaa	tgaatgaatg	169853847
caccacacaa	agtagcattc	tagcagaagt	gaaaacaagg	ttacctagtg	169853897

FIG. 1.53

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cagactttcc	cagccaggac	tcatactatt	tttaaacaca	tacacctgct	169853947
tcggtgatgt	actgaaggcc	tcaggctact	ctccccgccc	acatctccca	169853997
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agccaagagt	aaatgtgcat	ctagacctac	aggggagggt	ttggcagtta	169854297
cagcaaactc	aggggaatttt	aaatatgccg	gaaactttcc	agagccctga	169854347
ggtgagctcc	cagctctgtc	actgtctctc	tgtgctttgc	taaacagact	169854397
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tcttgctcac	gccgactttt	ctccagttct	cggacaccag	ttctgggtac	169854597
ccaacaattc	aatccagttc	tgacactaac	tatccagagt	tagcagaggc	169854647
cccacagggt	aaaggcctcg	tcccacaaaa	ctgccccac	ttcagacacc	169854697
agtggccagt	ctcagacccc	ctgtacttct	gaccaaccag	ctataagtca	169854747
aggattccta	agactccttc	ctcagggtcta	ataatttgct	aaagaagctc	169854797
acagaactca	ggaacacact	ttacttatgt	ttactgggtt	gttttcaagg	169854847
atgcaactca	gaaacagcca	aatgaaatga	ctgaatcagg	caagatatgg	169854897
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gaagttgggg	atggggctga	aagtctcaag	cttccagtca	aggcttggtc	169855147
tttttggtga	ccagcccaat	cctgaagcta	tcaaaggctc	accaagagtc	169855197
acctcactgg	aacaaaagat	gctcctatac	cctcatcact	cgggaaactc	169855247
caagggtttt	aggggctttg	tgctaggaat	gggagacaga	gaccaaatat	169855297
ctatctattt	atttatttat	ttatttattt	tttgagacgg	agtctcactc	169855347
tgtcaccag	gctggagtgc	agtggcaca	catctgctc	ccaggttcaa	169855397
gtgattctcc	tgctcagcc	tcccagtag	ctgggactac	agggtgccac	169855447
caccatgcct	ggctaatttt	tgtattttta	gtagagacgg	ggtttcacca	169855497
tgctggccag	gatgggtattg	attccctgac	ctcatgatcc	aaccaccttg	169855547
acctcccaaa	gtgctgggat	tacaggcgta	agccacctcc	ccgggcccct	169855597
ttctatgaca	ccacagatgg	gcacagtcag	aatcagagcc	tgagggtgcag	169855647
gtcaaataccc	ttagccctcc	accagtcccg	cccacttggt	ttctgtggta	169855697
gaaagttttg	tttactatct	gtatctgtat	ccccaccaa	atgcgagctc	169855747
ccccatccca	ccctgatgct	gaactgagga	cactcagggc	tttgtgtggc	169855797
tctggcagct	tgcaaatgg	gttctcagat	gaggtattcc	atgcccttct	169855847
tcttgagta	gtaagagtca	atgcttttca	gttcagcaga	aattcatgag	169855897
atattagaaa	gcacttccta	gatctgcgta	gaagttggaa	taggttgcat	169855947
atagaagcta	ggaaggttcc	atccctggag	atctttagga	agatcccat	169855997
gctctgggtg	actcagtcgc	tcattttcaat	catgaattac	aggcattatc	169856047
gagttaagtc	accatgggtg	ctggacctgc	tttctccaaa	gtccctccag	169856097
ctgcagggtg	gtgagcccat	agatgggggt	agtgaagcat	tggttggtcag	169856147
ctcaccagg	cacccttatg	agagtgaagt	agaccgtgac	tcctctgcag	169856197
ttggtttaagg	aagaggacac	tgaacaaagt	catgtgttaa	gagtggtgtt	169856247
tggttgga	attctgatcc	atctttcagg	accctgctca	agcatctcct	169856297
cttttgagaa	gcctggcctg	gccctctccc	catgccccac	tcttctctcc	169856347
ccaggtttaa	ttaaatgtct	cttctcagct	ggtgtgacct	cttggttgat	169856397
tgcaaatagt	gcatactcca	ctctctctcc	acggaactgt	gagctttcta	169856447
agggccagaa	ccatacccac	ctcatctctc	actgcctccc	tggtgccatc	169856497

FIG. 1.54

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gcaggacagg	tggggcagag	caggggcccc	gtgggtgctg	gctaaattgt	169856547
tggagggact	ggctgggagc	ccatacatca	cagacagcag	ataccccagg	169856597
gactggcagt	gtgggaacca	ggtgagaagc	cccagctctca	ggtctgcagc	169856647
cttcctcagt	ctcctcactc	agtagccttg	attcccagca	aaccacatca	169856697
atttctcatt	gcacaccctg	ctcaatgctc	atctgcatag	tgtcctccat	169856747
ccagagcagc	cctgagctgt	gggcacgaat	actaatggat	catgcaaattg	169856797
ccagcctagg	gcaagagtgc	cctggactgt	caattagctc	cccccagcac	169856847
cagctacagt	gccccacccc	ttcacttgat	acaggccagc	ccaatgcaag	169856897
aaggagcaac	agaaaaagaa	ctcggcttga	aggactgctc	tagtcaagggt	169856947
agtgtgttgt	ggcagcctgg	aaagggatct	tccatgtaga	gtgaggggaag	169856997
aagagagcca	gcctggcctc	tcaggaagag	gttcccacag	gcactcttgg	169857047
gaggaaagggt	ggtgctcttg	ggggcccagg	taataattgc	tacacgaatg	169857097
ccacggctct	tggaaactgct	gcttcactct	tttccctcca	cctggccatc	169857147
tatgtgccag	gccaccagcg	tacgtcctgt	gttgtcctct	aaaccaagac	169857197
caaagctctt	cacagccact	cttctctgac	ccagtaccaa	ctccatcctg	169857247
ggagggagga	tgacaggctc	cccgctccct	cacctcttct	tcccaatact	169857297
gctgtttcct	cccagttcct	tctcttccct	ccactgctcc	catctgcttt	169857347
ccttccttag	tggataaaag	cattaaattt	gaaggcagag	agatcggggt	169857397
caaaccaga	ctctacagat	cactcaagct	ttgtggcttg	ggcgaattac	169857447
accatgcctc	tgaacttcag	tttgctagtc	tataaaatgg	agaaaagaga	169857497
agtacctgcc	acagtggcat	tgtgaggatc	attttatgaa	tagctaagaa	169857547
tttcaggtaa	ctcactctga	tgtaccagaa	agttactttg	cttactgctt	169857597
caatcactga	acttaatttc	tactccaagt	tcccattcct	ctcagtggca	169857647
gagaacctc	aatcagttca	ggatgcccc	tcccagtggt	tgcctgaatg	169857697
ttttgggggtg	ggcttacgga	gcatggagcc	tgaagtgggc	tctacctctg	169857747
gtgggcagcc	ctaccattcc	tacagaaagg	cacccaaga	ggttctgctt	169857797
cctgtgcatt	ctgtggtcac	tgtgccattc	aggctgcagc	tggggcctcc	169857847
caggctctag	gaggggtttcc	tggaccgcac	cactgttggg	tgcaggggaa	169857897
gattccccct	ctccttaccg	gacttgcccc	ggagaggtag	gtcaggaacc	169857947
cctgcctgaa	aaagacacac	aagtccagtgg	ctgtgcaatg	ctcctgctac	169857997
acacagagggt	ggcaggcctt	agaggggaac	cctaggctgt	gttcactctc	169858047
ccaggctcca	ctttggaaaa	gccagggtct	gctctcagct	cccacattcc	169858097
gccaaagtct	gggggtttcag	tgccaaacag	gccaccaacc	ctcgaactct	169858147
gcctgagggtg	gaggacaagg	gcaaaccctc	cttgctcctg	ccctccaacc	169858197
agtcacatat	tcttcaggc	ctttcatctc	aaaatccaag	atgtgaccat	169858247
tgtttccgtg	ccacctctgc	cacaggtagt	gaatgccgca	gctcaaattgt	169858297
gcggcagggt	gtgtggtcac	aggaaataac	agaaggagcc	ccggttaata	169858347
tctcagttgt	atgtggcctc	atttttgcag	gccctgtccc	agagtcagtc	169858397
ctcagcacga	gggcagctga	gactcttttc	tcccccatto	cttcctcctt	169858447
ccctcttcct	gggtttcttc	ctttttcagg	ctccaattgc	agcagcagca	169858497
atgtctgggag	cggagatcct	gggagccccg	agccagctct	gacatgttca	169858547
gcgggcccgtg	cagggtcagg	ggcatgctca	tgggtctatc	actggcatga	169858597
ttactaatca	tcaggcagcg	gcagggttac	tgttccctcc	tccctcctct	169858647
gctcacttcc	tcagggtctt	caggctgcag	gagccgaaga	gggaaagacc	169858697
ctgcgtgcac	cctggcaggc	tgataatcac	agctgcagcc	cccaggcact	169858747
aaaaggatgg	gtgggagcat	catccaccac	tcaaagggt	ggggaccctt	169858797
gtccctccca	tgtgcatcca	tctctcctat	ctctgagtc	ccagtgaact	169858847
gctgcctccc	tagagaaaca	gtgctagaag	tcaagtggcaa	gagcagcagg	169858897
aggacttgga	gctacatgca	gagtgtgagc	tccggagtca	gaccagctga	169858947
gttcaaggcc	agctccacca	tctattcact	gtgacttcag	gaagggttgct	169858997
taacctctct	gtgccttagc	tgccctcatct	ataaaacagg	aaacaatgag	169859047
agtccttctc	tatgggggcta	ttgaaatgat	taagtgagat	caggcatgtg	169859097

FIG. 1.55

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atggcacaca	gtaagaactc	cataaacaga	ggtcaccact	gctaatagcaa	169859147
ttattctatc	acctcaggag	actaaagcag	gggaggaaac	accattgact	169859197
cctggacatt	taccaagga	gattatggat	ccatgttttg	cacacacttt	169859247
agaaagacaa	ggaattctaa	ccacagcatc	tgtctccact	gcccccgctca	169859297
tttcagtctc	accggtccac	cctcaacctc	accactgtgg	cccggaaatg	169859347
cggttgccca	gggccaactc	caccccacct	cagccctgct	ctgctcaagt	169859397
ctcacttcca	ctccttccag	ctcccatccc	tttctacca	gctccaccct	169859447
gattttctcca	ccatgacctt	tacctctcta	gtctgatcta	gacccttgat	169859497
cttgccgagt	atctaggact	ttggtgcctt	tgaccctcag	cagcagaggt	169859547
agagagggat	ctcgggtgaag	tctgggatgt	tatagtgact	tgtttatcta	169859597
agtgcctga	gactgtgagt	tccctaattgc	aggagacatc	aacctctgca	169859647
gagagcccca	gagccctgct	caggtgtgat	gaacaggagg	cactcacttg	169859697
atgcctcac	aaagtgtga	gtgaatgaat	gaatgagtga	atgaatgatt	169859747
gaatgaagat	tagtgattat	gttaatgacc	tgcctttttc	atgagccttg	169859797
caacctcca	ggtaccacac	taaagcactt	aatgcttcc	actcatttaa	169859847
tctcatagc	aaccctaaga	cataggcgta	attattgtac	ctattttata	169859897
gatgttgaaa	ctgaggatca	gtgaagttaa	aggcacacag	ctaagggatg	169859947
aatggataaa	atcctttacc	ataacctttc	ctccttagga	caaagtttct	169859997
tcaccaactg	tccaaggctg	tgtttcactg	gggagagtct	gaaattctac	169860047
accaagcatg	agcatgtgtt	catgcagcat	ggtaactctg	ggggaaaagg	169860097
ttcacagggt	ttatcagata	cttacagttt	gttagaacat	atgtgaatcc	169860147
atccatctaa	ccaccggtcc	cctttcaatc	cacccttctg	tccaccccca	169860197
gacagccatt	tgatcaatat	tcatgaaata	tctgccttgc	gccaaagcata	169860247
gtgctggcac	ccatgaattc	cctgggtctcc	agaaatatcc	ttccccctct	169860297
ccctgactac	ccctgcccc	gcctcaccac	acacacactc	cttgcaggat	169860347
ctgggtaact	gggagggtct	taccgccagt	gtcccagctg	cgtgggtggc	169860397
tgcactctgt	ctgaactcat	ctcagctctg	gtggagactg	tggcagcgca	169860447
gaagcgtgca	gggggaatcc	tcaggcagcg	cagccatcag	gacatgaagg	169860497
gcagagcctg	tgccccggct	tccccggctt	ccgctgcagt	ctacatcagt	169860547
cctgctccct	ccagaacatg	atcaaccggg	acagatgagg	ccatgcttga	169860597
tgcataagga	tgcagccagg	gagagctgcc	tcccaaacc	aagtcctatt	169860647
caaaggtctt	ttcttccctc	tggggaggta	ggggagaagg	tccaagcaaa	169860697
gggaactgga	aggggaaagt	gagggcatgga	gtttgtgttt	tctgaatcag	169860747
gactgtgttc	cagccaggga	gacctgtgt	caggcacttt	tgtaatcacg	169860797
atcactttca	gcctcaccct	gcgacctcca	acgacattgc	tgagattggt	169860847
ctccttgcaa	acatgaggaa	attgaggggc	tcaaagggtca	aataacttgc	169860897
ccaaagtcac	aaaacaaatc	cgggacttta	agcctgatct	gcttgacctg	169860947
aaactcatat	ctacttccct	gccctctgaa	gatctatatg	tcctatgtca	169860997
tcacttcact	gttcacacaa	ggtgatacct	ggcttctcca	agcacctgct	169861047
accctgaact	tactgcacca	ctctttccct	cctagCCTGA	ATGCAATTG	169861097
CAATGAGGAG	ATGATTGAT	TTTCTTCAGC	CCTAGACCTC	CAGCTTCCTG	169861147
AGAGCAGgta	ctcttgctc	ttcttgctca	ttattgatcc	atatatttag	169861197
aatagcgcct	ggcaggtaga	tgggtgcttaa	taaatattca	ttgaataaat	169861247
gaatgaatga	atgatccaat	gagccccaaa	gcaaataaca	ataaaggaca	169861297
tttgacagagt	gctctacaga	gagacaagtg	ctttcccttt	actttatctt	169861347
acccattct	cacaacaatc	ccctgacatg	attgggttca	tgtttcacag	169861397
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tcatatgagc	tcaggggtaa	atgatgacac	cctttccct	gccctgaagg	169861497
atctcagttt	gagtatttgt	agcacactta	ggatgttctg	ggccaggctg	169861547
agtggcggtg	gatgggggcg	gtggaggtgg	ggtatgcaaa	gcaggaaaact	169861597
cggcctttgc	tttctaaaag	ctcccagctc	atgtgaggcc	agacttatgc	169861647
atgcagaaca	tttgggaaat	ggtacaagac	agcagcaagc	atagtgtgta	169861697

FIG. 1.56



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attgcacata	atcaggtgcc	aactgcattc	ccttccttaa	ctaactctgag	169861747
tcttttaata	ccagatgggg	accctgagaa	tagattttcct	atcaaacaga	169861797
tgaagagcaa	agatggggagc	cgagggaaat	gctgtggcct	actcattttt	169861847
ataccctgt	aaccagcat	gatgtctggc	ccacagcaac	aggaataggg	169861897
cagtccacct	tcaataatgg	gccactctat	gtgccaggca	cctgctaagg	169861947
gccccacaaa	catcatgtca	ccaatccctc	acagcaaacac	taccacttac	169861997
taaaggaatt	atgaaagtaa	tccacaagaa	gctgaaagca	gggttcagag	169862047
atcgtactca	tcatgcccac	agtctcagag	taaaggggca	agctcagtgt	169862097
ttgaacccaa	ttctagcagc	ctcccaaatt	aatgctctca	atctgactct	169862147
atgctacctc	tgtgcctgga	aggaactact	gttgctccata	aggatgagaa	169862197
gaaacatggc	taagggagca	ctgagtaggg	aggaaggagg	cagcaggagg	169862247
gaagaaataa	attaagaaag	aaagagatac	aaagaggaag	aaaggagagg	169862297
gggagggagg	gaaagaacag	ggcttgtgtg	ttacataaac	tcagacaagc	169862347
acatgcatgt	tttaacagga	ttcctgcagg	tctgacaate	tcactccttc	169862397
ctccctgaac	aaccttagag	gggttgccct	aggagtccta	tatagaggct	169862447
tatggcagaa	ggaaggcctt	gcgtccagaa	ctttctgagc	tcattggattg	169862497
acactggggt	tgcgcacatcag	tctgcttgga	atgccttcaa	aaaatacccc	169862547
agtctgggtg	gcttatacaa	cagaaatcta	ttttctcatg	gttctgaaaa	169862597
ctggaagtcc	aagatcaagg	tgccagcagg	gttgggtgtct	ggtgaggcct	169862647
ctcaccttgt	gttgcaactg	ccttttccct	gtgtgctcac	atggtatctt	169862697
tgtgcgtggg	gggtcttttg	agtctctcct	tgtaaggaca	ctaactctat	169862747
cagatcaggg	ccccaccctt	atgacctctt	ttaaccttca	ttagtctcct	169862797
agaggtccct	tcttcaaata	cagccatata	ggggccttaga	gcttcaaacac	169862847
agggattttg	gagggacaca	aacattcagt	ccacaccggg	gtgcatgagg	169862897
gaggggtcag	agctggagaa	agtgcatgag	ctagttcacc	ttccagagta	169862947
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ctgtattgag	tacatcatgg	gagggacaac	aggacaaatg	gctcctgcag	169863047
tcaggggtgac	tcatgggagc	cttcttcagc	actccctctg	cacattcatt	169863097
ttgtcactcc	ctctctcccc	atgcagttct	ttgctctctg	ttgcaagttc	169863147
ccaggaggca	ggcagagggc	ctgttatcat	cattctttct	tcttgccctc	169863197
cacacttacc	tgtgttcttc	tacttagaca	cattctttgt	gagcatctca	169863247
tgggtgatgt	tggctgcatt	gtacagtggg	cacgtgcgta	tgtgtgtgta	169863297
tttatctgca	aataataccc	atgtcacaag	gcgtccgcag	gaataaatga	169863347
gctattgtgc	atgtaaataat	ctggtacatg	gtagatacat	gaatgaatga	169863397
atatttgttg	aataaataag	tgaatgaatg	aatcttcact	tggcagagca	169863447
tgtgtcttcc	tttaaggggc	aaggatgac	tggtaatcat	cagtttctgc	169863497
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tcagcatagg	ttggctgcac	ccctgtcaga	aaccggagg	taagcagaaa	169863597
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gacaggcaag	gaaaggaaca	atgagaaaca	aagtaaggag	tgctctgata	169863697
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agggagggat	ccctggagga	gatgacatct	gcagtagata	ttccagggtg	169863797
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ggaacagcac	gtgcaaaggc	cctgaaggag	aaccacaaca	cgcactctgag	169863897
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gttcagaggc	agccaattgc	aaacacgtcc	agaagcactt	tgctatttct	169864097
gatctgcaaa	atggagcaag	tcactctgtac	tctgcttctt	cagtgggttg	169864147
tggggaagca	gaaatgagag	gatgacattc	tagccttttg	tgacctctca	169864197
agtgtgtcc	ttatgggtcat	tcaggtacca	tgaaaattag	cagagcccca	169864247
agggggaagt	agcttggtgc	tcacccagtg	gtatccctga	caagttggca	169864297

FIG. 1.57

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aagacaccca	gggtggctta	actttctcct	cagcaaagag	ctctcctctg	169864347
ttccctgaat	cctggatata	ccactgggtc	ctctagtgaac	cccaagcttc	169864397
agcctcgcat	gccctcttct	cgaacagaga	aggcaggagg	gaagcaggga	169864447
ccagccccctg	ctccatcttc	caggattcca	ggcctccctg	gcctggacaa	169864497
gccctgagct	ggcagttagg	agagcagagg	ttgtgaatct	ggtgggaccc	169864547
ccagcaggtc	tttctggctc	agtgccctca	tctgtgagca	gGGGTTCCTC	169864597
AGGAGACCAC	GACAGAGGCC	TGGAACCCAA	GTTCTAATCC	CACATCCTGG	169864647
CTGGGCAACT	TCAGGCAAAT	TTCTAACACA	AGgtaagcct	caatttctct	169864697
ctggggtaat	gatcaggcac	ctgcttaatt	cacagggggt	tggtgggcat	169864747
cacgtggaca	atgtgggtgc	acagcagtg	gcaatgcaaa	ggaaaggaag	169864797
tatgttagta	agtgcctctc	ccctgttgca	caaaacagga	cacatgctgg	169864847
gattgcagaa	aagcaataaa	tgctgcacag	gtgaagaaaa	ctattcaagg	169864897
accctggcca	agtcacaggc	tacctgtggc	cctgagggga	cagctcatgg	169864947
gttggcatta	ggggaagcag	ctctcaaggg	gcctgtatcc	tggggattca	169864997
actctgtgcc	tatgtggcat	tgagcctgtg	tgaatgtgg	gactgtcatg	169865047
ctgttttgc	gtgtgtgcgt	ctgcatgcct	gtgtgtttgt	gtgtctctcc	169865097
accttcgtgg	ggggcaactg	taggtgtatt	atgagccttg	ggtctgtctg	169865147
tgtgtacaat	agcaatgtct	gtgcggactt	aaggacctgc	gccccatagt	169865197
ttgtgggact	ttctgggcat	gcatgcttgt	ttatgaggcc	atacatccgg	169865247
gtattctgtg	aactgctagc	atgggtgtga	tctgtgtggc	agacagaaaa	169865297
tggctgggtg	ggattgtagg	gggcagcttg	ggcaaaggat	cctcagtgct	169865347
aatcaaaatg	ggtctcagtg	ggaacccaag	cagctcagac	ttggggggagg	169865397
ggaagctctt	cctccacctt	ccagggagca	aaccttgcaa	ttcaacacca	169865447
caaggctttg	agtccacagg	cagggacgca	aactttgccc	attgggtgag	169865497
acgccactca	cagaagggaa	atggcttcc	aaatctaate	attgccccct	169865547
caagcactaa	caaccctgtc	ccaggagctg	atggctaatt	aattattgag	169865597
ctggaaaggg	agaagaggta	gaaccaagga	ggaaagaaac	agaaaaatga	169865647
gagagcaggg	cgggtggggg	ggctctcgcc	tgtaattcca	gcactttggg	169865697
aggccaaggc	gggtggatca	cctgaggtca	ggagttcaag	cccagccagc	169865747
ccaacatggc	gaaaccccg	ctctattaaa	aaatacaaaa	aaatttagct	169865797
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ggagaatcgc	ttgaatctgg	gaggcagagg	ttgcagtgag	cagagatcgc	169865897
accactgcac	tccagcctgg	gcaacagagc	gagactccgt	ctcaaaaaaa	169865947
aaaaaaaaag	aaaaagaaaa	atgagagtg	aaggggcccag	aggggctgag	169865997
ggctcctttc	tcctcccaaa	ctccctgtca	ctagaagggtg	ggccctgcca	169866047
taggaggatt	ctgcagaacc	ctcaaggacc	cgcgaggagc	gacggcacct	169866097
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ggcagacttt	ccccctcccc	atgagttcag	gcagtggtgt	aaataagatt	169866197
tcccttgaag	tcgaatgaaa	tcacaatgca	ccacacacag	ggacacacac	169866247
acacacacac	gcacgcacgc	acatcacaca	cacacacaca	cacacacaca	169866297
cacacacaca	cacatacaca	cacacagctc	ccctgggggc	aatctactgc	169866347
cccctgaacc	tcacccatca	gccaggtgcc	tggccccggg	tctgtctctt	169866397
agggttacat	gctcccgggg	ctcccgcaca	taccccgcca	gatgagggtg	169866447
cgcaggggtg	agggcgaggg	gctgggcgtc	ccccgcccc	accgtgcagc	169866497
cctcgcccc	gccccgcccc	tccgtagtgt	cccgccccgc	gccccctccg	169866547
ccgccccctc	cgccgctccg	actctcgccc	cgagcgctgg	cagcaggcag	169866597
caggcagcag	gcgggcgcgc	tgtggctccg	cgccgcgcgg	tcgggctct	169866647
gttcattcat	gattggtact	cggccctccg	agacccagcc	cgagcgcagg	169866697
gaggggagcc	gagtgtgcgg	caggaggggc	gggcggagcg	cggctcccgc	169866747
accgcacgcg	gcgctggctc	ggcagcctcg	gccgggcggc	cgctctggcc	169866797
ccgtgtccag	tgccaggcag	gcttcagggc	accgtcctcg	gccctgggcg	169866847
agggaaaccg	cgggcgggg	cctcgcgcg	ggaagcggtt	ccgaaggctc	169866897

FIG. 1.58



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gcggggagcg	gctagccctg	agtccctgca	tgtgcggggc	tgaagaagga	169866947
agccagaagc	ctcctagcct	cgcctccacg	cttgctgaat	accaagctgc	169866997
aggcgagctg	ccgggcgctt	ttctctcctc	caattcagag	tagacaaacc	169867047
acggggattt	ctttccagGG	TAGGGGAGGG	GCCGGGCCCC	GGGTCCCAAC	169867097
TCGCACTCAA	GTCTTCGCTG	CCATGGGGGC	CGTCATGGGC	ACCTTCTCAT	169867147
CTCTGCAAAAC	CAAACAAAGG	CGACCCTcga	aaggtaagcc	accttcttcc	169867197
ttttgttccc	ctgtctgggc	ttgggggtgc	taggcgccga	ggtgggctgt	169867247
gccacctgcc	tcccttagtc	cggactctcc	tctccacgag	gagcccggac	169867297
aggtgcttgt	atccaaagga	gagagaaatc	ggcgggaggg	ctggtgtgaa	169867347
caccagaggg	agggagccgg	agtggacgtc	tgccccagcg	gcaactggac	169867397
ccctctgggg	caccaggtgt	cgggactctc	ctcctgggga	aatctctgag	169867447
agccgaagga	agcggcatgt	tcacaggtgg	gggtgaccgg	attctctggt	169867497
ggaagtgtgg	tgaagctctt	cccattccca	tgacagctgg	cgtttgagca	169867547
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tcccaggcct	catgtcctgg	tggtccggg	agtccaggag	agcaaccgtg	169867747
aagggtctgg	tgcgagctga	gcttacatca	aggattaaaa	agcataatat	169867797
cgtggagtct	cttctgcctg	gacgtgttcc	cttcaccacc	tgtccccagc	169867847
cgaggcatgg	ctgatctcac	catccgtggg	agagtccctca	aatgggtcca	169867897
ggtgaagtgt	gaaccagtgt	gttgggacct	ggaggacaat	gcaggtctcc	169867947
ttaccagcag	ttcaaaagtt	agtgggttga	ataaagagac	tgaagcagt	169867997
taggaaacgg	gaaatgatgg	gttttgtttt	gtttaatgtt	caaattgtcac	169868047
tacgagtggg	aagattttta	gcagcttgac	acttaaacat	tcaaattcta	169868097
ccatcagagc	ccccatcctg	gatacaggtg	ggagttaagc	tcctacccta	169868147
caggcctgat	agtgagtaga	agtgtaatgg	ggtaaggggac	cccaagtga	169868197
caataagtct	cctcttagaa	cttgggttgg	ctcaccctgt	ttagaaccac	169868247
agagatctcc	ataagtaagc	tgtccttgaa	accccttggg	agaaggggtc	169868297
ccagcttctg	gcccagctcc	caggggcctc	aggctggctg	agccccgagg	169868347
aaagagatct	ctgggtgcag	atcttaggtg	ctgaagctgg	gttggcattt	169868397
acatcctaga	acataggaag	aggctttggc	ccatttgtcc	agctgagtta	169868447
catgtcctgc	tggcaaggaa	gggactgggt	gtcctgttac	cagtcctgac	169868497
cagaacaggt	ctgcaaagct	cagcccaagg	ccttgacatt	ctaagcctca	169868547
cctctcacag	atcctgggat	gctgcttgac	tggggacaat	tttcagcgcc	169868597
aaatataggt	cttctccctc	atcatctgtc	tgaccaccat	gcggtctcag	169868647
aggccagggg	actgtgggga	caggaaagtc	aggggcttgt	ttttaaatat	169868697
tttcaatgcc	tgtggctctc	ctgggagctg	ggtgtcacag	aaagatctca	169868747
agccctagag	tcaagtggag	tctgggtgtg	aatcccagct	ccatcactcc	169868797
ctgcctctgg	gaccttagga	aagtcccccg	cacctcccta	agcctcagtt	169868847
tttcatccat	gaaattcgta	tgctaacttc	cggagggaag	ggtatgtagg	169868897
aagtagagga	aggggaagact	ctgcctcata	tactgtgttg	gctgcagcca	169868947
ccagggaccc	agaggaagtt	gttgtaagga	tgtgagaatc	aaatgaatga	169868997
tgaataggga	gctccgtgca	tagggctggg	aaaagagtaa	gagctcagac	169869047
attgctgtct	accatttcc	tctcctgccc	caaacatcca	ggaattcacc	169869097
ctggatgaat	tcctgcagga	ttcccagagt	acaaaggtct	ttgcttctgt	169869147
ctcctcggat	tctaagaaac	agaagagggg	gtactggcat	tcagtgtgtc	169869197
cctactgtgt	gcttgccata	atgctcgggt	ttttatcaac	aactctcatt	169869247
taaccctcac	aacaatgttc	gtttgaggct	catagcaggt	tcggggccaa	169869297
tgggtggact	cccaagacaa	gctatcgaag	cactggggcac	tcagcccttc	169869347
ctgcacaaag	cccactggcg	tgagttgtcc	aggggtccag	ctgcataatgt	169869397
tccccaggt	atttgcccc	gaagcacagt	catctcactg	ccttgcatag	169869447
tggaatgcta	atcagcagaa	gacccttcta	tgggaggcag	cttggaacc	169869497

FIG. 1.59

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tggaggaagc	cctgggtgag	gaggctagtg	gtcagggagc	ctatcctggc	169869547
caggtcactt	ttccccactg	gggcctcggt	ttcttctttg	taaagggaga	169869597
aacttacatt	aggcatttcc	tcaggttcca	tttggttctc	aaatttcta	169869647
atTTTTatgg	ttgatgctct	caccagagct	gctgctatga	tctcagagac	169869697
gtgaggctca	gatctaatta	gaagcaaccg	gaagagagca	gttgggattt	169869747
ttcaactcag	gaatcagtct	ccctgctggg	ttcaaattca	ggctctgcc	169869797
cttactagct	gtatgactaa	gccttggttt	cctcaactat	aaaacagaga	169869847
tagtagtagt	taccatctta	aaatagctgt	tgtgtgtgtg	ggatttcaag	169869897
gatcatgcaa	gtcaagcatt	tagcacagtc	tctgctacat	aagtggtcag	169869947
caaatttgag	gtactattca	atTTatggct	ctattgtttg	gggcttccaa	169869997
atgtccagag	taaggccatt	ttcgaagtag	gcagtacatc	tgagagcctt	169870047
aacagctcat	ttctggaaac	cttatccagc	cctatccaga	taactaggac	169870097
caaaaacccc	agcacacaga	tgctcgctcc	ttgcttcaac	cctcactgac	169870147
ctctactctg	tggcttgctc	tgaaaacatc	aaagcctgct	caattaaaat	169870197
cctgaatgcc	ttgataatac	aatttagaaa	catacatagt	ttttaaatag	169870247
ggcaaaaact	ctgcatgatt	agtgtgcaa	gaagatatcc	agcccaacct	169870297
gggtgttcag	ggagcgctct	ctaaaggcaa	cagaaatcta	aagtaattta	169870347
agagccatgc	cactgaataa	aaatattcag	gttcatttcc	tgtccttctc	169870397
tctgtttggg	atctttgtgt	gtctttaatt	aaaagtagga	gagccctgct	169870447
tttgggattc	agcctctgca	tcccagtcct	agatagaatt	tctgactcta	169870497
gcagttttgc	atgtgcatga	cacaccaagg	acactgctcc	tggccttgaa	169870547
tgggtaagtg	agacaggcta	gggcattgag	gagaaccaga	ggaggaccat	169870597
acaggtgcag	ctgctgggct	tgtcagcggg	gcaggagaat	ttagggacaa	169870647
catcactaga	ccaaggccat	ctcaacagag	aattgcctag	aagcaaataa	169870697
tcccacacta	caggggtggc	tgggttagaa	atcctccatg	accgagtgc	169870747
agcatgcaga	actttctgaa	agggctgagc	ttcggatctc	cagaatagtc	169870797
atagcatagg	tgagctatga	ctcaacccca	tggctatcag	atgctttttc	169870847
taaggccaca	cggtgagtta	ataggttact	ggttaataa	gggcaaaca	169870897
tgggaatggt	ccgatagtc	ccatatttgc	tcctagatca	atgagcacct	169870947
cagggaaactt	atggaagcag	agtgtacctg	atgagactgg	gtttagggtt	169870997
tattggtcag	ggcagcattt	tcaacctaaa	gatatgggag	agtgacaaga	169871047
gacagacagg	catagagaag	cagtagccgt	gttgtcacat	agtcctgagc	169871097
ccaaggggca	ggcctttggc	aagtcatttc	accttgtaaa	tgctagtttc	169871147
tttatctgca	aaaggagaat	cctgatgtat	agaaatgttt	gtgctttggt	169871197
ctttaccat	ctttgcatct	ttgcctgtcc	ctttaattct	ataatgctct	169871247
cccacccac	cccttgctgc	cttgtcta	agttaaaatt	ccaccgacat	169871297
tccaagacct	cactcagcaa	tttccatatt	caggaagcct	tctccaagcc	169871347
ccagagagaa	gtgatttctc	ccatctgaat	tcccatatcc	ttttaagggtg	169871397
tacattttct	tatgactcac	aatcgcgctt	ggaattagac	aatcaacgga	169871447
ggtgttaacc	ccctttcccc	accaccagag	gtcaggggtc	ttgggggtag	169871497
gagctcgtct	aactcatcct	tcacaactct	ctgcttggtt	ctgtgcacat	169871547
agtaggtact	taataaaaa	tttccctagag	taaactataa	ataatggaat	169871597
ggttggtccac	tctccattat	ttgctagaat	tgcagaccct	gcaggaaaag	169871647
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gaatctgttt	accatttagc	aggaaagtgc	tgagaacagt	gattctactc	169871797
ccactccctc	ataatcacia	aggatatgagg	aaccacacc	cagcaccagg	169871847
cacagttctg	gtccctcaat	cccagaagaa	gctcaatgga	gctcaagata	169871897
aacagaaaga	gagagatgga	aaagaatgga	agacagagga	gaaggactta	169871947
ctgcctaaaa	tcagtgggat	tgttttgact	tggctctctg	aaaagggcca	169871997
aggcttagac	ctctttgtct	gcctggaagg	gccttgctcc	atgaatgctt	169872047
tgtaaatctg	taagtgaata	agtgagcata	tgctttaaca	aataagtga	169872097

FIG. 1.60

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aagatgaatg	attgaatgaa	tgggggaagc	agtaaaggag	tgaatgaatg	169872147
aagcaacaaa	tgaattatca	actgaatgac	agaaagaatg	atcgaataaa	169872197
tgaccacatg	aatgaatgaa	tatgtccata	aatgaatgaa	tgatgaagtg	169872247
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tcatctcccc	aaagttgaaa	aatataaatt	cagtcaagaa	gagtcctggt	169872347
aatttttttg	atactggtag	gtgtatagtg	tcttttgaga	aggtgaggag	169872397
atgtctctaa	gttttcactc	ttttgctgaa	acaaaagcag	ggactgactc	169872447
acagtgattc	cccttgtctt	cccttatatt	tcaggttcgt	tcacccttgc	169872497
ctgggtgaga	tcagaatctg	tatatattatc	cactcattta	tttgttcact	169872547
tagccagtc	cacaattgtc	cttcagcatt	gcttccttgc	ctaagatcca	169872597
ctctggcttc	ctcatcctcc	ctcttcctcc	atctcctcat	tcacctggcc	169872647
aactcctact	tatctttcaa	ggcctcattc	aatgccaccg	ctctgggaag	169872697
cctttcctgg	cttctgtagg	cagagcacat	ctctgccttc	tctctttccc	169872747
catagctgct	gctgcttccc	ttaactacaa	ttctgaacac	actatgaggt	169872797
tgtcattatg	ggtttacaca	tttatctctc	tgactagctt	tcaggcactg	169872847
agtcttatcc	cagggcctct	gtcaggcctg	acactgcac	caggcttgat	169872897
ggatgctggc	ggcatggagg	taaggatgga	tgggccagag	tgtgcgttct	169872947
tgatggctct	gagcgggtgtg	agaatgcggc	gggtgcagatg	aggaatccag	169872997
gtctgctcct	ggggagaagc	tctgcaaaat	tctgcataat	ggccgtggag	169873047
ctgatgttcc	cattcatcag	gcagggaagg	aacagttttt	agaaaagaga	169873097
gagagagcct	aagagtccca	gggccttcag	agaaacatct	ctttaaatgc	169873147
ttccctctcc	tccgggtagt	attttaaata	ggtcaccttc	tgggaagtagt	169873197
ggtagtcagt	tgggatattg	ctagcttccc	gtaccccagc	catgggagta	169873247
gtactttgga	ttaaatcttg	ttattcaagg	ccagactaaa	agcctcattg	169873297
gtgcgggtgg	gggaagtagg	aaccacattc	cactcaaate	aggaagctag	169873347
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ctgtaatccc	agcagtttgg	aaggtcaagg	tggacagatc	acgaggtcag	169873547
gagttcaaga	ccagcctggc	caatatgggtg	aaaccccatc	tctactaaaa	169873597
atacaaaaat	tagccggggca	tgggtggcatg	ctcctgtaat	cccagtcact	169873647
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accaggtgag	ttggcagtg	tggctttgct	gctgcctttt	gtcccatctc	169873897
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acccttggtg	atctcccat	ccctttgagc	tgtggcctct	gattccagcc	169873997
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gcttttagcc	ccatcccaac	cccgcctccc	cctagatctg	tttccatttc	169874597
atctgacact	gtggaagcct	gaatatgaaa	tgattggggg	cagaaggcca	169874647
attagcaaat	tcattaatag	gattaaacat	ctctcctctg	ctctaataat	169874697

FIG. 1.61

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ttatgtgaac	taaaattttc	tctctttgtt	atagccatca	ttgcctgtca	169874747
gtgaagatag	agtgtttaaa	tatcttccaa	gtatgttaga	attgcaaacg	169874797
ttcagaacca	gggaccagga	tcagagtttt	cacacgggcc	aggtgggcaa	169874847
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gaacttgcta	gtacattttgc	aagtacctta	ctgctcatct	cctttctctc	169874947
cttagccaca	tgttggtgcca	aatcacctgc	gtatgttata	cggttgttat	169874997
gagcatacac	tcctgggttag	gcagacctag	aattcaaatac	ctggctctgc	169875047
aactcattag	ctgtgtgaca	ttgagcaggt	tacctcgctt	ctgtgaactt	169875097
tcattctctac	ataatctaga	aaatgaaagt	attgttgata	attccctccc	169875147
aggttggttat	gaggattaaa	tgcagtcattg	catgtaagat	gcagcgggtca	169875197
gcactcagaa	tgcgctaaag	gtaaattgtt	actatctggg	tctactccac	169875247
ttaaagtgtg	ctcctccaac	caacagcctc	agcatcagtt	gggagcttgt	169875297
tagaaataca	gagtcctcggc	caggcgcggt	ggctcacgcc	tgtaatccca	169875347
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ttagccaggc	gtggtggcgg	gcgcgtgtag	tcccagctac	tccggagggtt	169875497
gaggcaggag	aatggcgtga	accaggagg	tggagcttgc	agtgagccga	169875547
gatcgcgcca	ctgcactcca	gcctgggcca	cagagcgaga	ctccatcttg	169875597
gaaaaaaaaa	aaaaacctca	actcagtgag	acctaccag	tcagaacctg	169875647
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atactggcct	aaagtacaga	ttatggaact	atgtgtattg	tattacacaa	169875747
aattatatat	caagccagaa	gaggcttttg	ctaagacttc	tgattttaagc	169875797
ctcattttac	aaataagaaa	atagaatcca	gagaagggtga	gtggtttgcc	169875847
cacaatcaca	cagctcaagt	gttaggcctg	acatccgaac	cccagccctg	169875897
gtcatctcat	ataaattgtt	aagaagtcag	atttccagat	ttgcattttct	169875947
gcaatcaagc	ttgtctgttt	ttctttctct	ctctttcttt	ttacaacaa	169875997
agaagtgcag	gatgatgtac	gccatttaag	ttttagttta	ctcattttta	169876047
atgttattcc	agccaacaga	gatcctgaat	cttgactcca	ccagccatca	169876097
tcttagctgt	acctccaagt	tttctgctac	ctgaagaaat	gataaggagg	169876147
cattctaggt	ctttatctaa	gttgcttcta	agaacatggg	ccagaacagg	169876197
gtgcaggaca	gagccatgtg	gactgcgaact	agagacttgc	ctgcataatg	169876247
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aggagtctaa	acagacacag	gtagggcctg	gggaatgaaa	gtcaaatgcc	169876397
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aagtaatcct	tttatttttg	taggagtcct	gtaatgggtt	cattattatt	169876497
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ccacctgggc	tcctgcctgc	agctggaggg	catatccagg	acaagcaagc	169876647
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caggaactga	aaatgacagc	ctcctcttgg	ccccatcagc	tcctcaccca	169876747
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gtctgccaaa	tttggttttt	tcccatgttg	actacttttag	tgactttttct	169877197
gaaataaaat	gtgctttcaa	aacacaattt	ttgatgcctc	tactttgcta	169877247
gtgctttaag	catctcttga	gtgtgcctgt	gagggtatttc	agcattggag	169877297

FIG. 1.62

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ttggaaccag	acaggaaaag	gaaagaaacc	gatctgtatc	gggcacctgc	169877347
tgcattgcaa	ggactgtgca	aggtgttgac	aaaataacaa	cagtaacaaa	169877397
cataacattt	aaatcgctct	tgtgacattt	atatagcaat	ctgtgccaa	169877447
taccactcta	agcgctttcg	gtacattaag	ctaatttaat	cctcacaaca	169877497
accctatgtg	gtaggtagt	tgattattcc	catgtaacag	atgaaatctc	169877547
acactatgag	agacaggcac	tgatccccct	attttataga	tgaggaaact	169877597
gaggcttggg	aagaagtgac	ttgcccgaag	gccccgatgc	ctggtggaag	169877647
aacagtgttc	acaccagctt	tggccacttc	caaagccctt	gatgttgaca	169877697
ctccaaatgc	aggcctcact	catttcctag	aagcgcttta	tgatttgata	169877747
tgtcctcagg	gtgcattata	agaggaggga	ggaaaacctg	ggactacaat	169877797
gagcattgaa	tcttgtcctg	atcttctcag	ggaccctctg	tcattcccga	169877847
ttgcctattg	catctgttct	cacctggtac	taccattccc	tcctccctgg	169877897
tttttccctt	gctaagtgc	cactctatac	gttggtccat	atcatgtagc	169877947
ctctgctgga	ggcaagtctg	gttcccatct	gccttcccct	gaagaagaag	169877997
ctgctggaaa	attagagtta	tgttggacac	agtctttgtc	cccaagggaac	169878047
ttctctctgg	tcataatcat	tatatataca	gcaaacctat	agcatgctat	169878097
gtgctagaca	cttttagcaac	ttggttttat	gtaagcctta	cagtatcccc	169878147
aggaagtgag	cactattact	agaccctttc	cagatgagga	cactgaagac	169878197
tagagggcat	aagcaaagt	ccaatgtctc	acttctcata	agtggaaaag	169878247
ccaggattcg	aaccagatg	gtttgcctcc	agtgcctgca	tgctgaatca	169878297
ctggactagg	ctggacctga	gcatttagag	gacattatag	attatgtaac	169878347
actgtgggga	ttcagaggat	ggagaaagca	cctctatctg	aggggcaggg	169878397
gctggagaat	tagagaagat	ggccgaaaga	ggcggcatta	gagctcaaca	169878447
aaagagctag	gggttggccc	aggcaagaat	gtagggttagt	gaagttctag	169878497
gcagaaggaa	caggataagc	aaagtacacag	aggcaggcaa	caagaagggg	169878547
aaagaaatga	aaactgacag	tgatgttttg	tatgcttgtg	acttggagga	169878597
tgttaacaga	aagaggatgc	catcagaagt	gggaggcaag	gagcagagtc	169878647
aggctgtcca	tggtcaggag	aatgggacaa	ggctcctagga	ggtagtagac	169878697
agcaaggatg	aggaaagcac	caagcaagta	gggatcgaga	ctgtgccctc	169878747
tcagcaccac	ccttgtcccc	ctaagtgtct	ccccgtgatc	actgcagctt	169878797
acatttgatt	cctccttctc	ctctcccagg	gaacttacta	tttgtcccca	169878847
tgatttagcc	tttgattacc	ttgaactggt	ctatcatcat	tcctgtaaa	169878897
cacgcttgac	tctccagcaa	gagtgcctt	tcctcagaga	cctggacctt	169878947
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actttgagga	tctccccac	cgcacaacag	catattcaca	agatacgaac	169879147
atcaaagatt	gtggcttggg	gtgaaaacat	agcacattgg	aggccattcc	169879197
ataacagctt	agagctgatg	aagagaaaaa	gatatggtgt	gttgggtgaa	169879247
atagaactga	aggccagctc	tagcttaccg	tttaggagct	gtgtggtttg	169879297
aagaaattgt	ttagccctt	tctgcatatc	agcttcttca	tctgttaaac	169879347
aataacaatc	atggtatcaa	ttcattggat	tgtcatgagg	attagtgaga	169879397
taatatgaat	gtgttttagta	agctataagg	cagtgcatac	gtggtgggga	169879447
tcagtattag	atgacaataa	tgggtcatagc	aataataatg	atgttgatag	169879497
tggttggtgat	gatgtttgtg	atggtggtgt	gatggtggtg	atggggatgg	169879547
tgttattcgt	ggtggttaatt	attatattat	ggatgtgtga	gtctgttttc	169879597
acactgctgt	aaagaactac	ctgagactgg	gtaatttatg	aagaaaagag	169879647
gcttaactga	ctcacagtcc	tacaggcttt	ccaggaggca	tggctgggga	169879697
ggcctcagga	aacttacaac	tgtggcagaa	ggctaaaggg	gaagcaggca	169879747
tattttcaca	tagtggttagg	acagagagag	agcaaagggg	ggtgtgctac	169879797
atacttttaa	acaaccagat	ttcatgagaa	ctccctcact	atcacaagaa	169879847
cagcttgggg	gaaactgccc	ccatgatctg	gtcacctccc	accttgtccc	169879897

FIG. 1.63

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tcccccaaca	ttattaacta	cagttcaaca	tgggatttgg	gtgaggacat	169879947
agaggcaaac	catatcaagg	gataatattg	ttgatgatgg	cagaggtggt	169879997
gggtgacagta	atgacagtag	gggcttcacg	gcaataatga	tgatgatgat	169880047
ggaggattac	aatatttagtg	gtaatggtga	ttattatagt	ataggtgatg	169880097
ttgattataa	gggtggtggt	gggtggtgaca	atggtgatgg	tggtagtgat	169880147
gggtgatgatg	atgataatag	taatgatggt	gatatggtag	tatgacagcg	169880197
atggtggtat	gggtggtggtg	gtgatgatag	tgacggtggt	gatgatggtg	169880247
atggtgatgg	tagtagtgat	gggtggtgatt	atggaggtgg	tgatggtgat	169880297
aatggtaatg	atggttagtga	tgggtggtggt	ggtagtgatg	atggtgaagt	169880347
gatagtgatg	gtggtggtta	tggaggtggt	gatggtgata	atggtaatga	169880397
tggtagtgat	gggtggtggtg	gtagtgatga	tggtgaagtg	atagtgatgg	169880447
tagtggttat	ggaggcggtg	atggtgataa	tggtaatgat	ggtagtgacg	169880497
gtggtggtgg	tagtgatgat	ggtgaagtga	tagtgatggt	ggtggttatg	169880547
gaggtggtgg	tgacgatagt	gatggtggtg	atgataatag	taatgatggt	169880597
ggtgtggtca	taatgatagt	gatggtggtg	gtgtggtggt	agtgatagtt	169880647
gtgatgaaag	gtggtgatgg	tggcagtggt	gatgatagca	gtagggctga	169880697
tggtggtgac	agtgggtgatt	atatagtgat	gtaagtagta	gtgttgttgg	169880747
aaggatgata	gtggttagtgg	tgtcaacagc	actggtgaat	ttaaggcaat	169880797
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tccaaccccc	agaacttgaa	ttcccccagg	tgtatttgtc	aaaagtagga	169880897
aagaataaga	caaatcagcc	catgccttca	gatttcttct	cttattcctg	169880947
gttggtactt	tcagaatcat	tttaatgtaa	gctgctttct	tgacatttgc	169880997
attccagcac	gtggcacagt	gccatggctg	gtacatcgtc	aagtcttcaa	169881047
taaatatattg	tgaaatgaag	ggatgaactt	gcagaaagac	acaggctggt	169881097
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gggggttatc	aggcacatca	gaatatacct	gcattaacac	tattgccagc	169881197
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cactttgccc	tcagaggtag	ggtctgttct	actgggattc	tgtgctaact	169881347
gatcacagg	aacagtggg	aaaatggcct	ctcccaccgg	ctgcttctgg	169881397
agagtcctaa	cctccctcct	cagtgcactt	gctgtgcggc	aggaatgaga	169881447
ggcacatcct	ggctctggag	atgttcttct	tggcagcaag	tcctcccaa	169881497
tggcaggagg	gattacagaa	gtgatttcag	gtgccagtgc	ctccacagcc	169881547
caccacacct	ctgctctagg	caagtcagag	gcacctgtag	agcctctggt	169881597
ctttgtgtgt	ggaaaaggaa	taatctcgca	ccagcattat	aaggttctca	169881647
tggttttttag	gggtgtggca	tatagtgagg	gctccgctaa	tggcagcagc	169881697
tattaatatt	ggtatcattt	attatttcca	ttactagtgg	agacattgag	169881747
ctgatatatg	ggtcaataat	gatagactag	agactttgtg	tgtctctttg	169881797
gtggaacatg	tgtggcttgg	attcaccttg	aatccctga	ttctggcact	169881847
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tgagatagat	agatggcctg	caggcatttg	ggttcaaatg	ctgttctgct	169881947
gaataaggaa	tacgatttgg	ggaccaaaca	cccttggatt	taaatcccag	169881997
acttggtttt	ccctggtggt	gtggccctag	ggaagtattt	ctgctgagcc	169882047
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ctttgggaag	aggatggaaa	ataaagtgt	aatggagcga	gggaggggaat	169882147
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ttttggatta	gagctgcctg	cagcctttat	ctgtctatgg	agttgattta	169882247
ttattctccc	aaatcttgg	acaaagtcaa	gaaagggagg	aaggaaggga	169882297
gagagatggg	taataagagt	atggaagaaa	atgtaaacad	gtagagtgca	169882347
gacagcggt	gcctgcccat	agcaagccct	ccgcagaggg	agaattaatt	169882397
ggctgttgct	atgtgtattg	ttgtgattgt	tcttattgtt	gaaagatgta	169882447
gaagagaaat	caggtagaaa	gaattcaagc	aaagacaggg	ggtgagcgaa	169882497

FIG. 1.64



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agcatgaaga	aatgaacaga	atctgggctg	aattttcttta	aggttataaa	169882547
gcactctatg	caatctgagg	caggcagtc	ccaagcttct	agtaccaacc	169882597
tgcgactcta	cgtgtcaaac	aggaggagtt	ccttaaagg	tgtttggtgt	169882647
gtgcatgtgt	gtagagggat	gaagcatgta	tacctctttg	tatacatcag	169882697
acactgtgct	gggcactgcc	cttaaattat	ctcacttaat	tgtcacacag	169882747
tcctatgaag	cagatgctgt	tattgtctca	gttttagaga	caagaaaact	169882797
gaagctcaga	gaaaagaagt	gatgaccagc	ccaaggtcac	atagctgcta	169882847
agtgcaggga	cagcatcaga	accagggccc	gtctgtgccc	ttaggtctca	169882897
gagattctac	acctactacc	tagtattagc	tcaatctgac	ccttggggaa	169882947
attaagcccc	aggaaagctg	tttccttcag	ttgcgagcc	aacttgaagc	169882997
aatggtagac	tgaatcccag	ttctgactgc	cagctccaca	gtccctccct	169883047
ggggcctcgc	acatcattgg	aactgacaac	acaagaatct	tccatctcct	169883097
tccttctctt	cctccttttc	ttggctgtca	tccaaaactt	taggggaatg	169883147
cattataaac	caacttgaga	gacagagaaa	ggctgtagga	agatccaact	169883197
caaaaacatt	ttggtgtttg	ctttacctcc	gcctgagcgt	ccctggagat	169883247
aaacctcct	cactctcgcc	caccattgct	ctgctatgtc	aatttcagca	169883297
gccggactct	ggggctgaca	tgcattgccc	cttctcaacc	cagacaccac	169883347
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cgggcagtg	tggtcagaac	ctggttctgc	ctttctcggtg	cgtgtggcct	169883447
tggataagtc	atctactctc	tatgagcctc	agatccttcg	tctgcaaaac	169883497
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tgggttggtta	cagtgtgagc	ccatgggtct	caggcaacag	acttgataaa	169883647
tacaggttcc	tctgcaacca	caatcctagt	ccttagcaca	agcatgacac	169883697
tgcttgcat	gtgctatccc	tcccatatcc	atcagccatg	gcagacacag	169883747
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tggttactgc	tccatctgct	cagtgcaggc	tgtctctctg	ctctgtctcc	169883947
cacctgcttt	tgtgagtgtg	tggttctatg	tttgtgtata	tgtgtgttta	169883997
aactcctctt	ccagagtga	agaccatttc	agtcttttgt	gtgctgattt	169884047
gtagaaatca	ttgaactttc	agaatcccat	ttgcaatgtc	atgtctgtgg	169884097
ctggggatct	ccaagtaaca	tcagcttacg	tctgggaagg	acaaggggaa	169884147
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gccaccttta	ggagtgcac	aagagatgg	gtttgaatat	aaatttgaag	169884247
tccttccaaa	gatttaacac	tcctttggct	gacaaccata	atctcaagga	169884297
ggtaggccta	ggctagagca	attatacttt	agggttaacc	tagctgctat	169884347
aacaaataaa	ccccaatatt	gcagtaggct	gaaacataga	attgttttta	169884397
tcattcatat	aacttcttga	tgggccagta	gccttcttcc	atgtagtcc	169884447
tcagggaacct	agcctccttc	catcttggtg	ctcccccaac	cctaaggcat	169884497
cctctacatc	taggtgaaag	gggagcagaa	aatgtggtct	ctggcccagg	169884547
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ctgcatggca	gttgcatttc	tcattgtggt	ttatatgttg	gtcacatgat	169885047
ctgagctaata	gggagtattc	gcctgacaga	tgagtccttt	ttgctgggtg	169885097

FIG. 1.65

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tgccagcaaa	atcaggcttc	caagccccc	aggctcactg	ccagaggctg	169885147
gggaattcgc	caaggtaa	gccacottgt	gaggtctttg	ggacacagcc	169885197
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cagcccaatg	gcattttgga	gccacatcca	caccocacgg	gtctgggtct	169885297
gtttccagct	gcaactgggac	attctggcag	attctccctg	atctctgtaa	169885347
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gagttttccc	tctaaagagg	acctcctgag	ccacttctga	acaggacttg	169885447
gaacaaagga	atcttggcgc	tttgatgatc	gtgtctgcag	cagttgttga	169885497
aatgagtcctg	acactcgcca	gtgccttagt	aggaattata	attacatcag	169885547
gagacccag	gcaaccaagt	aaactgatta	gctactgctc	cgagttgata	169885597
gatttttttc	tctctaggtc	ataaataggg	ctgtgggaga	tggtggaagc	169885647
atgctgggtg	gaacaggtcg	agatgggctg	tacattcagg	aagcccaacc	169885697
aagtgggtg	ggcagctccc	cctgccccac	cctgccaccg	gaagagacag	169885747
tctgacaggt	gccaaggtta	gagttcagtt	ccctcggcca	gggactgcac	169885797
tctgatcctt	gcgtgctgca	gagagctgtc	ctcagagcag	gctgagggtg	169885847
gctgaactgc	taggcgatgc	tctgggaagc	cctccgccag	gaaagccgat	169885897
gctttctgcc	aggcataatt	attgcatgga	taattacacg	attcagagcc	169885947
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cctgcacgtg	tcacctccct	gggacaatcc	accctgccc	attagcacat	169886247
atatgcggat	gacaccaagt	gtctttccag	ccaggcatct	gcaaatgcat	169886297
gctgggcac	tccttcacgt	gtctctccca	gccattgca	ctccagcctg	169886347
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aacctgctag	tcctttccca	ctccctgtgc	accatccgaa	gccaggatcat	169886497
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ggctttcttg	tggtggcctc	ctccctggcc	tcccaccct	catcccctgg	169886647
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gattcaatga	catattcatg	taaaagactc	agagcatgac	cagtgcacag	169887147
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aaactttgcc	taagatttag	gccttgggct	cagcctgatg	caccccatth	169887647
actgggtgcc	tgctctgaga	ccaggatacg	tggaaagaac	ccacgcctgg	169887697

FIG. 1.66



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gagccagctg	tcctgggctt	tggaaatago	tgtgtccgta	ggtgagacct	169887747
tgtctctgca	ggcctctago	agagggggcta	agagcatgog	ctctgcaggo	169887797
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ggagcctgtg	acctttaccg	ccgtgtgatt	ctctgactca	gactgcagtg	169888197
ttgcagtgcc	agccaaacat	ggtgacaagc	cccttcccag	gcaactgagg	169888247
acaggcagga	gtgttctgga	atcttctcct	ggagtgggag	taaggggtggg	169888297
cagagccatg	tgatgctgca	ctgtccacct	ggttgaagga	agtaattcca	169888347
gactctgtct	ctgacatctc	tattagccaa	gggtgagggg	gttaggttcgg	169888397
gtcatgttag	ctgcgcctcc	cacctgcat	cctgggccc	gaaaccacac	169888447
ccctgtgcag	ggcttctgtg	tcagagtcac	cagggaatg	ggctgctgag	169888497
gatgccagca	ccaaccaggc	tgctgtcctg	gggcgacatg	tctgccatct	169888547
tacaacctcc	cttccaatat	tcaccatgtg	ccagctccag	ctcagtcact	169888597
gagcctcaca	tcgctggacc	ccactgtgtg	ctcagggtca	tcaggcactt	169888647
tcgcctgtgg	ctgggattga	gacctggctc	ctccaccttg	cacttgtgtg	169888697
acctggccat	gctcatgtca	ccctcctggg	caccccaata	ccctcatttg	169888747
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tgcttagaac	agtgcctggc	tcctactaca	cactcaataa	tgccagctat	169888847
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ggaggctaca	ggaagggaag	gcatgtgcct	gggggtggatt	cgaactcagg	169888947
cctgtcgggt	tcagctctgg	gcttttctgc	tctttccagg	ccatattgga	169888997
actgccatta	gagggactca	ttcattccca	tacatgtcaa	atatgcactg	169889047
cacctcagatt	acatccatct	ttaattgaag	acctatcctt	ctgggctttg	169889097
gagatttgct	ggacttgggg	agtcaccaat	acaactcagg	tagtgacatc	169889147
tgggaggaga	agactgaggt	gtcatcagct	gcttcttatc	cccctgcctt	169889197
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cgcgctctgt	tgccagggt	ggaatgcagt	ggcgcgatct	cagctcaggg	169889347
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gacctcaggt	gatctgcccc	cttctgcctc	ccaaagttct	gggattacag	169889547
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gacctggtac	aggcatcacc	ttctctggga	tgcttccctt	gtccctccct	169889647
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gctcctaagc	agccccagca	tggagctcca	agccatgaag	ctctaataatc	169889747
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gagacagggt	actggcccag	tagaaaagta	gaaaatacct	gggcttgggc	169889947
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atcagccact	cacagctgca	gcagaaccag	gcagttgagt	ttgacattgg	169890147
ccttttaagc	tagtcacgaa	taatcagaag	acccatggca	ggctgtcact	169890197
agtgattttg	cttaggtaca	aacttgaatg	gtgctccttg	gagttctgat	169890247
gtgggagagt	cactgagctg	gacgttagca	cacacagtta	cacgctcaca	169890297

FIG. 1.67

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ggctcaccoc	agcatgcatg	tctcaaaaca	atatattttc	ctctattttg	169890347
cottggggtt	tcagttacag	caaaagtatt	ttcaaaacaa	aacaaaatgc	169890397
atcatgatac	aatctcatat	caagtaacat	tcattttggg	ggacgcactt	169890447
aaattaatag	tttcataagc	ggttggtgtc	ctgcattttac	agacacacga	169890497
caattctgaa	ggggcatgt	tatttttcga	ttatccttta	ctgcattttta	169890547
tgtgggacat	ggcatgctgc	agtgggtgtt	gtgagctgga	ggattttggga	169890597
gagccttagg	aaccctccca	ggagcctcaa	ggattgactg	cagtaggagc	169890647
tcaaataagt	tttgccctggg	gcctgccctg	gaggagacct	gcctctcagc	169890697
agccaatccc	accaggctg	ctctggaact	ggaggctctg	gctcactggg	169890747
ccctgctccc	caccacttc	cctctgcct	ctcccattcc	cttccccagt	169890797
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tgcataggctg	gcatgaggaa	taaacaaaat	ggttggtgtcc	agtgcctggg	169891047
gcatagcaca	gctcaaaaaa	cttagttcat	cctcctgagg	gatcaagaag	169891097
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taagggttcta	aatggacttt	agaccatttt	tcattttggga	aggaagaatt	169891347
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cattcaactg	ttcaatagtc	ctgggcagtg	ttattgcatg	ggagaccata	169891497
cctaacccca	aagattgccc	catagtctct	ttgtcagata	aagcataagt	169891547
gagcatccca	tctttgttag	tcagaacctt	ttcagtttca	aacaacagaa	169891597
aaccaactct	tcctgtttta	aggaagaaaa	gggggggtta	ttgggtcatg	169891647
taataaaatg	gccagggtta	gattaacttc	aggcagagct	gaatacaggt	169891697
gctcaaagaa	aatgtcgaca	agaacctgtt	gatttctctg	tctcagctct	169891747
gctctcttct	gtcttggtt	cattctcagg	aaatgctcta	accttggggg	169891797
tccaagagta	gtcaccagca	gccccatatt	tacagccccc	cagctcagca	169891847
acctctgtgg	gaaagagctt	ctcaatagtt	ccaggaaaag	tcccagggct	169891897
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gtaaagccta	acatcacact	gaggcaccac	ttgccccaaa	ctccagcctg	169892147
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ttctgttate	tttattccca	ttttacagat	agccaaccac	aaacttactg	169892297
ggtggagtaa	cagtgttgcc	cagagttaga	gcttataaat	ggcagagttg	169892347
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ccatgccact	gctgactaca	gctgggtgat	ttggttgctc	taacccttgg	169892647
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ctggcacaga	gtaggtgctc	atggctcata	acatgtttat	tgattgttta	169892747
gatggcaaca	cagataaaat	caaaacatgg	aagggttgctg	agactcaaag	169892797
acaggattat	tattgttggt	aatgatctga	tagctaata	gtattatatt	169892847
aataatagtc	aacatgtcag	gtactataat	agaggctttg	cgtaactgct	169892897

FIG. 1.68

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ccttttagtc	ctcccagtaa	tactatgatg	ctgatattac	tcttcccatt	169892947
ttgtagataa	agaaactggg	agtcaaggag	gtgaaatggc	tttcccaaag	169892997
tcttgcataat	aatgtatccg	gactgcaagg	atggggccct	ctggccccct	169893047
caacacccta	tctgcctctc	atacccaggg	acctgcccac	aaggtcagcc	169893097
ccttggcaat	cttgccaacc	ttggggctca	aaattcagtt	tatggcttcc	169893147
caagatctac	tggatgcttt	ttctaagttt	ggagaattca	tgacattatg	169893197
aatccttttt	ccccagggtg	ggtattcaaa	ctcagagttc	cagccacgct	169893247
tgcattccagg	gctcagatag	cagagggacc	tgcttgaggc	ttgatttaga	169893297
aggggtccacc	tgaggatgtg	gatgaagcgt	gaattcattt	ctggcagggg	169893347
tggcagcaga	ggcagacagc	tctgtggagg	cagaggtggg	gaaattctgg	169893397
tgtctccttc	ctagtgtgga	ccatcgcgcc	tgtgttgagc	agtggagata	169893447
gtgggggtcct	tcctgcagag	gcctccatgg	tagggctcaa	acattgttct	169893497
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aatagattct	gtagtttaca	accaagaatc	ctgactgaaa	ccccctgaag	169893647
cttgtggggtt	taggtatgac	catgtgggaa	ggcagcatga	gctctggact	169893697
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caacgagggg	aattattatg	atgatgggcc	tttggaacc	tctgccttct	169893797
acagcagtac	tttgaaactc	ttgtgcacac	agatcaccta	aggatgttgt	169893847
tagcatgcaa	attctgattc	aggagtttgg	ggctgggacc	tgggatcctg	169893897
catttccaat	acccttctcc	acttaagttt	tgctgatgct	ggtagtctga	169893947
ggaccaccaa	tgaggtgggtg	aggttccagg	gacgcttaag	cctccagcaa	169893997
aacatcacac	aagacagaag	tgctacttcc	aattgcatga	gataatgaga	169894047
ccaaatcatc	cccgggcaag	cccaccacta	acaattattc	ccatcattgg	169894097
taacatccta	agtcctaagg	tacotggagc	ttcaaattctc	ataattagca	169894147
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gagtgtgggtt	tgctatttgt	acctgtaact	cagcccaggg	agtgtctgaca	169894297
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cctgtcctaa	gccccaccc	tcccagcaaa	ggaaagtagg	cccctgaagc	169894397
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tcaacttagg	ttccccctcc	tactctctgg	gggtgcattt	ccaggccagg	169894897
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ctcttctctc	ttctctctct	cctcctctcc	cagtccaagg	aagttttatg	169895447
caaaggccag	aggaggggaat	aatgaggtgg	aggtctctct	gaccaagcat	169895497

FIG. 1.69

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gtagccttcc	ggatctgttg	tgctttccag	gagtccttca	aagctctaag	169895547
cttttggaat	tctgcaagct	caggaaattg	aaaacctttt	ctctcacaac	169895597
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gcggcattgt	tgttgcgcta	tccctgcaatc	ctacgctgcg	ggtagctgtt	169895947
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taaccactgg	gctgtaccac	ctcacaggag	ggcagggtggc	acagtgcctg	169896097
gaacttgga	gggtccagca	cgtggaacta	tgctctgtca	tttacttact	169896147
gtgtgtcact	ggatcagtc	ctcaacaccg	ctaagcctca	ttttccacct	169896197
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attctcaggg	agtcacattc	cgtctccaaa	tgcccatctc	ctgatccaca	169896397
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gtgtagtttc	tcatgcattc	attcagtttg	gcaccagaag	gtgcccagac	169896547
tcactttgca	gccagtctgt	ccccatagag	gtgataaagg	aaaaacatat	169896597
gcacatttaa	acttttataa	gtttatttga	acattcagcg	attcacaaac	169896647
ggtatagcac	agacagcaag	caactagcac	tcccttagga	ggggccaaac	169896697
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aatgggttgg	aatggaaagt	tccataattg	agggttcattg	gtggctcctg	169896797
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tgcttctcca	acaacaacaa	caatatctag	gtgtgcagtg	agctcccact	169898047
tctgctgatg	tgggactaga	caaaagatga	gaggggacca	ccctcagagg	169898097

FIG. 1.70

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ctccctcctg	cttggcccca	aactctttgt	aaatccagca	ccccaccccc	169898147
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tggtaagcat	ttaataaaaa	caaagccatc	aatggagatg	acgaaaccca	169898697
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aaggtggagt	gaggggagg	aagaggctac	agtcctccca	ctctgcccc	169899197
acacacctgc	agagacatta	aggaaagcgg	agctaccctg	ggctgcctct	169899247
ctgtgattta	acgtctctct	actcccacac	ctgcagtga	ccggagttaa	169899297
aatgacctt	ggcaaacagc	cttatgtatt	ctctgtctag	agcagaggac	169899347
agagtcaaag	aaaacccact	cagaagcctg	gagagcggct	gaaagtgggg	169899397
gagggcagga	aaggaggagg	gcaggatgga	agcatgcac	tcctgggcat	169899447
tagacttgct	ggattaagga	gtggagagtc	aaacatgggt	agctctgctc	169899497
agaaaaatta	ttactgaagg	agagattatg	ctccacaatc	tcaccagaat	169899547
gtggctttgc	aaagtgaac	gaggggtcgt	tcctctgcca	gcacgaccaa	169899597
ctctcccggg	acaccccctc	aggctccgtc	ttgtgccaca	ggccacctca	169899647
cttcagggtg	gtggctcaga	gaggtagcag	ctcccaccta	aatgtggcct	169899697
ctagaacctt	ctcttctcct	gctgagaaag	gattgtgctg	agtagtagaa	169899747
gcagctggca	ctggagtcct	ctggcctggg	tcctacaatc	ccaactttga	169899797
caattgtgtg	acctcggaca	agtcacctta	cccatctaag	cacatgttgt	169899847
tttaactgta	aaatgaggaa	aatagcatc	aactcagggt	atgaatgagt	169899897
ggagccatgt	ggagcaacag	ttaagggcat	ggacttgga	gtcaggcagc	169899947
caaggtctgt	gattctaggc	aagtgatgtc	accactgagc	ctcagtttct	169899997
ccacctgtca	tacaggcagg	agtaaatgcc	tcctcaccct	ctttgttctc	169900047
tgtacaaacc	cttgccctgg	atgttctgtt	tgtcctcagg	acccctctc	169900097
cactgttggc	tggggagggt	gacctgggag	gactctgtga	atgaggcccc	169900147
tgccttccga	cttcagctgt	tcatgacaca	ggcggagact	gcgggcagga	169900197
ggagagtgc	acgaggtgtc	aactcccagg	ctccctccct	gagggttata	169900247
gggcatggct	ctcttccata	gctttctttg	ctcggccttt	tgttgatggt	169900297
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tacacagtcc	ttttgttaca	cggccttcca	attccccaat	ctgaggggtgc	169900447
cattgtgtcc	agctgagacc	ctgaatgaag	caactgtccc	gtctggccac	169900497
agacctggca	caatttccct	tcaggcactt	aaagcaggag	taatgaacac	169900547
tgatgagtcc	agctcagtgc	taatccctct	acatgtgaaa	tctcagttct	169900597
tcagagagcc	ctgggaggaa	gctactacag	cctttcccat	tttaaagatg	169900647
agaaaactga	ggctctgaga	aggtttcaca	gccagagcta	agcctagagc	169900697

FIG. 1:71

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ccttaatgac	tatcctcatg	cctctctccag	tataggcagg	aggctactga	169900747
gtacacgtgc	ttgaacttcc	aaggcatggt	ctcaagtaga	agtgtcctcc	169900797
tcacaactgc	tctgaggcac	atgccatcgg	aaagctgggc	taataattaa	169900847
acaggggtga	ttttgtcagc	cccacatggc	ctgacaaagc	agaaacacaa	169900897
tggatggtaa	atattctatt	acgactgtta	ttcccaaccc	cctttccaat	169900947
gggggtggtga	gtaggaagcc	tccctatgac	cagtttcttc	cccacagtct	169900997
tgccagctcc	tgttcttctc	atcacaccag	gcttgtggcc	ttgattttgg	169901047
accctgttgg	aatgaggggtc	acaagaggggt	ctgtctgtcc	acacacacag	169901097
ttgttcctcc	tccttcttcc	ccacctccat	tcttaccocat	tctcagtcct	169901147
tattccagac	tcctcccttg	caccagctgt	gtccttggcc	tggggatgca	169901197
taatgagacc	cagatgctgc	ccccaaaact	ctcagtttat	ggactgtcca	169901247
tcttgaagag	atgaccacag	gatgctcaat	gctccagcaa	agaggaatcc	169901297
tgtgggtcac	caaaggcaca	caggtccttg	gcacttagag	aaatcatttg	169901347
tcatatgttc	ctctaagtgc	caaaggcctg	tgtgcctgca	gtcattcatt	169901397
aattgaacca	atattattca	atgagtcctat	ttctggccac	tccttctcag	169901447
ctagccttct	ttatgagatt	ttcctccact	gacactccct	gaactgctgc	169901497
tagccccagg	gotctgggct	ggctttctat	tcctccttct	gggggtgtca	169901547
ttcattctct	tggctttaaa	gaccatccat	atgcaatctg	caggtcctat	169901597
gatcatggcc	tcagaatct	gtctcatttc	gtccacatct	catcacctcc	169901647
tgttttctca	ctagcccaag	ccaaactcat	ctctagtcta	cactattgca	169901697
gacatttcag	gattgcctca	ttgccagcaa	atttgcctcc	tacaagtcac	169901747
tattaattca	tatgtcgggt	tgtcacttcc	tggttttact	tcagggtttta	169901797
ataagcctga	agggaaacac	ttgttttcat	tcccagcat	gaaactggga	169901847
catttcctct	ggtccttgga	gtgaaatcca	cactcccaac	cacagacttc	169901897
aaggccgcac	ctgctctgac	cctgctgacc	tcccatcttt	caccactggc	169901947
tgtggcttcc	ttgcactttt	gcaacaccaa	gctttttcct	gctttcaacc	169901997
cccagacctg	cccgtaggggt	gcaatttttg	ggcatccgga	tctcagcaaa	169902047
tgtgcctgct	cctcagaaag	gccttcctgg	ccgttctgoc	tgaagaagcc	169902097
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atagcgtca	tcccaaccta	aagtatcttg	tgaacgtgct	gctgggtctgt	169902197
tatccattgt	cctcgctaga	cttcaagccc	ccgaagagca	gggacctggc	169902247
ctgcctgttc	accattgtct	ctagcaccta	gaactcaggc	ctgggtacagg	169902297
ataggtgctc	aacaagttgt	taaggacaaa	tgtcaagaag	tacctggggg	169902347
aagtgagggg	ctgaattggg	gggaataggt	tcttttggtta	tggcccaaaa	169902397
attgctagaa	gtttaaatgt	gtcttctaag	cccagctctc	tgtgttotca	169902447
aggtcgcaaa	tattaagaac	tcagggtaaa	taaaaatgta	tcctttccag	169902497
tgccctgcatg	cccacactga	aatgagaaaa	gattttttta	ataataataa	169902547
taaaggaacg	atctttcaac	ctgcgtgcgg	gtctcagcgg	ctccacttgc	169902597
ctgctgtgtg	gatctgacca	gtgcactttc	actgcctggg	tctgggttct	169902647
tctgatgtaa	agtaaggctc	ccagtataag	ctgctttcct	tctagattcc	169902697
agggaaatca	tctcacaaaa	ctcaaagtgt	agacaaacaa	gatttcaggg	169902747
caaggaaaca	gactcaggag	ctttcctggg	ggcatggctc	cctcaaagcc	169902797
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gaggcacagt	aagcaggctg	ctagagccca	gcatacttac	agccctgagg	169902947
ttgtcagaca	atgagcctcg	tgatgagtta	ttgcaccaac	agctgttgcc	169902997
cagccctgct	atgtggatct	tggggacaat	aatttatcca	caattacact	169903047
ggagagcatg	gtgcttctca	ggtaacaggt	ggaaattcac	aagcccacca	169903097
tgtgatgaag	acctgccctt	ccctgaccac	aatgctatga	gtaatgactg	169903147
agaagattgg	gcagcccatc	ctcagtaatg	caggatgcac	tgtggcccat	169903197
gtctgaggca	tctgaaatat	cagaaactcc	agtgggctta	ccatgggtccc	169903247
actcctgcc	taatggttgc	cttacagtgg	ctttttcttc	caaaccaact	169903297

FIG. 1.72



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tgccttcaac	tgcagaaggt	gaggtcccca	aaacaccagt	aggccatagg	169903347
atagtgtgcg	gccggtagaa	taagaacctc	agacacttcc	cacttcccct	169903397
ggtagagaag	gtcttagtgg	ccacaccgaa	aggtaggtgg	aggctaacag	169903447
atctaaggct	gcccagtggt	ccatttctgc	actggatatg	aaatgtgccc	169903497
tctctgagcc	ctctctctgc	ctcagcgatc	tcctctatag	aatgggggta	169903547
tagagataga	caatctcata	tgtgatctta	ggcaagttca	gatctcacag	169903597
tttccaaact	tcagtttctc	cagctatgaa	gtatgagctt	gataatcttg	169903647
gctgtgtgac	tttggacaag	gcccttccac	tctctgagcc	ttggtttccc	169903697
atctataaaa	tgggccaatg	gtaggggtgg	gaaaaggatg	acctctgagg	169903747
tcccttccat	acagctgcct	ctgattcttc	attgcaagtg	acccagtgtt	169903797
ccatatgacc	catagccatc	tgtctgtcct	ttgtgccagg	cctgaagcat	169903847
tccttttgga	ctgggtcattt	ctcaccgtca	ccccctggag	tctgccccaa	169903897
tcattttctca	gtccttctga	ctgtgaagtg	tctgtctgaa	ctcataatca	169903947
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tgacagggat	ttatctttct	cagctgaatg	aatgatgtct	ccagccttgc	169904047
cccagaaatg	tgggctgggc	tattcaacac	ttgtcaccag	caagctcttt	169904097
tcctgaggct	gcatactcca	gccacccagg	tgactgagta	ctttgtcatc	169904147
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cacccaccca	ccttctgacc	tagtttggat	gctccaagcc	ataatgataa	169904247
agtaatgttg	tgaagagggg	aagaggtttg	cagtcagaca	gcctgaaccc	169904297
aggttctgcc	atgtacaggc	tgaagcttgg	caagcctctg	cacctctctg	169904347
agggtccattt	gcacctctct	gaggtccatt	tgcacatcta	caaaaatgcg	169904397
ataacaccta	cctagcagag	ttcttaggag	atccagataa	caaattgaaa	169904447
acatgccaga	taatgcctgg	cacatttttag	aagcttgaga	tctactactg	169904497
gttctcttcc	agttctccca	tcgtagtaat	atcatctaca	gagcaagatg	169904547
gggaaaaatgc	tcactgccag	atcccattct	aaagaggtat	ctccatctac	169904597
agatttattg	cacccgggct	cctagccata	cgcccaaaag	tcaaactgaa	169904647
caacagtaat	aatttttatt	cagccatgtc	acactgaact	gaggacctga	169904697
cttaagcaac	aattcagatc	tgccaacatt	tactaaggac	ctactatgtg	169904747
gcaggccgcg	tcgtgacccc	ctggagagag	aaagatggat	tggaaagtgt	169904797
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gatatggatt	gagtcataaa	ctccccatgt	ggcactgggc	aggttcatca	169904897
cttgaactct	ctagacctca	gctttttaaat	ctaaaatgtc	ccatagagtt	169904947
gctacaaaga	ttacatgaga	tatacactta	gcaaagtgcc	tggctcacag	169904997
taattgtcag	aaacagaaag	tgtcgagact	caaccctgca	tggaaaagaa	169905047
aataggacac	acatactatc	ttagtccatt	caggttgcta	taatagaata	169905097
ccttagattg	ggtaaagtag	tctcccctta	tccacagggg	atatattcca	169905147
agaccccccg	ttggcacctg	aaatcacaga	tagtgccaaa	ccctatatgt	169905197
actatgtttt	tcctatactt	atatacctat	gataaaggct	aattttataa	169905247
ttaggcattg	taggagatta	acaacaataa	ctaataataa	aatagaacaa	169905297
ttaccacaat	atagtataat	aaaagttatg	tgaatgtggc	atctctctcg	169905347
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aagtccaagg	tcagtgcaca	agcaaattca	atgtctgggtg	agggccagtt	169905547
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cactgcaatg	agtattaagt	ttcaacatat	gaatactggg	ggacatgagc	169905747
gttcacgcct	atgtaaatac	tacacagaaa	gatgtttatc	aggtaaaaga	169905797
aagtagacac	ggacagtccct	catttttcta	agaataattg	gtaccagtac	169905847
aaataccact	taaagagaaa	cttcttaaaa	caaagtgtga	ctattttactg	169905897

FIG. 1.73

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tgatagtgaa	ggaaaaaggt	tggagtaggg	ccaaatcttg	aaaaaataaa	169905947
attgaaagca	caaaaataag	tcttttttat	tgtctagtaa	caaaatgtag	169905997
gttttagtgt	caaatgagtt	aattttttcc	attaaaaata	ggaattacca	169906047
agtgttgact	ttgggggagg	catggcacat	tttttagaca	aaatcctatc	169906097
ttagcacagt	ctaacagttt	tgattttggt	tgactttcac	agcacaataa	169906147
ataaagaggg	tcatttgagg	caaataattc	caagctttat	ccattttccc	169906197
ataggcctct	tccaatcggt	agaagataac	atttttctcc	tttgaagcac	169906247
ctgacaactt	tgtcactttt	ctcttcttcg	gttgctaact	agttttaactc	169906297
tgocagtttc	tcatttgcct	gtagttaaata	gtgaatggaa	aagttatcca	169906347
acaatacttt	tgctattttt	atgaaatcct	gaatctgttt	aaagatttgc	169906397
acttttcttc	ttcatcaatt	tcctttgaat	ttccattaca	tcacagaca	169906447
tttacaacaa	ccaacaagcc	gaaggaaacc	aatagatcta	ggttaaataga	169906497
gtaaggctag	aaaccagcgt	taatgggagg	taaaacttaa	gcgtgcataa	169906547
aacgtttaag	tgaccggctc	attcgtaagt	atttttgtgt	tatgaagatt	169906597
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tagttgtcaa	attcaagata	accgacaaga	gaccgggctg	ggtggctcac	169906697
acctgtaata	ccagcacttt	gggaggccga	ggccagcgaa	tcacctgagg	169906747
tcaggagttc	tagaccagcc	taaccatcat	ggcggaaacc	caatttctac	169906797
taaaaataat	aataataata	ataaaaataac	tgacaagaat	ttctaaagta	169906847
gttcagaata	gaaagcttac	taagttgatt	catttaattgg	ttacccttga	169906897
tattttaaca	tgtactatta	catgttaaca	tgtaccact	aaatgtctag	169906947
atctcattga	tacttcattt	aactcctgaa	caataatagc	ttttcagtgt	169906997
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tagttctatc	ttgttacttt	tagtcattta	tatttactat	acttacagac	169907097
actgttgggt	ttatttttag	caccttccta	tttgtttttc	tatttgtact	169907147
atctcttctt	tcttccttta	ttcttctcatt	cctgtctttt	caaaaattaa	169907197
gtaaatagtt	ttattattgt	atttttttcc	ttatattggc	ttcttgtttc	169907247
acattcctga	attttgtgca	gtggttaccc	tagaagtttt	aatatatata	169907297
tttagtttat	tatagtgtat	ttttaagtta	agacttttac	ttcttcctga	169907347
acaatgcaag	aactttacaa	cagttaaact	cctgtaccca	cttctttctt	169907397
tttgtgctgt	tgtaaacat	tttacttctg	catagttata	aatctgataa	169907447
gacattattg	tcatttttaa	cagccaatat	tcctttatac	taaccctaat	169907497
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tctgaaaatg	tctttatttt	gtttcatttt	tgcaggattt	tttgcgtgtg	169907697
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agatttttct	agagtccatc	agtgtttggt	gaaaaatcca	ccttatttgg	169907797
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ccatcttttt	ctctattctc	tttaacagaa	taaccatagt	caaagtcctg	169908347
tctgatgaat	acaatagctg	ggctcatctat	ggatctgttt	ttattgttag	169908397
ctttcttttt	ctctttgctt	tgtctctttt	ctttctctct	cttgcttttt	169908447
cacatgcctc	ataattttga	ccataagctg	gacattgtat	gtaaaagaac	169908497

FIG. 1.74



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tgtggagggtt	tcagctgata	cattccacca	gagcagcttc	cccccttcc	169908547
ctgttggaga	gtcaggggtga	aggctgatga	cctcagtcct	gtcagaaatt	169908597
taagaggatt	gcagtttgag	aaagactgaa	tcgaccacct	ctggcttttc	169908647
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ctgtctcctc	agccctaaaa	gcctgaagag	attcagtcct	gctctttaga	169908747
agttttgagc	ttttctgggt	atcttcaaaa	tctggcaaatt	atcttgaggg	169908797
gaaaaacagg	gatttatgtc	aggcccttcc	tctctctcat	ggaatgttgt	169908847
ctcctaagtc	ccgtgagttt	agcagaaatt	tcattccaac	cttccatcct	169908897
catttcccag	ccacctgagc	tgcatagagc	acttagcagt	gtcctatgcg	169908947
ttaaagccaa	cagtcacttg	gcttcttata	tttcaggctt	ctcttggttc	169908997
caatccatca	tgccagccct	gcacaactgc	caaaagtgtc	gcttgggttc	169909047
tgctttctcc	agtagacaac	ctctgcttgg	gccaatgcca	gtcctcaacc	169909097
cacgtccaga	atcagcagtt	gcccacaggg	aagaaaactg	tcaggagtta	169909147
tcagcctaca	gaggaccacc	tttgtcctca	tttccacagc	tttctgatgt	169909197
cttcaaattt	tctatttttg	cggttttct	tttttttct	taatagtgtt	169909247
tgtagtaggg	gagtcagcct	gccacaatct	actacatctt	acctggaagc	169909297
aataccttat	cttggttattt	ttaagtcaac	aaattagaca	ttattattat	169909347
taatataatac	agcaatatatt	agagtcactc	gcacataaat	attaatttag	169909397
agttaatacac	atattttgctt	tgtattcctt	tttgaatctc	tgactttcta	169909447
tctgtgctaa	ttttccttct	gactaagcca	catcttttag	aatttcctct	169909497
gtgaggacct	gttttatttta	ttcaaacata	aaaaatttgt	ttgctctcat	169909547
tcttgaaatg	taattttcact	aagtattcat	ttacagttgg	tcaattgttt	169909597
cctcttgaca	catggaaaat	atcattcctc	tgccctctggc	tttcatttgt	169909647
attgttgaga	agacagatgt	tagcctaatt	gctattttatt	tgtagatggt	169909697
ctaacttttc	tctctaacta	cttttaatat	ttctccgtca	caggttgtga	169909747
tggtactttc	atcttctgga	attgttcttc	cacatcttat	catcgtcttc	169909797
cattattttc	atctttgtct	ctctagcttg	ttttatttat	aactatctaa	169909847
gagtttacta	attgtctcct	tagttccttg	ctccatctat	atctgtccat	169909897
tgtgacttaa	aatttccttt	ttttaacttt	tattttaagt	ttaggggtac	169909947
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acttataagt	gagaacatgt	ggtattcagt	tttctgctcc	tgtgttagtt	169910197
tgctaaggat	aatggcctcc	agctccatcc	atgttcctgc	aaaggacata	169910247
atcccctttt	taatggctgc	atagcatttc	atgggtgtata	tatacctcat	169910297
tttctttatc	ctgtctattg	ctgatggaca	tttaggttga	ttccatatct	169910347
ctgctattgt	gaatagtgtc	acaatgaaca	tacgcgtgca	gctgtcttta	169910397
taatagaata	atttccattc	ttttaggtat	ataccagta	gtgggatttc	169910447
tgggtcgaat	agtattttctg	tctctaggtt	tttgagaaat	ctccacgctg	169910497
tcttccacaa	tgtttgaaact	aattttacact	cccaccaaca	gtataacatc	169910547
gctccttttt	ctgcacaacc	tcgccagcat	ctgttatttt	ttgacttttt	169910597
aatagtagcc	attctaactg	gtgtgagatg	gtatctcatt	gtggttttga	169910647
tttgcatttc	tcacttaaaa	ttttgaacta	atgtattttt	cattttctaga	169910697
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ttttgccatc	tcattttctg	tgctaataaa	aattctaata	tcggaagctt	169910847
taataatcag	attctgctat	ctctttttcc	tgcaagcctt	atctcacagt	169910897
accttggttt	cttggtgtgtt	ttacaattgt	tgacagtga	tattcttttag	169910947
aactttatcc	ttgataatta	ttagaggaat	gaattaaaaat	ttcactttctc	169910997
cggaaagtac	tgtgtttgca	cctttttaata	actcaagaga	ggtaacaacc	169911047
caagttcatt	ttcaattaaa	attttccattt	gagggtttttc	agaccacaaa	169911097

FIG. 1.75

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cccatgtgag	agctcacata	tggttacaaa	ttcttgaaga	aaatgaggct	169911147
ccttccttcc	ccatccacct	tcttagtacc	aaagtcagga	cagacagggt	169911197
ttctgtgtta	gttcacttct	cattcacctt	tgtattaaag	gtctagctct	169911247
ttgaggttca	agttttatgt	tgggacctct	tcccacttgg	tagggcctgg	169911297
gttttaccta	ctgggtttct	aagcatattt	tgtggttaac	atcagaggcc	169911347
aggagactca	tcagtgtata	attaattctt	gtataactaa	ttattttaag	169911397
gcagtggacc	tattcactag	cacctgctt	toggagtcac	tgaattcatg	169911447
tttgccttca	gctaaagcca	tcttgaacct	ctttagatgg	gagaaccctg	169911497
atgctggtag	ctgtagcatg	ggggctgggg	ctggagaagc	caagtagtac	169911547
actagggacc	tcacggtcac	tgtgagggat	gggggtctct	gcttggcttc	169911597
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ctgggatcct	ctcataagaa	gctatattta	ctctaataaa	aaaaaatctc	169911697
acctgggctg	aaaaagcgta	tgctatacat	gagccttggg	taacctaaac	169911747
tttcatccag	agtttcaagg	attaaattcc	taagtctctt	ttaaagcaaa	169911797
gagaagttag	ttccagtcct	aggccatgat	aatgctcttg	gctgagaaaa	169911847
cctccttcgt	ttttttaaaa	tatggattct	gagggtgcaa	gtgcagtttc	169911897
gttatatgga	agtattgcac	agtgatgaag	ccatggcctt	tagtgtaccc	169911947
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accccccctc	tctgttttaa	ggaactggca	tttatgcaac	taattgataa	169912047
aattatcatc	tgtctcttaa	ccagattaat	agtataatta	aggaaatctg	169912097
ggatgatgat	agcaggttta	ctgttgatga	aaccattgaa	cacttgattt	169912147
aaccatttaa	cagtgtttct	gaaagtatgt	tccttgaaac	actagaccat	169912197
gaaaagtcct	ttatgttgaa	atatgcttaa	gaaatattat	atgcttgaaa	169912247
cttctcttgg	aaactcacga	agtataattag	acattaaagg	ctctaagaaa	169912297
tcttgcataa	aagaagccta	tttaatttta	tttgactcgg	tgttttcaaa	169912347
ttatgtgtga	ccacagaaat	agaagggaact	tggaggagta	ataattcatt	169912397
ttttgggtag	aattcactac	tgtcacagat	atttgatgc	tgtcaatgaa	169912447
cattttaaag	tggattatag	agaaagtaag	atttattcaa	caaataattg	169912497
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aaagatatag	ttctgtctca	tggagcttgg	aggagcattg	gactgtcgtg	169912597
gaggcattaa	gaaagaagta	gcaagtgcct	agaatccagc	tgcccctcaa	169912647
attgttggat	cacagccgtg	gaacaggccc	cagagctggg	aagttgactg	169912697
ggcagttggc	tgttgtatcc	agcctgggag	atgcaaaatt	tattgacata	169912747
actgtacccc	tcaagaggac	cataaagaag	accaagcaga	aacacacttg	169912797
gttctggaac	agaaaaaagt	ttatctagga	aaggaagttt	aggaaagact	169912847
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tctgagaatt	cctcccaaaa	caatccctct	aaaagtgcct	gattcataat	169912947
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gatgacaatg	atgggtgatga	tgatgggtgat	gatgatggca	atgatgatga	169913147
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ttatgccttt	tttgtgttct	tctctacttg	tgttttctcc	ttcttgcctt	169913697

FIG. 1.76

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ttagcaagac	atgtactcat	ccttcagggt	ccagctcaat	ggtgagagcc	169913747
totctggggc	tttggctgat	ctcaccctgg	aatgcactgc	aatgttcctt	169913797
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gacagctatg	cagaccagag	cccccttctc	ccaggttctg	tgttgccac	169914047
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gtaagactca	cctcagagga	agggtggg	tttcattcct	agctgcaatt	169916247
ccttacaaagt	aagaaggaga	gggcctcaaa	caggaaacct	ggggtgaaga	169916297

FIG. 1.77

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ggtgaacctc	agatgcctat	cttgtttaac	cttctgtctc	caggcttagc	169916347
acagtgcctg	gtacagagga	agtcctcagt	aacattgttg	agtgaacgga	169916397
tggatagatg	tgtgtggacc	cgggttcac	cttcacatga	gaaagtccgt	169916447
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gaaaggcaat	gtcatggctc	ttgccctcac	actctagggc	ctagactggg	169916547
gtgacaatgt	ccatgcttac	atgtcctgtc	taaggaaagc	agctcccgtt	169916597
ggtcatgcct	gtggaaatgt	ggccctgtat	ggccagctct	tctgattttt	169916647
cataagaacc	tggatggaca	gatgccatgc	aaagtTTTTT	TTTTtaattt	169916697
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ggcccagaat	ggggactggg	ttgggtgaaga	ctaagaagaa	tgagaagctc	169916847
cctggagcct	ccgagaggaa	ggtacatttt	gcacgccagc	ttatccggat	169916897
tccgagacttg	ctcgatgttt	attttctggg	tgtcactcca	ggatttttagt	169916947
taagtcttgt	ctaactttgc	agccaggctc	agccattctg	taggaggatt	169916997
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agctcttgag	gccagaagag	tgggggaaga	tggcttgatg	acagacggaa	169917097
tctcaggcac	ctgaagagtc	ttagaagcca	gatttggggc	tgagccgccc	169917147
ttccccaagt	ggagattcac	cagccatggc	cagactcgag	gatgtgagat	169917197
ttatttttct	taagatagca	aatgtctttg	caggcatgct	tcccagttgg	169917247
gaaattcttt	ttatgtctca	tgtaatccgt	ctgccagagc	ctcctttgac	169917297
tctgtttatc	ggttctcttc	ctgtatgtgt	catgctctcc	ttccctctct	169917347
cctcttctcc	ccttctctgc	accacccctt	tgctctgcac	cacccagagc	169917397
ctgttaggaa	gaaagggggg	atacactcat	cctggctcca	tttaggggtg	169917447
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ggctctatct	ccatatctta	ttttgacaag	cactgtaatt	atccctcatt	169917597
gctggcaggc	ggagcagaat	cacgttcggt	cccagcccca	tcttctcaga	169917647
acaagagtac	tcaggctcct	ggttgctcca	ccactaaaca	actgcctgtc	169917697
tcagttcccc	agcgagaccg	agactgagct	cagccattac	tcaggagatc	169917747
gcaggcgggc	gctcagccta	ctttttgaca	gcacgtgga	ggtgatttca	169917797
gagcgcttgc	tgcatgcaca	tgggaaatag	cttccaagga	ggatcttttg	169917847
gggcagaagg	aatgaggtgg	gcacccatgcc	ctccaaaaag	acagaagtta	169917897
cccctccagg	agccagcatg	aatggagcac	ctaccatgtg	cccattttggt	169917947
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ttgcagtggc	ctcagaattc	cgaccaagag	ctagctggcc	ccacggtttc	169918097
ttcccttctc	actttacagc	attgtggctc	agggagagca	cacatgccct	169918147
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ttgtcaaaat	cgtgtgtcta	gaaaaccacc	ctccttactg	gttgtgttcc	169918847
aggggttccc	aaactcaagt	tcttcttgga	ggagctgcaa	gaaatgattt	169918897

FIG. 1.78

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gaggggtgata	gcaaggaaga	atgcatctga	gatgccagge	tcaggagatt	169918947
cctggagtc	tgcactgtgt	gccctttggc	ccagaaggcc	cttgtaagca	169918997
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cctgggcctc	tcttctcagc	tgcaatacag	ggctaataca	ggcatgcac	169919747
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gccgaggtga	gtggatggct	tgagcccaaa	agttcaagac	cagcctgagc	169920897
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aagcgctctc	acagtgaccc	tactgggctc	tctggaagct	gcatcccagc	169921147
agctgtgcag	cccctgggac	cagccaggag	tgacctgggt	gctgccgttc	169921197
aaccacctg	tacatttccc	aaaaagaggc	agccaagtgc	tgattcaggg	169921247
aatttaaact	ttaatggctc	ccgggtctat	tattatgttt	taatgaactg	169921297
gaaaagcaca	aacagaaatc	cttaagagca	tcagccgtga	cacagaaatc	169921347
taatacaata	aaacaaagtg	cttataaacc	ccagagttgt	ttaaaaccca	169921397
gaaattgcc	attgacatat	gggactatat	ccttcttagcc	cctagtaaac	169921447
tgagtggctt	caaacaagtc	cctatcacct	cccagggcct	cagtttcttc	169921497

FIG. 1.79

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acctgtgaaa	taagaggatc	aaaaaaagat	aatgtttctct	ctgtttctctt	169921547
ccaaccgagg	caggcatctc	aagtattttct	tagtcagttc	tactctaggg	169921597
tacacagtat	ctgtatctgg	cagctgtatg	aactactggt	gaaaatcctc	169921647
ttcccaatcc	cagtttcaac	atcactcctc	aaggcagcat	ccaccttcac	169921697
tctagactga	attaattcct	ctgtcttacc	acctaaactc	ctctagaaaa	169921747
cttgatagag	gtaaagataa	atgcattttt	tcaaaaattc	tacttttcta	169921797
gtcccaaggc	attgtgtata	tcattcttat	gtaagttatc	acaataaacc	169921847
cataattagt	tacttccatt	tatgtcaa	cgcctacaaa	gcagaaacat	169921897
gtattattca	tttttggcct	cctccccagt	atctagcata	cgaactgttt	169921947
gcaaacatgc	ccagttcttc	aaactttgta	acttcatgcc	ttttctatct	169921997
actacttggg	atgggcccac	cctccctttg	tcctctaagc	acactcctat	169922047
tcactcctca	aagtccagca	caaaaatccc	ctcctctggt	aaacttcaac	169922097
tgctccaggc	tgagtcttat	gtttgggtcc	ttcatacgta	cccctcttct	169922147
attgtttggg	gtattgtgtg	ctgtggggtc	tgtttactct	cagttctccc	169922197
ctctaggctg	ggttccttga	aaaacaccct	ctggacattt	cacctctaca	169922247
tcctctgcat	tcttggccag	gctctgagag	ggcattggta	aatgttaact	169922297
gcctggcaat	ggtgatgctg	ttaacctgat	gtgtcagggg	tctgaataaa	169922347
gctgcctcaa	ggtaggcaga	tgcccacaac	caagcaagaa	ctcaaagctg	169922397
caggctcctc	agcctgaacc	ttagacagcg	tcttggtcac	catttcaaca	169922447
ccttgaccac	atttctcact	ctcccaaatt	tcctcctgct	tattcctcat	169922497
ccacatacat	aaggctgtgt	ctcccagggg	aaattcaact	acttggtaat	169922547
tatcctgctt	cttaagtttg	gggctagggg	attcatagat	gatgttcagt	169922597
attatgctgt	gcaatgtaga	tgtctcctaa	accttctcag	gagctaccac	169922647
tgagtggcac	ctggggacct	ctcaggaaga	gccagttttc	tgggagctgt	169922697
ggggcaggac	agagctcatt	aaaccagcct	accacctgtc	ttccagctcc	169922747
tcctctcagc	ctctgggctt	ccagcagaaa	gcacacgaga	gcattcttgt	169922797
tggttttctt	atgacttgag	ccagcgagac	gtacatgccc	agcacctggt	169922847
acctgggctg	gctcttggtc	gagagcatac	atgcattggg	tcagggtttca	169922897
gatctgctgg	aggaacacag	ccagaatgtc	ttgacaggca	gccctggcaa	169922947
agccccagaa	aatataagat	ctgagtctta	tgatggactc	tgtgaccttg	169922997
agcctctcac	ctcgtgacct	tgggcatctc	atgttctctc	cacaggctctc	169923047
ggttctggac	tccttcatgg	gagctgtcat	gccctgttca	cacagcagtg	169923097
ttgtgcccc	ggggatcagg	gaccaggatg	gtcctttctt	ggtggtgaag	169923147
ggggcatttt	gcatattcca	gagattcaag	tttccagacc	tatctagaaa	169923197
gaaacatttg	agtttacagg	ttggcgcttc	tcagcctctg	tctctcttcc	169923247
tctctgttca	tctccctctg	tcctctctat	gtatgtttgt	gtctctttct	169923297
gtctcctctg	cctttctttg	tcattgtctt	ctgcttctgt	cctatactgt	169923347
ctctcacctc	caccctgggt	ccccccgccc	cagatgctct	tctctctgtg	169923397
gggttttttc	ttccctctca	tttcttctct	ctctcccact	ccttctctcc	169923447
cagattctcc	ctcactacag	gcttctctct	aatctctctc	taactgctta	169923497
ttcttctcac	aagaaggagt	cccctctggg	gccagaggcc	caggcaaggc	169923547
attgtggaca	aggaggccat	ccgtgccatc	caacgggcag	gagcccagcc	169923597
tcctgggctg	tgctgtggctg	tgctgtgggt	ttgtttccac	ttaccaaagg	169923647
gcatctgtaa	ttaatgtggg	cagtgtataa	ggagctggag	atgtgtttat	169923697
gctccttcga	gggctgagat	gaaacaccca	taacatttaa	tgtggcgcac	169923747
tgacatttaa	atgtcaatta	gaaagtcccc	gctctgcttg	gctggccccct	169923797
gcatcctcag	atgagaccgc	cctcctccct	gccttgccag	cctgctggg	169923847
accaccagct	cacaaaagac	agtggccaca	cagcaaccgt	gactgaagag	169923897
tgtgcagggt	ccaaagaggc	taaagtggct	ttaagagcac	tccggagggg	169923947
gaggactctt	ggaacagaga	aaggaggagg	atggtgccag	gccaccacca	169923997
aaggcacgtg	gaagggggct	gggcaaatgg	tgaaggagca	tgtgggagac	169924047
aagtttagag	gtagcgttgg	cttctcctc	tcttccctca	gtacctacag	169924097

FIG. 1.80



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ggcagaatct	agagcttggt	tgtgccttgg	cccttagggc	ctatgtttct	169924147
gcctctgtgg	ttgatcacc	tccattagac	caagggttc	ttgagaccag	169924197
gttcccatct	cttcatcaca	caggacgcct	atgcacacac	ggtgcctggc	169924247
acacagtagg	tacacaaggt	agtctattca	gttcaataca	gtatatattc	169924297
gttgagttcc	cactgcgtgg	tgggcattat	cctaggaact	gaggctacaa	169924347
caatgattgg	gactgagacc	tgccccaca	gagtgtacag	atgctcttca	169924397
aattaccatg	gggctacctc	ctgagaaacc	cattgtaaat	caaaaataca	169924447
gaaatcaaaa	acgcattttag	tacccccagt	taatccatca	taaagtcaat	169924497
aaattgtaaa	ttgaaccatt	ctaagtccag	atgctcctta	acatacaatg	169924547
aggttatgtc	tcaataaacc	catcataaag	tcaaaaaatc	tgaagtcaga	169924597
ccgtcgtaag	tcagggatca	tctgcgttac	atttttaaag	acagacagaa	169924647
aaatagatat	gtggcaaagt	tttagatgga	agcaaagaaa	agaggcagcc	169924697
ggccccacct	ggatgacaag	aaagcttctt	ggaggaagtc	aaatagagct	169924747
gagacccaaa	gaataaatgt	gcatttgcaa	gacagagagg	cagaggggaat	169924797
actggacaga	gggcccagca	caagtgtgga	gccaggaggg	agcctaggag	169924847
tgcacagggg	ttggtggcaa	tgggcacagc	agcttccttg	tgaaatctga	169924897
gctcagagac	cacatgactg	catgggggtc	tgcaaccagc	acgtgagctc	169924947
tgtgagggca	agggcctcat	ctgtcttgtc	cactgctgtg	ttcccagagt	169924997
tggggaaagt	gcttgatgtg	tagcaggcac	tcgacaaaca	tttattggat	169925047
gagtaaata	atgctgtctt	cactggcctc	tctcctcttg	tccagttccc	169925097
aaagctcagt	gggtccccgc	aaatgcattt	attttgcaaa	agcctttccc	169925147
aaagcctggc	atccaatggg	tgcctcattt	cctcatcccc	tgcacgccgt	169925197
ctctcagtc	ctgagctgct	gtgcccacga	catgctccat	tttctcataa	169925247
aagcccttcc	aacaaggggc	acatttgcat	ttcaagtttc	ctggaattgg	169925297
agtacagaga	aatctgactt	ccagagccca	gggctctaag	ctgcagctgg	169925347
agaactgaaa	cacagcaagc	aggacacctg	cccagaataa	ggttcaggcc	169925397
ctggaatata	acatgggacc	catgctcctg	tagctgtctg	cagtctcgag	169925447
ccccaaagga	gtagaacagg	tgttcatctt	ctcctgcact	ctggaaatgg	169925497
agtcaggggc	ctgagctact	gagttttag	actgcaactt	tggttagcaag	169925547
aggcatttct	cctcctcacc	tccaccaca	cacagatcta	gttcccctcg	169925597
tacgctgccc	tttcagtctt	ggacactgca	gaagacctgc	taggagagcc	169925647
taagaaaccc	aaagccttcc	cacctgcca	ccaccaacta	tcatttactc	169925697
acccccactc	ctccagagt	cagatgacta	tttcaacttac	tgatttggea	169925747
ggcgtgctg	ctcctcacct	tgggtggagt	agagtttacc	ctgcccagcc	169925797
ctgcaggccc	agtggtaag	ggaaggaggc	tagtgattat	tccgactttg	169925847
gatcaatcag	ttgctcagtt	tattggaatt	acatcccagt	ggctgctatt	169925897
gatggaactg	ctggactcgg	gccacaatc	ctcatgccag	ttttataaca	169925947
ctgacatcac	ctgctcacac	acagggttc	ctctcccatc	ctgtcccat	169925997
acctcactct	gtagcctgag	atttctaagg	tgggggatct	gcactgggtg	169926047
tttggcataa	atgatgtaag	agatttcctt	tgtattgtct	tcagctacat	169926097
cttacctttg	tgtaagaatg	caaagtcata	agcacagttt	acaattgcaa	169926147
tgggaggtat	gtgctagttt	taaggtgttt	tgtttttttt	tttgtttgtt	169926197
tgtttgtttg	agacagtttc	actcttggtg	cccaggctgg	agtgcaatgg	169926247
cacaatcttg	gctcactaca	acctctgcct	cccagggtca	aacgattctc	169926297
ctgcctcagc	ctoccaaagta	gcttggatta	caggcatgtg	ccccacacc	169926347
tggctaattt	tgtattttta	gtagagacag	ggtttctcca	tgttggtcag	169926397
gctggtttcc	aactcctgac	cttgtgatca	gcccgcctga	gcctcccaaa	169926447
gtgctgggat	tacaagcgtg	agccactgca	tcaggcgttt	taagtttcta	169926497
ccatttgggg	catattcagg	aagattccta	tcccaacaca	ccccttcctt	169926547
ctgcttttat	aaacacacag	agtccccaac	cacctacgt	cctcttctct	169926597
ccataaccac	gtcacagtgc	actgtaaaca	cattacgaac	cagctatgca	169926647
ataacaatct	gctgaatctc	agagatgcag	aaagaaatca	ctgggccttc	169926697

FIG. 1.81

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tattgataca	ttcttatggt	atcatttttta	attttotataa	ttatgtttttt	169926747
aaggtacatt	gtgtatcagc	acagcagcag	atgctaataa	tatattaaaa	169926797
actgtactcg	tgttctggga	gtgttcacaa	attatagctt	cacactattc	169926847
tcatcttctc	ccgcctctgc	tcagatgtcc	ttgaaacatc	tctaaggatc	169926897
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ctatgacacg	tcttttggtt	tttccaatca	tcaaaagcaa	gaggtagcag	169926997
gagaccgagc	tgtaggcac	tgaccgtggc	attgcctcca	gggtgaattg	169927047
cgggggcaca	ggaaaaacag	ctcagattcc	tagcttttcc	ccaccttcc	169927097
gatctactga	accacacttt	ctccagggat	gtggcccgtg	atctatatatt	169927147
taagaaaaca	cctcaaataa	cttcccagcc	aggtgtgtgc	accacagtgc	169927197
tgggacgtgg	tattgttctt	gccatgggag	gtgggagatt	cttgtccatc	169927247
cttcacccag	aagcctgcat	gtgggttgtc	aatttttttt	tattttatga	169927297
aacttttttt	ctgtttacac	tcttgcagaa	caaacagaca	aattatatag	169927347
ctgatgtcac	atcccttttg	aaaatctatc	aggtttcatc	cattcattca	169927397
acaattgttt	ttaccagtta	cacttttttt	ttcatttgcc	atatacagaa	169927447
actgaggctc	agtgagactg	agagatttgt	ttctgactta	gcttgtaaga	169927497
aagagattca	ggaactcaac	ctagggtacc	tggccccaag	tcctgtgccc	169927547
ttttaatttt	acttccgtac	attttaatga	aatggctgcg	agaccagagc	169927597
tctgtgtgtg	aacaagttgt	gcctttcaac	cttcctttat	ctccccctt	169927647
ctttccccc	caccaagagc	aggctgatga	gaaaattaac	attcaggaca	169927697
cgttctgctc	ccttctgatt	cccacagaga	gaacacagcc	tctgcctgcc	169927747
aattagtgtg	gttcagatct	ctattagaga	tggggacagc	tagttccagt	169927797
tatgcaaattg	cccttgtctg	agagtagcca	tgggccagca	gcatgccagt	169927847
ctcacctctc	cccatggagt	caccatggat	gtgacttgca	cctcccgtgt	169927897
tgttttaacc	aataatcaaa	tcagtatcta	tttatataag	caactggcaa	169927947
ggtactgcag	gaagctcagg	gacagatttt	atttcagcct	aaaggaactt	169927997
acatgagta	gagagtgtgg	ccagggaag	ggcagatctt	tcaaagacac	169928047
tctgttcttc	tctaaacact	cacagtttct	atttattacc	caaaaaata	169928097
cataaggaaa	aatacctaac	atttgtttaag	tacctactat	gtgccaggca	169928147
ctgttagaca	ctttatacac	attatctcat	tcaagtccat	taattttata	169928197
taagaagcaa	tatgctattt	ggttcaaggc	atgtgtttta	agtaggaaaa	169928247
actaggattt	ttaaaactag	gatttttaatc	ctgccacttt	ctccatgtgg	169928297
gacttcttga	cctcagttat	tcatctgcga	aatggaagga	aacaatgtct	169928347
gtttgccagg	aatatatttca	gaagcaatta	gataagggtat	ttaaatccaa	169928397
gcacctcatc	ttcatatgac	acagcatagt	gttaagatgc	ctaatatgta	169928447
gggaaatgac	aaaaatggac	aaatgcagga	tattattagc	aacaatgcaa	169928497
aaatatctgt	atatggatga	agagtgggaag	aggacaatta	tgggggaaac	169928547
ttgttgtctt	ttaatttctg	aactatctgt	attattatta	ttatttttaga	169928597
tggagtctca	ctctgtctcc	taggctggag	tgcaatgggt	caatctcagc	169928647
tactgcaac	ctctgcctcc	cgggttcaag	cgattctccc	gectcagcct	169928697
cccggttca	agcgattctc	ccgcctcagc	ctcccagta	gctgggatta	169928747
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taggctggtc	ttgagctcct	gatctcaggt	gatccaccgc	cctcagcctc	169928897
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gtattattat	gtattttcat	ttaagctttt	aaaggaaaat	ggaaacactg	169928997
cattaaactg	agcctcagag	aaattcagtg	acttgtccaa	ggcatacaaa	169929047
ggactggagg	gaccaaggca	ggatctatcc	attttcaatg	cccatgcttt	169929097
ccccacaca	ccatgccacc	acatgtccct	caggaaacag	gtctgcaatg	169929147
attcaggaga	cctcgtagtc	tacattgata	gatgtaaaca	gcattgggtt	169929197
ctgtcttaga	gagtgggcca	gtgaggaagg	catggatcaa	agcaaaaaga	169929247
aaagccaagg	agggggagga	tggagattaa	acaggtcctt	ggttgtcagg	169929297

FIG. 1.82



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ggcaaaactg	ttaatgacgg	tggagcacca	tgaaattaat	gacccaccca	169929347
aagcacctga	gaaattgaac	tggttattaa	aatgcaaate	ataaaccagg	169929397
aaaaggagga	aaacaagcac	gaggaattag	gaagaaggaa	gatatggcat	169929447
ggagtaccac	gaacagaaag	tctgtggcca	gcacctggat	attcagagaa	169929497
agagtgtgat	ttaggcttca	gaagggcagg	ggtctgtagc	ttagggactg	169929547
ggcagagctg	ttacctagaa	aagctagaaa	cagaaatgca	taaatcccag	169929597
ttgtccctga	cagtgggata	cagtcagggc	ctgaagtgca	ggggaaggcc	169929647
atcttaggtc	agaggcagtg	gttcttggca	tacagtgggt	ttccccctaa	169929697
gaatgttagg	caatatttgg	tgacatgttt	aatgagcaca	accagggttaa	169929747
gtatctactc	actgctaate	tctggtgagc	agggagacca	ggggtgctgc	169929797
taagcatcct	acaaggcctg	gggacctccc	caccaactac	agttatccag	169929847
tccaaaatgc	catagtgtcg	ctggggagaa	accctgatct	aaggatgagt	169929897
gagaaggtgg	atacaggagg	tgaggagggtc	agaagtcaga	ccaacatca	169929947
gatgggaagc	taggaggaaa	agagggtcaga	aaaggagtta	tgaaccaaag	169929997
gacaaaagga	agttaagtag	tcagtcagga	gatgaggatc	atagaggaga	169930047
tcaggcaaag	agaagtccag	aggtggaaaa	aagcttcaga	gctcagacgg	169930097
gctgggctct	aacaatcatc	acagaagcag	caaagatcaa	gaagcaatgg	169930147
ggaaggacag	ttgaggctag	cgccaggggg	aagggccatt	ggtgaggagc	169930197
ctttctgata	agaagttgga	tggagaacac	catggtggat	gtggatggag	169930247
gtcaaagtga	tgatgttctg	gaaagcagtt	taaacaaaac	aaggggcctg	169930297
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ctgggcccag	gctacatcct	tggcaaagga	tgagatttgc	acccaaggtc	169930497
aggatggctc	gggtgtgtgg	agcacgggct	acggagccag	gtcaatggag	169930547
ttctaaatcc	ctgatcagca	accttctaca	catgtggcct	ttgataggtc	169930597
actgcctctc	tctgaagctc	agtttctcca	cctataaaaa	tgggatcgat	169930647
aacagagggt	acatctgtgt	ggatcaccta	aaactgtagag	gattttgcaa	169930697
atgtgttgtt	gtgggttgcca	ttcttattgc	tggaaacataa	ttccctcatt	169930747
agtatttctg	agtgtctctg	tgcatatctg	ctgcagcaga	atccttcatg	169930797
catccagcaa	acatttctctg	ggcatgtagt	atgtcccaga	cactgtgctg	169930847
aacactaaga	ttacatggag	gaatagagat	taatttctgt	tctttgttta	169930897
ctaagctcct	aggggctgaa	aggcatctta	aagtcataa	acttctcct	169930947
gatgcttaag	tacctccac	aacatcccac	ttatgtgtcc	tgggcttgca	169930997
cacttctggt	gctgatgagc	tcaccgcctc	ctgagacagg	tgattccttc	169931047
tacagaccac	tcagactatg	agaaagttca	tgccgggtgc	agtggctcac	169931097
acctgtaate	ccagcacttt	gggaggccga	ggcgggtgga	tcacctgagg	169931147
tcagagtttg	agactagcct	ggcgaacatg	gtgaaacccg	tttctactaa	169931197
aaaaaaaaaa	aaaaaaaaaa	aaattagcca	agcatggtgg	cgggcacctg	169931247
taatcccagc	tacttgggag	gctgaggcag	gagaatcact	tggacctgag	169931297
aggtggagggt	tgcatgagc	caagatcaca	ccactgcact	cccgcctggt	169931347
tgacagaatg	cgactccatc	tcaaaaaaga	aaagacaaaa	gaaagttaat	169931397
atatacctgt	attgagctga	aattctgggt	ctggcccttt	ctctgcggt	169931447
accaggtctt	gtgttttcat	ctccacatt	acctcctatt	agggacttta	169931497
atggatgaca	tattgtcacc	cagcctcctc	tgctggatcg	ggatagcttt	169931547
ccatccagac	aaagaatttt	catgactgag	tgaccatccc	caggatgggc	169931597
tttgggtgtct	ctcttccctc	agaaagtggg	aagctccaag	tgctgcccc	169931647
tgaaaccctt	ttccagtaac	catggcctcc	aggggtcctg	gggtgatctc	169931697
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tcctgaaatc	tagagaacag	agcaactttg	caagcttctt	caaaggagcc	169931797
cgttctgacc	caggtcgatg	gagctcccaa	aatctgcacc	cccaccccc	169931847
gctgctgtgt	gcaacaggag	aggggctttc	cgggaccagc	ttttccagaa	169931897

FIG. 1.83

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acatgaattc	tttttgacac	ttggcaaaca	tttggggacc	ctctcagacc	169931947
tcactctggg	caggcccgaa	ctgtcttttc	catgccagag	ggcagtcag	169931997
gttcctatca	gagttatttg	aataatcttc	ccaacacctc	tgagctgcag	169932047
tttcttcatg	tgtcaaatac	agataacaat	agtacttcac	tcataggatt	169932097
ggtggacaaa	gtcagtgagg	taccaggtgg	aaaaagaggt	agaacaagct	169932147
gggctttgcg	gcatgccacc	gtagtcctag	ctactcggga	ggctgaggta	169932197
ggaggattgc	ttgagcctgg	aagttcaagg	ctgcaggag	ctatgatcac	169932247
accaatgccc	tccagcctgg	gagacagaac	gaagccctgt	ctctaatttt	169932297
ttttttttaa	agaggttgaa	aggtgtctgg	cacttagtaa	gccttcaccc	169932347
tagttagctt	tgctaggatt	atgatttcca	tccagacaaa	gaagttgccc	169932397
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gtggacttca	gctctcccag	taactggctg	agtgatatta	gaaaagtcac	169932697
tgagcctcta	ttttctataa	aattaagaaa	aatcacactc	ccttataaaa	169932747
tccttaggga	aattaaagat	ccttgggaaa	atagatctct	tacaggcata	169932797
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cctgggagaa	ggagaagctg	atctgtccat	gcctgtctcc	tttggaaaat	169932947
gcacgctgtt	acacttcccc	acatgttcaa	attcatactc	tctccccac	169932997
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tcacagcatt	cctcagcctg	ctcaaaaggg	ctcaaaggaa	tcgattcaga	169933197
agtggtaatt	atgactgtgg	cccctgtcca	ggcgggcggt	cagcattgga	169933247
gcaccagcga	cagacggccg	gcactgactg	gggagggtgc	ctcccagggtg	169933297
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tttaaccctc	agataactcc	tggagggtatg	tgctcattatc	ctgattttata	169933497
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ctgcccggtc	ctcactcact	ttcctccctc	ttccccaca	ttgtcttttg	169933747
gactctgggt	gactcttgct	gtcctctggc	tactgggatt	catccatgca	169933797
cattagaacc	cagttagggtc	actaaccttc	tgaccatcac	agcccagctg	169933847
tcataatcct	ccctagactc	atctcttccc	tggccctttc	acctccatgc	169933897
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gtccatctga	ctcaccacag	tccagggtta	agcagggttg	ccggtacatg	169934247
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gtgcttaaat	gtggacattt	ctgggggctc	agggaatagg	tcattctgtg	169934347
ggccagacaa	agcatgcaag	tgagcagagc	tggcccttcg	cctacaaaat	169934397
accgaagaat	attottcaat	atcacaagaa	agtatctttt	ccatcatttt	169934447
tcttgaaaaa	tgcattccctc	ctgatctatc	tttcattttc	tcacatttaa	169934497

FIG. 1.84

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tagagatgtg	aatacagaga	actatatctc	tactataaga	caaatagcac	169934547
cctacgcaca	gtaatgacag	cccaagtagt	ctacttgtag	gaacaatgaa	169934597
aggaagtgat	gggggctggg	gtgaatggag	gtgcaccgag	cctgtctaaa	169934647
gaggctgctg	cttctcaacc	tcagcctggt	attgccccag	gaaatgtgaa	169934697
ccagtgcagc	cagatttcct	gacttcaaga	ggagctggaa	atcgactgta	169934747
tgcgtaatgt	cccaattttt	aagagctgcc	tcaattgaac	acgcacaggc	169934797
acaaacaaaa	acaaaataaa	caagccaaat	gcaacatctg	ctgagagggt	169934847
ttggttcttg	gattgcaacc	tctgcacaca	ttttccact	aaataaagaa	169934897
aagctccttg	cagatggacc	ccggtgggac	ctccaatacc	cggaatgcac	169934947
cgaatggctg	ggatttgtgt	ggccccaaaa	ccctcccttc	ttgcgctcac	169934997
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aaatcactcg	caattgttct	ctgtttcctc	tctgccatag	gatcaaatgc	169935147
ttccagtttc	aatgattaat	cgctctcag	ttttcaccac	aagttgtaca	169935197
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caaacacaag	ctctggggcg	gggctgatga	tgaactgatgg	cacaggttgc	169935297
tgcacatggt	tctgtgctat	cggattcaaa	ccaccctga	gactgctctc	169935347
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ttagtgtgac	tttattaatg	gccactatcc	atggaatgtt	tactctattc	169935447
cggatacggg	gccaggaaca	ttacctatac	catctcattt	aagcctcata	169935497
acaccactg	ttatatattg	gaaggagcct	tggcagtaac	attttatact	169935547
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gggccagtcc	ccagcccaga	gtccccacct	cggctctggc	attgctctcc	169935647
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catggttgct	ctccaggaat	gtcccagggc	agtgcctctc	taactcaaat	169935947
cctgggagat	attctccagc	gtctatgaat	tctccaggta	acctctttac	169935997
aaaattttaa	atttttcatc	aaataataat	catgtaaaca	tcaatttact	169936047
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gtctactact	gaagaatggc	ttcatggtct	taaccctattg	agaaaaaaaa	169936197
aatcaaaaaga	aaaataatat	ttcatgacac	ttgaaaagta	tatgaagttt	169936247
aaatttcagt	gtccataaat	aaagttgtat	tgagacagca	gttctcattc	169936297
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gtgaaaagac	atataaagaa	accaatttga	ccagaagcta	attgaaagaa	169936797
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atttacccaa	gtttggtgaa	ttagcgagtg	ccagcagtc	tagtggtggg	169936997
ctgttggatc	aaggaataaa	tgtttgaaag	caaaagttgt	caggagcacc	169937047
tcctcctacc	acacagttca	aaaacaatta	cagatatggc	aggctcgcca	169937097

FIG. 1.85

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agcacttoca	taccacatgg	tttattgcct	tgcatttgta	cgattatctt	169937147
ctgctttaca	aatttttatt	ttacaattac	ttttattcat	tgactgattc	169937197
atttttccaat	ccacttattc	cagttcaggg	tcacaggtgg	ttggagccca	169937247
tcccagcagc	tcagggtgcc	aggaaggaac	ccaccctggc	caggacgcca	169937297
tcccattggca	gggcacactc	acacacacct	acatactcac	actgggaacca	169937347
caccagttca	cttcacatgc	acagctctgg	gacgtgggag	gaaactggag	169937397
tccttgagga	acaccctg	agacatgggg	gaaacgtgcc	gattccacac	169937447
agacagtggc	tctgccaggg	tttggtgttt	gtttgtttgt	ttttcatcaa	169937497
tgttatatga	agcaacagta	ttcgaagacc	tgctgtacag	ctttccagca	169937547
gttccaggaa	aaaagagccc	tgggagactt	aagccatcac	agtacaaggc	169937597
agtagaggca	gggtgaaata	gaatggaaaa	aaaaaatgtg	aaccacact	169937647
gcagtcatac	tgggaagcagc	aatcccat	caaccaaaca	acctcacatt	169937697
aaactaatgt	tgttaatttg	aagtttattg	gttttgagct	cgtattttgtg	169937747
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ctgttaggtg	gaaaactttt	ttttcggttt	actgaaaagt	ttaaccagg	169938447
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taaagacttc	aggagtaagt	attccaggaa	gcaagatata	agctatgtgg	169938897
ccttctaaga	cctagcctca	gaggtcacat	agtgtaacct	ctatcacacc	169938947
ctattggtag	atattgtaac	agaagccac	ccagtttcac	agatggggac	169938997
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gtcaccatat	gtctttccca	agaggggtgac	tgacttctctg	ctttggtccc	169939647
agtttccctg	agattttcct	gaaagccctt	ccggctagcc	cagttgggag	169939697

FIG. 1.86

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tgtagtaca	tcagatocca	tgctttggtg	aaaaatgtaa	acacagacct	169939747
gatttttcat	tttaaataaa	gccaagcata	ttgctcccag	cagatgccga	169939797
gtgactcaat	ctgtcctctc	ggttctgaag	ggaactgaag	aacaacatgg	169939847
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gagttcatac	tatgaacca	ataattcaga	tcctagggcc	ttatcctaag	169940297
gacataatag	aaatgagcac	atattataaga	acaaagatgt	tcaatgaagt	169940347
gttacttaca	acagcaaaaa	aacttgaaag	tcacctaaat	gtttgttaagt	169940397
caagagcttc	attgatattg	actgcaaagt	ccatgttatt	ccatgtgacg	169940447
aatttttttaa	tcaatcacct	cttgatggat	tttaaatttt	ttacaatttt	169940497
ttgctatcct	aaaaaaaaatg	tgtcaatgaa	caactttgaa	ctaccctgac	169940547
taccacttta	ggatagattg	ctagacgtgg	aattactagg	acaaagccta	169940597
tggtataata	ttcactcagt	caacaaacat	gtcttgagtg	cccactatgt	169940647
ggtaggcagg	ctttgctcta	aacctcagag	gccccgtggc	agatgaaagg	169940697
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aggaatctag	tagacagtag	cagatgctga	ggagactgag	aacagtggaa	169940797
aggctacaca	cagggatctc	tgagtgccat	ggttcagaga	tcattgaatg	169940847
aggtgagatt	caaagagtct	gagaaaagtgc	ctgatagaag	aggatgggtg	169940897
gctctggagg	gacagaagtg	gaggggtggga	gtggggggaac	tggccttgcc	169940947
tgagtgtatc	caaagagcaa	atctttctca	ctgggctgac	tgacctcgag	169940997
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tgagatccgt	ggagaatcac	cgcagagctg	gcagcgttta	tctaagaatg	169941147
tggcattggg	aaaagtgggtg	caggctacat	tccaggcgat	aaggaccaag	169941197
caatgaaata	acaaataagt	catcttaaa	ttaaaggaga	tggacaatag	169941247
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gggttggaga	gaggggttcta	cttagatagc	ctgatcaggg	agaatctctc	169941347
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gaaagagaca	gtcatgaaga	gagattggga	gcgtaagatt	ccaggcagaa	169941447
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accttctctat	gtacaatcca	ctttctctta	aagtcacagc	agcctcagaa	169941747
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tctctgctag	attctctggc	attgcaagaa	attcttcaga	ctgccccaa	169942247
agattcgttc	caatctaggg	gctccttatc	cccagctcag	agctggattt	169942297

FIG. 1.87

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ggctcttgct	tggaggcggg	aagccctgct	gggccagggc	ttagaggggc	169942347
tcacaagaaa	tcaaagcaag	cattctccgc	ctctctccta	cagccctgca	169942397
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caccactggg	tccacgtcca	gtgggtagag	gtaaagggga	tggagatata	169942747
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tctaggaaga	caaggtggta	ataactaaca	tcaaatagag	agttcctatg	169942897
taccctgtac	atgtcttagc	caacttcata	cttgtaacaa	acctggaagg	169942947
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aagtcttttg	tgcaagggtca	tgcagagttg	aggcccccac	gtcggtagac	169943047
ttcaggagcc	agaccctcaa	ccccctcaat	gcctcccgcc	tcatgctgca	169943097
ctgagcagac	cataccogga	tggtcatggt	cagggttggt	atcaatgcag	169943147
accacgctgg	gcatattcag	gggacggata	ctcagaacta	tataacataa	169943197
ggaatagagg	aaggactgga	ggatgtatta	acatgaagaa	aaggtagact	169943247
catggcagga	gatgagcagg	gtaaagaggt	gcaagacata	aaaagccaat	169943297
ttcatataca	tgaagattta	tcaagagcca	gaaggccctc	tatgggtcca	169943347
agagttacaa	ggcctaata	ggtgaattaa	tgccagcata	taaggaaaag	169943397
cttttgataa	ctcagaagtg	tccaaaaagg	ggtcaggctg	ccttggaagg	169943447
tagtaagctc	tccatcagag	gcttggcaac	ttcttattag	ggatggtatg	169943497
agtatctcaa	gtacagatac	agatgaccca	aataaccact	gaggcacttc	169943547
tgaccccaag	tataagagat	tctattgtaa	cgcacaggag	tccatctcaa	169943597
gcagcacact	gagccatctc	cttgataaac	ctaaaggtag	gtattattcc	169943647
tcccagatgc	tgtcttctta	gcctgggatg	caaaagccat	aggatcactt	169943697
cacgtccaac	ccccatcagg	tgatctgtca	tgaatcacia	gttattggag	169943747
ccagatggaa	ctacagagct	aaaagataca	tgaagacacc	gaggcctgca	169943797
gacaggggact	aactttccaa	ggtcacagag	ctaacaagtg	tcagagtcag	169943847
gctagaccca	ggactcacia	gttgagctca	caattagttc	cacttcctac	169943897
accacctgga	tcatgagtg	caagaatgaa	ggaccttttg	cagtcttctc	169943947
atccagcagt	gacaaacagg	atgcacttca	tgtgccagct	tttaattcat	169943997
tggtcatggt	ttcctgaagt	gctgttgtcc	agaaatatte	tgaggccata	169944047
tctggatcca	gtggacatga	gtgaatcatt	tatgatgtct	gctttggaca	169944097
cagggtggga	agtgacaacc	tgtgtacca	gggtttggca	gccttgagct	169944147
aatccatctt	aatgactttc	tgacatgct	gcctggaagt	gatattaata	169944197
ttgcaaaaga	gattataatg	tgtgataacg	ttgtagtacc	tcacttatta	169944247
aaataattca	aggatccatc	tttgatgggt	aaaccactg	tctatgtctg	169944297
tttgtgttcc	tacaaaggag	aaccacaagg	tgaataattt	gtaaagaaga	169944347
ggtttatttg	gtcacagtt	ctacagactg	tcaagaagca	tggatccagt	169944397
gtctgcatct	ggtgtggacc	tcaggctgct	tccattcatg	gcagaaagtg	169944447
aagaggagct	ggatgtgcag	agatcacatg	gcaagaaagg	aagcaaggga	169944497
gagggggaga	tgccaggctc	ttttaaacaa	ccagctcttg	ggggaaactct	169944547
cttaggacta	atagagttag	aactcacttc	ttacctggac	aatggcacca	169944597
aaccatttat	ggagaatcca	ccctgtgac	ccaaacacct	cccatgaggc	169944647
cccaccccca	acactgagga	tcaaatttca	acagatgaga	tgaggaggat	169944697
caaatatcca	aactatagca	cccacctaac	gaatgcaaaa	gatgtgcagt	169944747
gaccttaagc	cccaacaata	tagagcagat	gacagttgat	atgtagatag	169944797
tttgaatgac	agtttaagg	agcagggttg	cagggtggctc	caccatatac	169944847
ttgttgagta	gtcctgagca	ggtgtttctc	tgagatcctt	tggctgggtct	169944897

FIG. 1.88



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gtaaaatgag	agataatgac	tctctcacaa	ggttgccatg	agaaatagag	169944947
aaaataccaa	gtactcagca	tagcctaaca	tttagcagtt	gctcaataaa	169944997
tgataggaag	tattggcttt	ataatattgc	atctaccccc	ttctctctat	169945047
gttagaacct	ttccaggcat	ttaaaagggtg	agcagcaaag	gccacccata	169945097
aatgtgctgc	tagagagcac	atagggtcacc	aatctcagac	tattgggtctg	169945147
aggcagatth	ttggagtctc	ttattcccga	agagatccag	ggacctgctt	169945197
tgcagggtgac	tgagaagacc	aaggccagga	gggaaggcca	aaaagctcca	169945247
agcagatcac	ttatctgtat	aacacttttc	accttccagt	ccttcttcat	169945297
ggagtttccc	aaagtacaca	cccacagtcc	tacaaattgg	ggaagagcca	169945347
gaggcaataa	atgtgtggga	gcagtcagct	gagaactgga	tggtgaagga	169945397
ttgtacattt	tcttgaatta	catgggagca	aactgcctcc	tgagcctgct	169945447
gtacccaaat	ttatcaaagc	acaaagcatt	tttaaagacc	atttaataaa	169945497
ctgattaaat	gtatttgaca	acggagctag	aaagccagtc	aattcatgtc	169945547
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ggcatgctgg	gaggccgtcc	cagcccatct	tcctgacatc	gctgcttttc	169945697
ctgtactgtg	ctaagtgcag	agaagggtcca	gcgccttccc	tgttttttcac	169945747
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actagcatct	aagtttatcg	cttctctctc	gttacctctg	tatcctccaa	169945847
gtacatgata	tacctctaca	gctcatctgc	caatgctgca	aagtttactt	169945897
atttataacc	ttcccagtg	cttggtgata	ttagatgcag	gagtaagatg	169945947
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aggaggggga	gaagattagg	caagaatgta	aaagccctca	tgggtcttgg	169946047
aaatcacagc	atctaagttc	tctccttcc	ctccctcct	tcccttggtt	169946097
tagagatgct	ttagctagcc	taagggcaga	atagcctgcc	tcttcatttg	169946147
ttcttcaaaa	tccattgttt	ggggcacaaa	atgatcttca	gagtttaggc	169946197
tcttgagggt	caataaactt	aaaatctttt	ctcagctttc	ctgtagatc	169946247
accacccccc	gaggcaatga	atgctgctga	gctgatggaa	aaagggcggt	169946297
gagaaactcc	agaaatatth	tccggcagtg	tttcttcttt	atctctgtcc	169946347
cccagtagct	cagtgaagga	aagataatca	tcagttttta	attttttatg	169946397
ttattattgt	ggctgcataa	cagttgtaca	tatttatggg	gttcatgtga	169946447
tactttgata	ccagcatgta	atgtgtaatg	atcacatcag	gtcgttattt	169946497
taacactgag	gatatggatg	ctcagaatgg	acattggcct	cactgaggtga	169946547
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gactcaacta	cctgaagatg	gaatatgggt	tgtgctaact	aaattaatga	169946647
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gaacttggtg	agaaaagaag	tgctgtgac	tattagtaat	gtctgccatg	169946747
ggcactggac	ctgggagcag	ccacgggagc	catgccatga	tccccagact	169946797
ccgtgcttct	tagaaattct	gattgttgtt	tggtcaatag	ataaatgaat	169946847
gcagaaactg	cttctttaat	gtaggcttag	agaaggggat	tggagttagga	169946897
agcaagagag	gcagctcctg	ggcctgttca	tggtgtgtcg	ggaggccagg	169946947
ctggacagta	agagataaga	acggcagggg	agattgagac	cagaacttgg	169946997
aaaagcttac	aatgccaaac	taggaagcct	gagggtcgtg	aaaggtttgg	169947047
gctcagagga	ataagtaaga	aaagctgcat	ttaacaccag	gaatctggca	169947097
gggacacgta	gagtcaagga	gacagaaaga	ccagcttgga	gagtgggtga	169947147
gtctgcacga	ggcgtggagg	ggtgcccagc	ccccggcaga	ggcaggtcac	169947197
agtgacaagg	acagaaagcc	tggagggaca	actccgggga	cttagtggtc	169947247
ggcagagggg	actcttttcc	ccagtgactc	atatgctcct	ttttttctag	169947297
ctgaatttca	gtttttattt	cagctccaat	cagtggcaat	agaggaatcc	169947347
gtgtgcttta	tttctctctg	tccacattcc	tccccacagt	ctcccagagg	169947397
ctaacattct	cccctcctcc	aaagagaaga	aatccacagc	ccagagcaga	169947447
gcaggcctgg	tggttctcatg	acagtcacga	gtgtggcccc	atctactagt	169947497

FIG. 1.89

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gctctccaag	tccagcaatg	tgtaaacct	ttacaggcat	tatcccatgt	169947547
aaccctaac	agccctagga	agtagacact	actagtacct	ataattcaca	169947597
ggtaagaaaa	ctgagggtca	gaaaggcaaa	gtaactgggt	gagggtcaca	169947647
cagctaagaa	gtcgcaaagc	cagagtcgaa	aatattcaaa	acaaaaaga	169947697
aaaaaaagaa	aaaaaaatct	gagttgaaag	cttgctctct	taacgatata	169947747
gctctggccc	aattaagcta	taaaatgtca	caggtagcag	tgtccttaga	169947797
gaacacctaa	gctgagaact	ccctcatttt	tcagaggggg	ggatctgagg	169947847
gtcagtgagg	agatctgttt	tgtccagggt	catcagtgag	ttaggggatg	169947897
agccgggact	tgaaccctac	agtggaagaa	atgtgagcca	cagaacttac	169947947
catgttgctt	gttgacttcc	tctggcacat	tccactgtat	tttccccgaa	169947997
gcctctcccc	agcctctcag	ccccactcct	cgtggctcca	ctccctatta	169948047
ctcagagggtg	ttcagctcca	cccactagtc	tcccagcatg	gcagtttctg	169948097
cccattacag	gcctacaata	cctgcgagcc	tgtcagcccc	ctgcctccca	169948147
cctctcacc	cccgccccgg	aaatgggtct	gttggtaccg	gaccaatcag	169948197
ggcaccagc	agcgtctaga	acttggggct	gataatggca	tcgtgaatag	169948247
aggaaattag	agctgaatgc	attcacagtg	aatattcctc	ccagggcaga	169948297
cggggccatt	cgctgagtg	cacatgacag	atgttcacat	ggaacccagt	169948347
cgcagggcc	ccttcactcc	tttcaccagc	acggctgtct	cccagccctg	169948397
gccgtgcttt	agagcactct	gcacccccaa	ccctggccct	ccaagccctg	169948447
caggagccag	tgggtctgca	tgtctcctct	agtacctctc	aagcacatgg	169948497
ccttggccct	gaagagcgta	gtggttgatc	gcacagccct	tgggggttaga	169948547
tgtatctgct	tccaagtccc	aaccttctgc	ctcactgctg	ggcaggcccg	169948597
gcaacatgcc	tgaatctcag	tgcccccatc	tgtaaaatgg	ggataattaa	169948647
taccaccccc	acagtggtca	tgtgaattca	atgtgattat	gagtgtaaag	169948697
agtttgtccc	catgcctggt	atacagcagg	tgttcaataa	acgatggcta	169948747
ttatgatcat	cgattgctct	ctgtcacctg	tgtatcctcc	aaatgcatga	169948797
ctggcctctg	caattcatct	gcctcaaagt	ttacttcttt	gtaaccttcc	169948847
cagtaccttg	catatattag	gtgcaggatt	aagggtgttg	gattgagatg	169948897
atggtgacga	tgatgatgaa	gatgctgatg	gggatgcaga	ggagggggag	169948947
aagattaggc	aagaatgtaa	aagccctcat	gggtcttaga	aatcacaaga	169948997
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tgctgaaatt	tactgtcagc	aacaggaaac	tcacacacc	tgccgggtcc	169949097
atgccacatt	gttctgtgtg	gctggggaaa	gttacctcat	ctctctgagt	169949147
ctgggtctca	gtccctcatc	ttctccagg	ctgttgtag	gagtgaatga	169949197
agccatgctc	acaaagtgtc	tagcacagta	cctggcctag	tgggtgttcg	169949247
attcacagtg	gatattgctg	ttgctactct	tgtcagtata	tttctgatct	169949297
ccccaaactta	cagatcacca	ctccocttga	gagcagagtt	gtacacttca	169949347
ttgtgtgtgc	ttctggagg	cagggatgga	acatccattc	atttagtcaa	169949397
caactgtgga	ttgagcagtg	tctctatgcc	tgccactgtg	ctcagctctg	169949447
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tcacagccca	gtggggaaga	cagatatata	ggcaacaagt	ttttaattgc	169949547
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aattatcaca	aattcagtg	cttaaaacta	ataaaaatgg	gccgggtgca	169949697
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gtcctagcta	ctccaagagg	ctgaggtggg	agaatggctt	caaaccatga	169949897
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aacagagcga	gactctgtct	caaaaaaaaa	aaaaaaaaaa	aaaaaagcta	169949997
atataaatgt	attatcttgc	agttctggag	gtcagaagtc	caaaatgagt	169950047
cttatgggac	tcaaatcaag	gtgttgtagt	gctgtgttcc	ttccgggggc	169950097

FIG. 1.90



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tccaggggaa	agtgtttcct	tgcoctgttac	agcttctgga	ggccactcac	169950147
attccttgctc	tcacggcccc	ttcctccatg	tcctaagcac	atccctccaa	169950197
tctctgcttc	tgatcatcaca	tgcccttcct	ctgaccctga	gcctctgcct	169950247
ccttctgaga	aagacccttg	tgattacatc	aggttcacct	ggataaattca	169950297
ggataaatctc	ttcatctcaa	aatccttaag	ttgatcacat	ctgcaaaaatc	169950347
tctctttacca	tgtaaggtaa	catattcaca	gcttctgggg	attaggacat	169950397
gcacccctag	ggaacccatga	ttcaacctag	catgggggaa	cccactacag	169950447
gcaggtgttg	tccttgccat	cgccagctca	gtgcttgcca	cagtagaggc	169950497
catggatatt	cattcagaga	gagcatgcac	tgaggcaagc	ctgacctcaa	169950547
gatcaagaca	ggaaattggc	tttcatgggt	taaggacctg	ttactttgct	169950597
catcaatgta	tccttaataca	tcagagggtca	gatctgctgg	agagtgcatt	169950647
ctttcagttt	ccaaaagtaa	gactggatgc	cttagaactt	aaagtccagg	169950697
aggtagccaa	gaaagcaatc	atagactgag	tcctccatgca	gtgcactttc	169950747
tcggatggac	aatttctctg	ttctgacagt	cactgttgac	tccattttctc	169950797
agatgaggga	ccgaggcaca	gagagggtgca	gtcagtcacc	tgaggccaca	169950847
cagtccaggaa	gtggaaatcc	atggaaaactc	atcatcagct	gcctcgcatc	169950897
agggccagtg	ctctttatct	ccaccccaca	cattataaag	ccactcagct	169950947
ttacactcaa	gggaacttcc	tatttcccta	ctggattata	tgtataattt	169950997
gtagtattgc	aagatttgaa	cagaagcgag	cagcagcttg	tagttgtgtg	169951047
tgtcactcac	tcctgcctgt	ggggatgcca	cgtgattgtt	taaagggttg	169951097
gaatcaggag	aaaggcaggc	tcagagcagg	accaagagag	agcccacccc	169951147
tcgcctcccc	aaatccttca	gcttcctgaa	gtgtggctgc	tgggtagcag	169951197
ctccccagg	gaagaaaata	taagatatc	ccaagggacc	ctggaagctt	169951247
tatcccaagg	cttcacatgt	gtaggctgtt	tcctgtgatt	cggctctggc	169951297
gtcaatgatc	taagattgag	agccaaggct	agtgaggggg	gaaaagggac	169951347
atgtagtgc	ggggttcagc	atccaggcct	aggacttaga	ctgaggctct	169951397
ttacctcct	ctgtttcttg	ctgatggcct	taggcaagtc	gcttcccctc	169951447
tctgacctc	agtttttccc	tctgatgaaa	tgggtgtaat	aattgtgcct	169951497
acctcttcag	gggtgctgtg	ggataaaaatg	agctcatact	tactttcttt	169951547
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tgcagtggcg	cgatctcggc	tcactgcaag	ctccacctcc	tgggttcaca	169951647
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ccatacctgg	ctaacttttt	ttgtattttt	agtagagacg	gggtttcacc	169951747
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caaatacgtg	gtatctgcta	ttttctgttt	taattaggta	ttcagagtct	169951947
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gtattgttgt	agatgccagg	agtacagcag	ggaataaaaac	aacatccctg	169952047
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tgcaggaaaa	caaagcaaag	tgagggtatg	agagtgcgga	aggttggggc	169952147
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gtggtgactt	catctccct	agtgttcctt	tcctccctctg	caaaatggga	169952547
atggggatgg	ctcagaactc	ccagcgggag	ttaggaggaa	taatgtatag	169952597
gaagtatgag	cagagtgcct	ggcctggagc	atagcgcag	gccgatcata	169952647
ggttaagtgt	ggtgttgatt	ttattggaca	caagtttgga	aactcagagc	169952697

FIG. 1.91

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ctgcagggat	ggccttgaag	gtaaagaaga	ggtagttggg	agttttacac	169952747
ttcccaggac	ctaccctcag	agagacaggg	gtcattccag	agtatctgga	169952797
taccagttt	gggccaaga	tacttccagc	cagggcactc	gtcaaccacc	169952847
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gcaccttcag	cctcagctac	ctcaccacct	aactggggag	gattaactat	169953197
aactctgacc	attcctggga	ctgtctccat	ttcaaaacaat	cagatccctc	169953247
gccagactgt	attagtccga	gcagtgcata	tgctgtataa	aacagcccca	169953297
agtgtctgtg	gctgaaacca	tgacagttta	cttctcgttg	ccatggcagc	169953347
cagtgcagct	cagagtggat	gggcatgtct	gcattctgcat	gcattgcaggc	169953397
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aagggagcct	ggaggaagcc	tcagggtttg	atggggcagg	cctggaagtg	169953497
aggtgcacca	cctccactcc	tatccctcgg	gccagaactt	gggcatctga	169953547
ccacacagac	ttcccttgga	aggagaagag	aacaaggaca	ctgtgcacct	169953597
ttgtcaagcc	aaccaccatg	cccatggagc	atctactatg	tgcaagagat	169953647
tcagctcctc	cagacaatgt	tctctgtcat	tttccatctg	ttcaagctga	169953697
gtcagagggt	tgtacatgtg	caaatgcgaa	caatccaggc	tcacttcctg	169953747
cttccctgag	tcctaggcta	acctctagca	cagcacagat	cacaagagtg	169953797
atgactgcct	gaccgtgtgt	ccttcctccc	agtagagttt	gagccacatg	169953847
gaggcagggg	ccacagcctg	tattctcagg	acttggacag	cgggtggaagc	169953897
tctacttagc	ttgctgaaga	ggaaagggga	aagaaaggag	agtgaattgg	169953947
cacttgctga	gatctcccag	ttcggttttt	aaaaattgtg	gtaaaatata	169953997
tgtaacagaa	aattttaccat	cttaaccatt	ttggagtgcg	cagttcagta	169954047
ccaccaagta	ccttcacggt	gttggacaaa	cttcaccacc	atctgtctct	169954097
agaatgttct	tcatcttgca	aaaccaaacc	tctgtaccca	ttaaacgact	169954147
ccccattccc	tcttccccca	gctcctagca	actaccattc	tattttctat	169954197
ctctacaaat	ttgactactc	taggtacctc	gtataattgg	aatcaacagt	169954247
atttgtaccc	tggtttattt	catttagcat	aatgtcctca	gactttattc	169954297
atgttgttgc	atgtgtcaga	atttccttcc	tttgtaaagc	tgaataattt	169954347
ttcattataa	gtatatacca	cactttgttt	atccattcac	ttgtcgatgg	169954397
aaatttggtg	tgcatccacc	tttttttgct	attgtgcata	atgctgctat	169954447
acacatggct	gtgcaaatat	ctaattattg	tccctgcttt	cagttccttt	169954497
ggatatgtat	ccagaagcag	aattcttgga	tcatatggta	atcctatttt	169954547
taattccttt	aggaactgcc	atattgtttt	ccacagcagc	tgcaagcatt	169954597
tacattccta	ccagcagtg	acaagagttc	caattttctc	atatcctcac	169954647
caacacttgt	tattttctgt	tgctgctgtt	tggtttttta	ttaatagtca	169954697
tcctaattgg	tgtgaagtgt	tttctcattg	tggtttgctt	tgcaaggttt	169954747
gatttgtaga	ttttcctgat	gattagtgat	gggtgcattc	tttcatgttc	169954797
ttactgacct	tttatatata	tttcttggag	aaatgtctgt	taactctact	169954847
catacttttg	taaatagtat	tcccaatcct	tctaactccc	caatgagggt	169954897
gatattagta	tgttcgtgtt	acagtaaagc	caactaaacc	ttagaaagac	169954947
taggttaatt	atccaaggtc	acacagctag	aaaatgacac	agcttgtatt	169954997
gaaacatcag	tttttctctt	tccaaacctc	acgcacattt	catgaaacct	169955047
acattattgc	accataacat	catgttgatt	tacttatctg	ctctcctgcc	169955097
tgtcccatct	actacataaa	ttgagtgtgg	tttgaaatca	gagactactt	169955147
ctcatctttg	gcacagtggc	agccatggat	cagaatctct	tacatgctgg	169955197
ataagtggat	gcaagctcaa	ggccacacct	aaagtcccca	ggtgacttga	169955247
tcacttgagt	tagctgctgg	aaacctgggc	ttcctcttct	gcaaaatggg	169955297

FIG. 1.92

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gagagaaaat	aaattctcag	tggattgttt	agaagatttg	agcaaagacc	169955347
tctgcaaagt	gctaagcatg	tggctagcat	gtggcagggtg	ctgcctaaat	169955397
agtagaaatt	aacactgcc	tgcttataag	ctccggacaa	acacaagaag	169955447
cccgaaacat	aatctgtgcc	ttctgcttgc	attcctocta	gttggggatg	169955497
taaaatagcc	cagctacaat	caaagaagaa	aatcaaagtc	agcacagact	169955547
atggatatgc	ttctatatgt	gtagattatt	tccagactca	ttcggaagaa	169955597
tctggacata	ctggttgcct	cagagggtcaa	gaaaattggc	tcattttactt	169955647
ctgtaactta	atttcgactc	tctatgcttt	tacatagttg	gaatttgcca	169955697
tgcacatata	ctacatttta	aagagcgtgt	acgcgagaat	aatgtggtca	169955747
ggtggcctga	tccacagggtg	ggtgggagag	acaacagaga	cagtcttctg	169955797
accccatctg	gcttctacct	gccaacccca	tgtattctgg	agactctcca	169955847
cacctcctgg	catgaagcag	aatccctctc	aggggggtcac	ctcacctcct	169955897
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gcacctata	gagatatcac	ggagagggga	gcatttgtaa	tttactttgg	169955997
aggggtgtgt	ggaggccgag	taacaccgcc	ttccatctca	gtgacaacaa	169956047
actcattctt	cactataatt	aaaatgtcac	tttgataaat	aattccatca	169956097
gcccccttcc	acctatgaat	agcttcttgc	tataattgtt	cacattctgc	169956147
tgaattagaa	gtattcaagg	gagaatttaa	gaggtattta	ggcaacaaag	169956197
ataaatcggg	tgtgttttcc	accctcccac	aatccctcat	taagcgagac	169956247
atcatccccg	gctgggcagg	gcggggctgg	ggggcctcat	ccctgtgttc	169956297
tcagtcactc	tctccctgag	tggagggagc	cggaggggtt	gccacagcag	169956347
cgtggacctc	aggaaggggc	tggagtgttg	ggatacatgt	ttgggggcct	169956397
tcccttccca	gctattactg	tagaaaaaga	agaggatgcc	tgaggtggtg	169956447
ggaagaacgt	aggctctagc	ttcagggtgag	cttggaaaag	tcagtgaaca	169956497
tttatggacc	tctgttgtat	aacagaatac	aagatataat	tcttcattca	169956547
atcttgtgtc	aagagcctga	gtcaagatat	aattcttgga	agagacatct	169956597
gacattgagg	gtccccctc	ccatgttatg	ggaactcaagt	cttccaaagg	169956647
atgactttcc	ctaggagaca	cagctagaga	ttggcaaccc	caggaccttt	169956697
gaatattcaa	caatacccag	taggggtatga	agcaccgtag	gagttccgtg	169956747
actattccca	tcttccctca	tttttgttgg	tacctcttcc	ttcctgataa	169956797
atcacatctg	ctgggaataa	tccaataata	ggatgcacag	agccagccac	169956847
agtgtgttgg	acacctcagg	aagtgtccca	tcttgggtat	gtctgtcctc	169956897
accttgggta	gaaagagatg	gtatttgact	ctttcccccac	cagaagaggg	169956947
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tacagtttct	ttttttttat	tattgtttga	gacagagtct	cgctctgcca	169957097
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cccaggttca	agcaattctc	ctgcctcagc	ctcctgagta	gctgggatta	169957197
cagctgcccc	ccaccacacc	caactagttt	ttgtattttt	agtagagatg	169957247
ggttttcacc	atgttggcca	ggctgctctt	gatctcctga	cctcagggtga	169957297
tccaccccac	tctgcctccc	aaagtgtctg	gattacaggc	atgagccact	169957347
gcaccagcc	taactacagt	ttctttatct	gtaaattgga	aataacaata	169957397
gtcccactga	tgagttatgg	aaagttagggc	cttccacggg	gtctgcatgt	169957447
ggcaaacatt	acccatagct	cctgttgggt	ttctcgtgag	gagtgttaaca	169957497
gtttggccat	gcagttttta	atgccacatg	agcggctagg	tgggagggag	169957547
taccgggcca	atccaactca	gtcaacacag	gtccccccaca	ccatttcctc	169957597
tgtggcagg	ataagagtca	aggcccactt	caaggccacc	aaagtccaag	169957647
catctcccca	gtcctagctt	ccccagagag	tcctgaatga	cagggtattca	169957697
ttggttgtga	tggggcttgt	ctgggggttg	ggactggggg	tgaggagtgg	169957747
ggtgggggtt	aaaaatggag	ggcagcggta	ccagtgaagg	ggaagcagtg	169957797
ataaaaccca	tttgagtctt	tgctctgaag	cagagtccat	taggatgacg	169957847
gctccttgga	ccaggggagct	gcgtctgagg	ggctgtgccc	agttccatca	169957897

FIG. 1.93

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gtggtgggat	tgggagtggt	ccatgaaaat	aactcacatg	catgtgtggc	169957947
tggctgaaga	agcagagaag	cctgcatggg	cagccaatcc	ccatgctgag	169957997
cgctttgott	ggaatggctc	tgataaagaa	gcccattgatg	ctggaaggaa	169958047
gggctccctg	caggaccctc	tgggatgatt	ccctgcccatt	ctccaggacc	169958097
accctccaga	atatggtcta	ggatggcctt	gagtgcgtag	gtttcagaat	169958147
gtgggaagaa	ggggcaagga	gaaaaaaaca	agcacctatt	gatcacctgt	169958197
gttagctcat	tcaatctttc	taacatctct	gcaggttaaa	tattctatcc	169958247
cattttacag	agggcaagct	aaaactgaga	gatctaagat	gattttgcca	169958297
aggttacact	gctagcaaat	ggttagattt	gaacccaaga	ctctaactcc	169958347
aaagagccaa	gctctttaca	gtggatcagt	ccatcatctc	tttacatttt	169958397
acaagtttgt	gtcatgggtt	tagacaatat	gtttgacatg	caagacgctc	169958447
tgctaaccct	aatgaagggt	tgcatgtgag	atgcatgtgg	gagtcagtgt	169958497
ctcgggtggg	gagcttcctc	cagactcatt	tcaaaactagc	ttgcacagca	169958547
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cagggactca	aaaagtttgt	tctgaagctc	cagggccttt	ataacggggc	169958647
ttcgaaagca	gcagaaagaa	acagcacaca	aagtgtttgt	ttattctctt	169958697
gtattcaaga	aagagccaat	aattcaaaca	actaattcta	gaagaataga	169958747
attccccag	tccccacctt	aatacaggca	ggctcacctg	tccattggta	169958797
agtcagcaca	tttctctgtg	aacactgatg	ccctgtgccc	atcacacca	169958847
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cagctgctc	ttggaccagg	agctaaggga	gaaactcctt	ccttagagac	169958947
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gttctggaga	tctgcgagca	ggactgtatc	catgaatcag	gactctgtct	169959047
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cgtagcatgg	agccatggag	agagcatgag	tttagaagcc	aggagcgcca	169959147
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accatccagt	ttgagacctg	cttaatcagt	gggggttctgg	gaggccagag	169959297
ctggagctat	gatcagggtt	aaaatgcata	cagaaagcac	agatgctaga	169959347
agccaaatgg	aggttgtcca	gggggtcccc	aaccatggga	ctggaagcag	169959397
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gcagctgcta	acagggaagg	ccagggtctg	aaccacagctg	atccggctcc	169959647
agcatccgag	ctctgaacca	ctggtctatc	ctgcctctgt	taggacttgg	169959697
tccaatgtca	tcactctaga	aggaacattt	aggcccgac	ggtgggtggc	169959747
tggttcaatc	cagtttaaag	gccaggagca	ggacagtgc	ttgcagctgc	169959797
agcaatccta	tgactcaaac	caaagcagct	gtgacaaata	aagggaactga	169959847
ctctcattct	cccgtgctag	ggaaggatga	gctatcaggc	cttgttgag	169959897
gctgagtcag	tcactccaca	aaccacctaa	gtgaaacctc	ttcactgagc	169959947
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ttattccata	ccaggctggg	ttcggtttcc	caagccacct	ccacttgatt	169960297
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atatatatat	atatatatat	atatatatat	gaaagaaaga	aagaaaagag	169960397
agagagagaa	agacacaaag	gggaagcttt	catgccaaagt	ggaaacaaga	169960447
caaaataaat	gcaccgaatc	cgatttcaaa	agctgtttga	aaactctgtc	169960497

FIG. 1.94

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cggaattgct	ggaaagggcc	ccagcatcca	caggaaatgt	atccctgcc	169960547
agccctgtgc	tactgaactc	tgtggccccc	actcctgcct	cccgggtgact	169960597
tgtttagaac	tacttcagat	cggaacaaat	cacagccaac	tgcagtcgct	169960647
gtctctagcc	cttcaatcac	tcctaatacag	accgtgtatt	ttagcaacag	169960697
aatcttccct	ggctgaggag	ctcattcatc	tgccctccac	cagctcgaca	169960747
ccctttgaat	gggagatgag	gggaagccac	ctgcttctct	ggcagccaag	169960797
ggaagctggg	aggaggcagg	aattgccagc	cctccctctc	tgatagatca	169960847
ccagtgggag	tccagaccag	caggaaccag	gaaaggaggt	ggcagggtcag	169960897
agagaaggca	ctgaaaaggg	tcatctgagt	ccatgtttgg	tgaatgccc	169960947
ccttgagctg	gacacctggc	tgtggtccct	ggagttggat	agcctgggtt	169960997
caaattcttt	aactaccatt	ttctggccaa	cccattctct	gtgtgccccg	169961047
gacaagggtac	ctaccctgtg	agtatagaag	caaaccccc	gaaaaaagca	169961097
agtggaaaaa	gcaaagaacc	aggacatggg	tggactcgag	tcctagagag	169961147
gctcaggaaa	cttttatcca	aagacacaga	ggagctgggt	gcagaggaga	169961197
gcttaaaactc	acacagagag	gggaggcctg	ggaggtgtca	acaagttatc	169961247
ttctcacttc	agaagggccc	tctcgagaac	agggatttcc	cctgctctgc	169961297
aagggaccag	tggacagaag	tcagcagagg	ccatgtaggg	gcaggagctt	169961347
cctgtcatca	tagatgccaa	agctgaagca	ggatactgaa	tgcaaacagg	169961397
ccctgaggcc	atctgatgtg	ctcgttccca	tagccccgct	gtgtgtgtgt	169961447
gcgcgtgtgt	gtgtgtgtgt	gtgtgtgtgt	gtgtgtgtgt	gtttgggtgg	169961497
gtgggagggg	aggcagaaga	ggaagagagg	gcagagagcc	aaagactgag	169961547
gccccggccc	ataagtaagg	cagtttgag	atctcaatat	cctgtgcaga	169961597
cccacaggct	gccgtggggg	tgagggtctg	tggtgtctta	accagaggca	169961647
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cacatttctt	ctctgaaaat	ttgccattaa	tcacagggtga	cgatggaatc	169961747
agcaattaac	atgagctaaa	acaaactact	aggcatacag	tagcgtctca	169961797
taagtgctag	ctattatgat	tacaatggag	ggaaaagttg	tcaccgcagc	169961847
acaccgtgca	tccctttttg	gtctggggcc	tctcatccag	acacaggtaa	169961897
gaagactcct	cactccccga	ggaatcgctg	gcaatgtcat	gatggcatct	169961947
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aacccttcag	acttacatac	cctgtgtatc	aaggaatgag	tctcccatca	169962047
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agtggagctc	agaggtgccc	tcccaccccc	agattccatg	atgctcagga	169962147
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aatgaccagc	attttctctga	acacatcatg	ctgtatttag	cgtccaggct	169962897
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ctcttgggag	ccttttttgg	tgcccccac	cccatcaggc	cacgtagcac	169963047
ctggtagcac	caggtagcac	cccatcctct	gtgtgcccac	gcctacctcc	169963097

FIG. 1.95

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tctctacctc	acccacccctg	gacagaccct	cacaccacac	ttctcacatt	169963147
acattgaaac	tgatgactgc	cttgtcatct	tctccctgga	gcatgtcatt	169963197
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gcaagcagat	ggccaatgaa	tgtttgga	cactgcactt	cagaatcggt	169963497
ctctacctag	acagacttca	tatcaaattc	cagctctccc	acttaccagc	169963547
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aacacaacac	ctgcgtcgct	tcctctgtg	tacagagcag	cggtgttgca	169963697
gtttgcgcgc	taaggctgta	gactgggctg	cagtgccttt	taaatacacc	169963747
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agacatcaca	ggagaaggag	gcagaagctg	gaacatcatc	cgggagctgg	169963947
actagaacgt	cccgggaaac	ttcagcctgg	cttctgcttt	gtcccgaaaa	169963997
cccagggtc	cagctccagg	gctctgtctt	agaatgaggg	agtttatctg	169964047
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aggagcagag	acaataaata	attcagcagt	gaaggaagca	gaaaaaagat	169964197
tgactcatt	tcgcccttca	acaattatac	taaacacctg	ctctgggcca	169964247
cagaagggcc	agatcccatt	cctgtgctca	ggaagcccac	aggccggcag	169964297
ggagaggctg	gttggaatgt	gtgctttgca	ctgtaacgga	ggcatcgagc	169964347
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aatgggggat	ggagcaggca	gcaggggaca	gatgctgcca	gaaaccgaga	169964497
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gaccctagaa	tcccagtggc	catcacccca	cagcacatgc	caacctttct	169964647
gtgataactt	tctcttgtgg	aactgtgaaa	gtgtaagacc	agctcctgta	169964697
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cttataaatg	gggtcctggg	ccgtggcact	gatctggtcc	tccaccttg	169964797
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aagaggacgg	gatgcctggc	ttggctgctg	gtctggggca	ggtgccaggt	169964997
tacagcagtt	ggaaaaatcc	tcagtgttgg	aaggaaattt	ggaagtgagc	169965047
atctacctgc	ctgccgtgca	gtttgtgact	tttaagatgg	ttgacagaac	169965097
attcccaaag	gaccacagcg	gtgaccactg	ttctcgtttc	cotttgggtg	169965147
ctcactcact	cagtgtctga	cacagtggtc	ctgacaagac	agtgtgtgtg	169965197
cttccatgaa	cctaggacag	ggatagactc	aaggactaag	aacaaaccag	169965247
gaagaagcat	caccacaggc	tccttgccag	tcacctcatc	tcacctcct	169965297
ggccctggcg	gatgggtctc	catatttaca	ggggccagat	gaaaaaacca	169965347
gaggagccag	gaaaaggagc	ttccccttcc	caagggcgca	aggtgaggtg	169965397
ccagtcatga	gatgcaagcc	ctgagctttc	tgattccact	gcatgtggtc	169965447
ccaaggttcg	gcgccgcac	acacagttag	tgagcacact	ctcctcccct	169965497
ggccccgagt	gagccagctg	gatggcagat	cagaaagaga	agtcccgggt	169965547
gcccccaaca	tggttagctc	cttccaggac	caggggctag	gccccagcta	169965597
aggctggtgc	acacagcagg	gcagggggcg	aaggagtggg	atcccaccca	169965647
gggatcccac	ccaccccaaa	cctgctttcg	gacatctttc	caatgcataa	169965697

FIG. 1.96



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tgtgcagatg	aggccctttg	ataaggacca	aatccctttc	cgttgcttgg	169965747
caacctggct	cacaagtcac	agcaggggaag	taattttacag	gaattcaaag	169965797
tgtcgctgga	ggttctgctg	agctgaattg	ctgcaaagag	gaacctcaat	169965847
ggtccaaatc	acacctctgg	cggggaggag	gggctgaagg	aaaagcttcc	169965897
acttccgtca	cttgagagta	cagagccctg	agctcagact	cagcgatcgt	169965947
tttccattaa	cggattttact	ggttccatgt	tgagctcctg	ctgtgtggca	169965997
ggccctgtgc	tgggagccag	ggacacagtg	acaaacgaga	cagatgcca	169966047
ccccggatgc	acagagctca	aagagacaga	ggagtaaaca	gggctacaca	169966097
tgtgacaaga	taggctgtgc	acaggggtct	gagcaggacc	cttggggcag	169966147
gaggaggcag	tggagggatg	ggagggtagg	gacgcagtgg	tgaccagcta	169966197
gccagataga	gaacagaggg	tgtcccagca	cagggccaca	caagcaaagg	169966247
cagaggtggg	gagagaagag	cctgccacac	tctcagatca	ccatgtgggt	169966297
gggccagggc	cccagctgag	gctgaggaca	catggagccc	agatccggca	169966347
gggccttgaa	tgccaagtca	gaaagcatct	gaaatttagt	ctacagatga	169966397
tgtgggttat	tgacagccag	gacaggggaat	gacatttgtg	tttcaggaaa	169966447
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aggggaagaa	actgtgagta	aaggagtctc	tggggtacag	gtgaagtttc	169966547
tgtgaaactg	gagaagaaaa	ctgttgaggc	aagagttgac	aaaacttgaa	169966597
gtaggatgga	gaggaaggga	caagttcccc	tggcatgggt	acggcccggg	169966647
ggtgggaacc	aggggaaggg	aggggctttg	caggtgtctg	acttgcccaa	169966697
caggtggcgc	catttaccac	gatgggaagg	gccggggaga	agggaggggt	169966747
ccattctagg	gaaatctcag	gtcctcgtca	ttaggattct	ttcggttgcc	169966797
agtgaactgaa	accagctga	aatggacttg	ggaacatact	ggttcatgac	169966847
atctggtgga	ggtgaggtca	gggtgcactg	gagccctggc	agcccactct	169966897
gatgccagag	cccatgggga	cagcgggtga	tgttggaacac	agtagtcctt	169966947
caagggcggg	gatcggagga	acagaagaaa	ggaacagcag	atgccccact	169966997
gaggctgagc	agaacattta	ggatccttgg	ccccatctca	ttgtgccctt	169967047
tgctgtggct	catctcacac	ttgcaggag	aagccaatgg	atctctgtga	169967097
atggcgaggc	tttgtatgca	taaatgtggg	ccattttgtc	cccaagaatc	169967147
cctgggggtg	aggaagccac	agaaaattga	ggtcctattc	cctgctcact	169967197
cctggtatgt	agtggaagct	ggagagcctt	tgtccaggca	ctgacagcag	169967247
gaggtttcat	gcagagctgc	tcagggcatt	tcccagatct	gtcccacccc	169967297
tgggaactgg	ctcagtggcc	ttgccccacc	agaagactgg	gaactgcacc	169967347
caagacaggt	tcagcccccc	caggagagga	cctgctgggt	tgcgtgtcca	169967397
cacacagcac	agaagcaagg	aagatctggc	aaacaacctt	caacaaaaaa	169967447
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aggcctgggc	ttcgcaggcc	aacttgggtt	tgatttttgg	ctctgtgtca	169967647
caggcctcat	gagatgtgct	cacctcttag	ctccctcatt	tcagaatggg	169967697
gatgagaatc	tgccatgccc	ctgcccacca	gccacctgcc	caccctccct	169967747
tatcatgtgc	cccgacctcc	catgggtgct	gctcatctga	gtccctctgt	169967797
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agaccattta	gcctctgctc	ctgcttccct	attttcttgc	tatttcccag	169967897
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ttaatttttt	tactgtggga	aaatacacat	aacataaaat	gtactatttt	169967997
aaccattttta	aaggatgcaa	ttcagtggca	ttaattacat	tcacaacggc	169968047
atgcagccat	caccactatc	tggttccaga	actttctcat	cacctcagat	169968097
ggaagccccg	tattcactaa	gaagccactc	cccattccca	cctcccccaa	169968147
ctcctggcaa	ccaccaatct	gctttctggt	tctgtggatt	tgcctattct	169968197
ggatattttca	tttaaaggca	tcgtgcaata	tgtggccctt	tgtgacctggc	169968247
ttctttctct	cagcaccatg	ttttagggtc	tatctacgtt	gtagcatggg	169968297

FIG. 1.97

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tcagtacttc	aaccctgttc	tttttttttt	tttttttttt	ttgagatgga	169968347
gtatccctct	gttgctcagg	ctgaagtgc	gtggcacgac	ctcagctccc	169968397
tgtaacctct	gccccctggg	ttcaagtc	tctcctgcct	cagcctccca	169968447
tgtagctggg	attacaggca	cgtaccacca	cacctggcta	agttttgtat	169968497
tttttagtagc	gacgggggtt	tgccatgttg	gccaggctgg	ttttgaactc	169968547
ctgacctcag	gtgatctgcc	cacctcggcc	tctcaaagt	gtgggattac	169968597
aggcgtgagc	caccacgcct	ggccacttca	tcccttttta	tggctgagta	169968647
acattccatt	gtgtggatat	accacacggt	tttgtttatt	catcagttga	169968697
tgaacctttg	gattgtctca	cattttgacc	attgtgaatc	atgctgctat	169968747
aaatattcat	gtacaagttt	ttatttgaac	acttgtctct	aattcttttg	169968797
ggtatatacc	caggagtggg	atcggtggct	catatggtaa	ctctgtgttt	169968847
aacttattga	gaaactgccc	aacagttttc	cataacagct	gcaccattgt	169968897
acgatccctc	aagcaagggtg	caagggtatc	agtttcccca	catcctcatc	169968947
aatgttcttg	tttttatggg	ccttcacagt	gggtgtgaggc	tctttttact	169968997
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catcttccag	ggctgtggac	tggggcagttt	gggacccggg	aggggcaggc	169969197
cgtgagacct	gtctagtgc	catgtgcgac	ctcatccgat	cctcatagta	169969247
acacttacta	aaattcttaa	ccattacccc	accagtctat	gtccacacgg	169969297
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tttgcagaac	ctcatgatga	atgcagcatc	cactgtttcc	ttcttctgct	169969397
gctctgggtc	ccctccaccg	aagcactact	ttgtccaaga	aactgctcct	169969447
tcccaccagg	cagcgcccta	ggctggggcc	aaactagcca	gtatcaacca	169969497
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gcctcctggt	gaggctagag	gaaggaccac	ctcctgttca	ccagcatgca	169969647
cagactagac	aggacggctc	cgtctgtcgc	gcttctgttg	gtctctcatg	169969697
cccaagggtg	tggctctggg	atcagcctgc	cctgggttcg	atctacttaa	169969747
ttgtcactgt	cacttttcagc	togttattta	gcctccagt	cttccatttt	169969797
ctcaggggtg	tagtgggatg	atgaaaacaa	ttcccgtttc	gtagagtagt	169969847
gatgaagagt	aaatgagcta	atcccagtaa	aaagctttta	ctcctgagcc	169969897
acagtaagt	ctcagtttat	ctaagcatca	ttatcaaaca	taaacaatca	169969947
tttacagagt	gatgaccacc	gtatgctcca	aaccacgggc	tgggggcctt	169969997
tctacttct	acagtgacct	ttagaggtga	gcagtctagc	ccccacttta	169970047
gggataatgt	gacgaggtgc	tgagaggtca	tgatctccca	gcagtgagtg	169970097
acagagcctg	aggtgaaccc	caaactctgtc	tgactctaaa	gttcatgctc	169970147
attccaatca	tggcaaagaa	aatgcagtg	cttctcacga	agggttcac	169970197
cctgcctcct	cagtggctgt	ttcaaggagg	gccctttggg	ttgcccagat	169970247
agactattca	cactgaaagt	gacaatggag	aaactggcca	ggacactcca	169970297
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aacaatagac	atttattctc	tactgccct	gaaggctaga	aggtccagat	169970597
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cctaggaaca	aggacaccac	tacattcatt	ccagaaaaga	ccccttttgt	169970747
ctgccagcca	tcctcagagc	cgaaaagcaa	acctttgctg	ctgagagctg	169970797
ctgatagaag	agcaggaagc	acagttaaag	gggaacaggc	tcccaactct	169970847
ggggcagcag	atcttttggg	cttcatgtca	tagtattgta	aagacaattg	169970897

FIG. 1.98



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ccaaagtcag	acaagatcag	ttgtgtgac	ttggcaattc	actttgtttc	169970947
tctgagcctc	agtttactca	cccataaaat	ggggagaacc	acgtctacct	169970997
gactgactcg	tgatgaagat	gaaattaaca	caaagacaag	gctgggcgca	169971047
gtggctcacg	ccagtaatcc	cagcactttg	ggaggccgag	gcatgtggat	169971097
catctgaggt	caggagtttg	agaccagcct	ggccaacatg	gtaaaacccc	169971147
gtctctacta	aaaatacaaa	aattggccag	gtgtggtgat	gggcaccagt	169971197
aatcccagcg	actcgggagg	ctgaggtagg	agaatcgctt	gaaccgggga	169971247
ggcagagggt	gcagtgagct	gagatgcact	ccagcctggg	cgacagggtg	169971297
aaactgtctc	aaaaaaaaaa	aaaaattaat	gcaaagacaa	aattagtgtg	169971347
ggaaaaccct	ttgtctcagag	aaatgatggc	cacaaagtca	tattactccc	169971397
cccttactct	gtaaaatctc	ctttgctaga	ggaagagtta	aaagtccaag	169971447
tgggaagcac	agtcccgggc	ggaggcaggg	aaggctatcc	tggctctgag	169971497
tcgggctctg	tctacctgga	ttttgtgcct	ccacgttccc	tttcatcact	169971547
ctccaacagg	gagatgtctg	tctccctca	gtgtgatagt	aataataatg	169971597
ggcctcctgg	tgctcctcag	aatcacgtgc	tctgggcagg	aaaaagggtg	169971647
aattctcctg	cagaatgtac	acagcaaaga	ctggaacga	gaaaactgtc	169971697
ttcccagggg	tggcttccta	acaaatataa	tgagaaggcg	cttcctctct	169971747
tcctttcagt	cacatgggga	ggtcaacaga	gagcaatgac	tgtcctgagg	169971797
ctatttattt	attttttgcc	tgataataat	tataataatc	acttgcattt	169971847
attgagttgt	ctgtgtcagg	caccgggcta	ggcacttcac	tgcattgagt	169971897
atcgcaagca	atctttccaa	agggattagg	aagcaggagt	tattttacag	169971947
atgaggaaac	tcatgcatag	agaggttgag	tgtgacgctc	atgtttagcct	169971997
aacatgagga	tccaagagct	tatccattta	ctcagacttt	ttgattattt	169972047
tttgtgcaat	ttcacagact	tttgggtgat	cataaaattt	tttttagagta	169972097
ctagtgttggg	cctggcatgg	cagctcactc	ctgtaatctc	agcacttttg	169972147
gaggctaaag	cagcagaatc	acttgaggcc	aggagttcaa	gaccagcctg	169972197
ggcaacatag	cgagacctca	ctaaaaataa	aacaaaaaat	aaaaataata	169972247
caaaaaatta	gccaaagcat	gtggcacact	cctgtagtcc	caactacttg	169972297
ggagactgag	gcaggaagat	gtcttaagcc	cagaaattcg	aggttgagct	169972347
gagctataat	cacaccactg	cactccagcc	tgtagtacag	aacaagatcc	169972397
tgtctctaaa	aacaaacaaa	caaataaaca	aataactact	tgctcattca	169972447
tttaagtcag	taaattgtga	caaattgaaa	aatgcaagaa	aaaaaaggaa	169972497
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gatctgttag	gtaaatctct	atagcagtgg	ttcccaagac	atggtctcct	169972647
gaccagcagt	atcagcacta	cctgggaacc	tgtagatttg	tcctctccca	169972697
ccctcgaatc	tgggagtcag	gccagggcat	ctggtttaac	gagcccccta	169972747
ggtgatgatg	atacatgctg	aggagtacga	accacttatg	ttagaataaa	169972797
tacacaccag	cttctaaccat	tgatatcgca	gagaaatttc	tgcattgacac	169972847
agtgagctat	tatattgacc	aaatcccat	tataaacacc	atcatgtact	169972897
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ctcaaggcac	agcttaatat	aattagttcc	agaggcacca	agctatgtca	169972997
cccagacaca	cagcatgatg	ggctgggttt	atgctcatgc	acacttctga	169973047
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ctggagccag	gctgacccaa	atttgaatct	taggtgcacc	tttcattaac	169973147
tgagtgcact	tggccaattc	ccttaattcc	ctccctctgc	ctcagtttct	169973197
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ctaattgagtc	cttataaatg	ttcccacgat	tatgaactgc	tagagtgtgt	169973347
ttcctgtagg	taaacctcca	agccatcaaa	cctatgtcca	tgtctcctgc	169973397
caccatctgt	cctggatgat	tattgttcag	atgcatatcc	caaacttact	169973447
gagtacctag	tatgtgcggg	gttctttcac	ttatatcatt	tgcctttaaa	169973497

FIG. 1.99

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cagctctgca	ctgtagttat	tattacccat	tttctgcac	aggaaactga	169973547
gttcccccca	aaatgaactg	acttttcaaa	agtcacacag	gtattaagtg	169973597
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tgtggaatca	tccacatagc	ccttgcaagg	aggtatcaca	tacatccact	169974097
cagggtcgaa	gacacagaca	gcatgtgtct	ctctagcctt	ccctctctcc	169974147
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caacacctcc	caagcccact	ccaccttctc	caaagggtaa	cctcttccctg	169974247
acctaactcg	tttcagagga	aagagcagga	actttggagt	caggcctggg	169974297
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cagtggggct	gggaaggaca	gagagagaag	ggagaatcgc	tactgaatga	169974397
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cacttaactg	tctaccctgt	caggtttcca	tatgtgccag	acacatcatg	169974647
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agacagacag	acacccaatg	acaacattga	aggcttgca	gcacgagggg	169974747
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gcttcccagg	gtgagccaga	ggtcaggaat	cagaaggcct	ccccagagct	169975147
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gtggagtccc	gttgtcatgg	tggcaggagg	agaacagacg	gatcgccctg	169975247
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aaggttcctc	tgcgccccag	ggctaagtcc	tggtcccatc	cgctcttcac	169975547
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ttatatgcac	taattttatt	agcttcccaa	aactccatta	ataggtacta	169975997
ttaatgcccc	ctacttgaaa	gattaagcaa	cagaggcatg	aaaataataa	169976047
agtgatatgt	ccaaaactac	acagctaata	agtgagagag	ccaagatttg	169976097

FIG. 1.100

aacctgaagg	agatgggagg	gagagaaata	gttggggaga	ccacagggaa	169976147
aggaggaaga	agagaagga	agaaaaggag	gcggggagg	ccggggagctg	169976197
gaaatgtacc	tttgtattt	aagtcattga	gatttggggg	ttgttactgt	169976247
cacagatcct	agcctgttct	tactaataaa	ataaataaact	aaattttataa	169976297
agaagtgtca	gaaaaaaagg	tcatattaga	ccacgaagga	tgacaaagag	169976347
cttcttataa	agggaactca	aggcccaaac	atgggtattg	ttgtgtcatg	169976397
tgaatccttc	acagggggcca	cttggtgtct	gtgtggctgg	ctctttgtgg	169976447
ccctggagag	ggaacaagca	tgaatgcatc	agtggcttcc	agcctgaaca	169976497
gaataagttc	aacaagagat	ggccccagct	ccggtgtcta	ctggggaggt	169976547
gatgaagtga	agtgttcaat	tcctgcatag	ccaccaacaa	gtccctggaa	169976597
acacaattgt	tgaggatgtg	tcctcggggg	aggcatgggt	catctggctg	169976647
tgtcacaaag	cagatgggaa	cagctggcga	ggaaggactg	cctgtcctgg	169976697
gaattgccct	aatcatcttc	ctaaatattg	ccgcagccag	gaggaaagcc	169976747
tgattccctg	cagatggggc	cattgacagg	atgctactgg	tccgggttgg	169976797
gagaaaagga	atgctgtaaa	cacagtcagc	ccattcggca	ggcagtggaa	169976847
gctgtctgag	gcttcagggc	cccctcctca	ctaggggcta	taattcatgc	169976897
agtttcttat	ctgccagatg	gccaggagga	cacatgcatt	ccagtgggtgc	169976947
catcttctaa	gtgttggcag	cttgccagtg	atctcaactt	cattttcatc	169976997
attgcctttt	gagacttttt	gttcttaatc	accccaacca	accatgaaat	169977047
tttaatacca	gaaatatatt	ctctgtttac	atactttatg	caaaatctgt	169977097
tttttaaacy	taaaaagggg	attttttcac	acgtgcattc	ccacaagaac	169977147
caattctctc	cccgttgag	aatgcctgtt	gtacactaaa	ccttcagata	169977197
accattttct	gcaatcagcc	ctatcagatt	tggagggaga	gaagcaactc	169977247
accaggaaac	aaatgctctt	tgcattgttt	tgtctcttcc	cagaagcctc	169977297
ccatccacct	tcagctggag	ttgagctttc	taacatcact	gcattcctgc	169977347
acatccacat	taccatcttt	atgtatttga	ttcctccttg	agggcaaggc	169977397
ctgtttctct	gttgttttaca	cccctctca	gtgcgtgctg	taaggtagga	169977447
gcttcacaga	tggttaaagc	aaaacagaa	atggggccggg	tgcagtgact	169977497
cactcctgtt	gtctcagcac	tttgggaggc	caaggcgggt	gaatcacctg	169977547
aggtcaggag	ttcaaggcca	acctggccaa	atggcgaaac	cccatcttta	169977597
ctaaaaatac	aaaaaatagc	tgggcgtggt	ggtaggcgcc	tgtaatccca	169977647
gctactcggg	aggctgaggc	aggagaatca	cttgaacccg	ggaggtggag	169977697
tttgcagtgc	gccaagatcg	cgccactgca	ctccagcctg	ggcgacagag	169977747
tgggattcca	tctcaaaaat	caaaaaacaa	aaaaaggaaa	aaacagaaca	169977797
tgaaagccac	tttcccacag	cctgggcacg	tagctactgt	ggtgaatcac	169977847
ctttcctggc	agagcacact	caggaaccgt	cagctccaaa	agcaccaaac	169977897
agtttcatta	agaccgtggc	tccttcgcag	aagcacacgg	aacgcagact	169977947
gacaagcctg	tgataacatt	ttaatggcct	gagttcagtt	cccaataaaa	169977997
tacttaagtt	tctgcaatca	tggagctggc	attttcatta	atactcctga	169978047
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taaagctggc	aaagggcaag	gaagactccc	tggcacctgg	taccctccac	169978197
ttgccattgt	aacagaggt	tacaggctct	aagcccagct	gctgtccttg	169978247
cattcagacc	tcaccactca	tacactggga	cctggaacta	cttaaatgtc	169978297
ctcagtttct	ttatgtgtca	aatggcgttt	gacacataaa	gcactaatac	169978347
taatagtact	tacataataa	ggttgttgta	aggattaatt	gagttggtac	169978397
aagtaatgtc	ctggcacgca	tctggcacat	agtgagtgtc	tcctataata	169978447
aacagtagct	gggtttgttg	ttgtttttact	attatttttc	ctccagaaag	169978497
gcgagagttg	catcagcctt	ggaagaggca	ggactgagat	gtttgggaac	169978547
aagaccactt	tcacaggggg	cagcctttttg	agaaatgtca	tgtctacttg	169978597
atagggcctt	aaatatggag	tagtgggaat	ctgcacattt	ggattcaa	169978647
cctggccttt	ccaatggctg	atgatggaac	ccttataggc	tcaaatcact	169978697

FIG. 1.101

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cacttctctg	agcctcccca	aaaattgaga	ataacagttt	ttattccata	169978747
gggtagtttt	gagaattggt	aagatgatca	taaatgtaga	agggcctggg	169978797
actcataact	gttttcttca	tttattttatt	tagtcaacaa	tgttttctga	169978847
gcacctaccc	tggggccaggc	acactgaggt	gggccttggg	attcatcagg	169978897
gatcaaaggg	aaaaggcatc	ccatctccgt	ggagcttcac	atcatcgtag	169978947
ttaagggtgga	taatgactgt	ctcgacagat	aggacagtgg	ccaggacaca	169978997
ggccttcagt	ctggagcatg	cttctcattt	tgaaataatt	tcttggtcag	169979047
agtcagggtt	gaaggaaggc	cttgcagggg	ctgggtaagg	atggcgggcat	169979097
ctctgcgttc	acgtctgtgt	gctcaccatg	agagcccacc	tctctctggc	169979147
ccaagtttcc	ttctgtaatg	tgaaagaggt	ggggttccat	gctctcctct	169979197
tcagcatcct	ccttagatac	tcaatctggc	actcatcagt	ttcggaccct	169979247
ccatgctgcc	ccaaaggaag	ccacactgca	ccttcatcca	gtttcttaaa	169979297
cctgcatgtt	ctctcttgcc	tctagacctt	cgcccagggt	attccatctg	169979347
cctggaacat	gcttccatac	acctgccttc	acttggttaa	ctcctacttc	169979397
tgcttctgtc	cactgcttgg	attgaatgtc	ctctggaatt	cagccttcct	169979447
ggatgtccct	gagctgggct	agggctccct	ctgcccacct	ctgctctttg	169979497
attttccctg	ttcatcacc	cagttatgac	actgagttgt	aactgggatt	169979547
tctaactctgt	cgctccacc	aagcagcaca	ctctttctgg	ccagggtcca	169979597
tgtcttattt	gtcttggtat	ctctagggcc	cagaatctgg	tacctagtga	169979647
atgtgtaaca	aataatttct	ctgagctaaa	ataggaacac	agggctccctg	169979697
caatgaagac	cccagggtctg	gaggggaaga	caaggtagca	ttacaagata	169979747
acaggccttc	cctgcaaagc	gtcagcactc	agactggggc	attgtggaca	169979797
agaaggggtg	agaggagaga	aggcatgaag	gcatcccaga	tagggacaca	169979847
gcagaaacaa	agacaaaag	gccggataag	caagatctct	ttgagccggc	169979897
aggttaagat	gggtagtgga	aagctggacc	actgtcaggt	tttgaccct	169979947
ccagacaatg	caccgtgac	ttctggcttc	catatgtccc	tggctgctgc	169979997
tgcttctgtc	ccactgaggg	acctcaccct	ccagactcta	agtgatctta	169980047
agccaccagc	cttacaatt	acagcagaca	gaggggggtcc	agggccttct	169980097
agagatagt	ttcacagcac	tttcccaaag	ctggttctgc	tcaattccct	169980147
aaaagatctc	ctgcaatggg	gcctccaggg	tcctaaaagc	accatctgct	169980197
cttaaagagt	ctcactgctc	attagcatat	caaaggctct	gaaatgtcct	169980247
gcaggaaaaa	actctgggct	aacttttgta	gccctgttcc	ccaaactaaa	169980297
ttgaatgaag	gattcttttt	ttatgaccca	cctacagttc	tgagagatc	169980347
ctccaggga	tgagatcta	acctattctc	tgtgcagtga	atggcagaga	169980397
aaattaaagt	gattgcatct	attgcacact	tacttttctc	tcgaggtagg	169980447
tgagagagta	aataagatgc	aggagagaat	tacaaccgga	gatataaaac	169980497
agttgtctta	cagggaatag	tctgtttgcc	caggaggagg	gttttcagaa	169980547
tacaaagtac	catttcttct	ccacgacatc	cccaggggag	aaaggaaagt	169980597
gaaagaagcc	ctccaaccga	ccactggaga	tgggagcatt	tctgctgggt	169980647
tcattttacat	aagtgtcctt	ggcaatttgt	cccaatttgt	ctcattataa	169980697
atgatgtaaa	catccggggc	taatcacaga	caaaatggga	tggttttaaa	169980747
gctgcctgat	taaaaaccct	gggttggctg	caatgacttg	caggcatgct	169980797
aacggcttcc	ctgcaaggga	ctttgggttc	aaagtctctga	gagctcagga	169980847
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tccacataga	gocctagcaag	aatgcatcat	cttctctata	tctcttataa	169980947
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aaggaaagaa	gaaaagaaag	gaaagaagga	aggaagggaag	ggaggggagg	169981047
aggaaaggag	gaagggaagg	agggaaggag	ggaggaaagg	aggaggagg	169981097
gagggaaggga	gggaggagg	gagctaactg	acattttccc	ctttgccatc	169981147
tgattggcat	gaagggcaat	gtaactgagg	agtctgggga	ccaaagtgaa	169981197
tcctagtaat	gtcactcact	taatatgtgt	gatttttttag	accaatcaca	169981247
tcatttgccc	aagcctcagt	ttcctagtct	gtcaaatggg	aatgatgatt	169981297

FIG. 1.102

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tgacatctgg	tgtgtctctc	actactgttg	agacattata	taatgagagc	169981347
atagcccttt	ataaagacag	ggtttctgtc	ctctttctta	cttcattctt	169981397
tccttctctt	ctttccttct	aatagaaggt	atagagaaga	cagcacattc	169981447
ctactgagct	ctatatggag	agctgcagtc	atgggggaca	ctgtctagat	169981497
ctggggaccc	tcccaagctc	tcagagcttt	ggaaggaagg	tccttgcagg	169981547
gaaactgtgt	gtgtttcttc	aacagtgtat	cctcagtgcc	tagcacatgg	169981597
taagtgttcc	ataaacagct	gttgaagaga	cggatggata	actgaatgaa	169981647
tggatgcttc	catgggcaat	gacacactaa	tctgaaaagc	cctgtatcaa	169981697
tgaaagaatc	acttaatagt	ttaacttttc	cctcatcctt	cagaacacag	169981747
atggcatgcc	atcttccctt	caaactctct	cccagtgccc	cacacagaag	169981797
aggcacactt	ggacactggg	gtctgatgga	cccaagttca	cagcctgtct	169981847
ctgggtcatca	ggtatcatga	ccttgggcaa	gaagcttaac	tctctgagcc	169981897
tcagtttccc	cttctgtccc	ccagggaaaa	tgagtccctgc	ccctcctaag	169981947
ggaggtatga	gatgtaagac	cccgaaggac	acaaagggtt	gccaggagcc	169981997
ttcaggtagg	aggcaggtaa	ggaggtctgc	tagattggaa	tgagtttctg	169982047
gaaggcccca	aggagctcaa	aatcagacct	ggggtgaagg	tgtcttgacc	169982097
aaaatgagac	ccatcaaaga	agcctggatg	aagggtgcca	cagcatccat	169982147
cagtgccaaa	aacagaaaaca	cttttagcca	ggatacaagg	aacattttta	169982197
agcaacagag	ataagagata	gttagaactc	aggcctcctg	gctcttgctg	169982247
ttcttggccc	ataattagtt	gttatgggac	cttaataaac	ttcttgccct	169982297
cttggtacct	ttgccaaaca	atctgatgag	gagaatattg	agtcatggtg	169982347
ccagggaaaa	ttagcatatt	ctgcaaattc	ctggcactgt	taacactgga	169982397
ttctgtccac	ctttagaaat	cctcagatca	ctatgtcagc	atcccccaat	169982447
cacagctctc	caacttcaag	gaggggtgag	gggtctgaag	aaggagagag	169982497
aggcaacaga	gccagaaaacc	cttcagaaga	tgccaagagc	aaggtttgga	169982547
cccatagtc	accacttact	aacttcaaga	gtgttatgag	ctacaaactt	169982597
ctcagtcctc	gttgactcat	ctcaaaaatg	gaagtaaaat	tatttaccat	169982647
gcaatatggt	gtcaaaaatgc	attgggttta	gttcatagca	ggtgctcaaa	169982697
gaatatcagt	tcacttccc	ttgtccctag	agagccttgt	agtggatggt	169982747
gatgtgtctt	ccaacacatg	caccaacctt	tcctgtcct	gtagcagttg	169982797
agatggaatc	atcccactcc	cagctccagg	aataggctct	gatgggcttg	169982847
aaccacagcag	cttaattcca	ttggttctct	aggccttcat	cattagtaca	169982897
ggaaaggcac	ttgacctaaa	ttagtctgat	aagattttaag	ctcagaaatc	169982947
tggtttggtg	gatggagaaa	gagatgcttt	ctttctctct	ggaaggagtt	169982997
tattgcaaaa	gtaagggtctg	gggctgctac	agccattgtg	ctaccatgag	169983047
ggaactagcc	atgataacaa	aacttgctctg	gggaggggct	acgcatacaca	169983097
gaaaatgatg	ccaaagtcc	gctcaaaactg	tgcttgatgc	ctgcctgatc	169983147
tatggacttc	ttagttccat	gtaatggatt	ctctctatct	ttaaagccgt	169983197
atcaggttga	atttttggag	aaataaaaaca	aaaagcatct	tgactaattt	169983247
aaaaaatctt	ctttgggtat	tcaaccctcc	taaactcacc	cccaaattcca	169983297
ctggggagcat	gtcaagattt	ttgtgagccg	atttaggaga	tgcaaatttca	169983347
tttgcccttaa	ttggatctcc	aggaaatgac	ttctgcccc	tcttaaattca	169983397
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aagaacacca	actccagact	cagggagact	caggccagaa	tcctagctca	169983647
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cccactctgca	aaatggggat	actaagggtc	acctagctgg	gctgccctgg	169983747
agattccaag	acattaggca	tagaaacagt	ctggcctaga	ccctgtaggc	169983797
cagtaggcat	ttgatcaatg	gcagctgtgg	ttgagatttt	tatcatcatt	169983847
atggctgccc	ttcctgcttt	ccagggctag	tgtagatcta	agattatagg	169983897

FIG. 1.103

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ggctgcaacg	ttcctcagtg	gagcagatgc	agcaaggtag	taagagaggg	169983947
cattctcact	tgtccccaca	gagtgtgggtg	tgggggagat	ctgtgagcac	169983997
cccagcagcc	atgaggggtca	gcacttgaat	ctctgcagggt	cagtcatact	169984047
cctcttttatt	atTTTTtattt	ttattttatgt	attgatttat	tgctctgtca	169984097
cccaggtctgg	agtgcactgg	caccatcata	gctcactgca	gccttaaact	169984147
cctgggtctca	agtgactccc	acttcagcct	cccaagtagc	tagagccaca	169984197
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gtctcactgt	gttgcccagg	ctggtttcaa	attcctaggg	ttgagtgate	169984297
ctcccgcctt	ggactcccaa	agtgtctggga	ttacaactgt	gagccactgc	169984347
acctggcctt	attcccttct	ttttatcagt	tttcaaagcc	atcagtatgc	169984397
agagcactag	gcccagaaat	gagaggagaa	gagagatgga	acgacgaaga	169984447
ccaaaacctc	tgtcctcaag	ctgctcataa	gccagtatag	agacgtgtgg	169984497
agtctgtctg	cctgagttcc	agtcccagtt	ccccttgcaa	gcagccgtgt	169984547
gacttgcagc	aagtcataga	atccctttga	gcctcacttt	ccttgtctag	169984597
aaaacaacaa	aaactggaaat	aatactgctt	cccttccagt	ttgtcaagga	169984647
tgaaggtgct	ttgcacggtc	cctggagcaa	aatgtgttct	caatcaagat	169984697
tccgtctgtg	gtgggtggag	ccgcgtcctt	cccaaattca	tattcactca	169984747
gaaccttcaa	atgtgacctt	tttcagaaat	agcatctttg	caagtttaat	169984797
tcagttatgg	gtctcaagat	gaaatcatct	tggatttggg	gtctatccga	169984847
aatccagtga	ctgatgtcct	tataaaaaga	agggatacag	gccggggcca	169984897
gtagctcacg	cctgtaatcc	cagcactttg	ggaggctgag	gcaggcagat	169984947
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gacaagcgtg	agactctgtc	tcaaaaaaaaa	aaaaaaaaaag	agtggataca	169985197
gagaggcagt	gaagaaggct	gtgtgcaaag	acaggcagag	gttagtggga	169985247
tgcagcgcga	ggctaaggag	tgtctggggc	caccagaagc	cagggaagcc	169985297
taggaagggg	tttccctagag	ccttttgagg	gagcacagcc	ctgctgacac	169985347
cctgacttca	gactcccagc	ctccagagct	gggaagggat	aagtagctgt	169985397
tgcttttaaac	cagtgggtccc	caaccctttt	ggcaccagaa	accggttttg	169985447
gttcagtggg	agacaatttt	tccacggaca	gggtgtgtgg	ggtgggagat	169985497
ggtttcagga	tgaaactggt	ccgcctctga	tcatcaggca	ttagcattag	169985547
ttagattctc	ataaggagtg	agcaacctag	atccttcgca	tgcgcagttc	169985597
gcaatagggt	tcatgtcctt	atgagaacct	aatgocggcg	ctgatctgac	169985647
aggagcggag	ctcaggcggg	aatgcttgct	cgccagctca	cctgctgtgc	169985697
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gaagtctggg	acgaaaaggg	atagttagga	tggcgggagg	ggctgaactc	169986247
caaattgggt	tatcaaggct	ctgcaaaatg	gcgtgacggc	gctgccccct	169986297
tctggtggcc	tgaagactaa	cgcacatgat	gtcaagtgcg	gggcccaggt	169986347
actcaggaaa	aggttctcat	ttggacactg	ggaggtctta	cattggggggc	169986397
cctgagcctc	cagcccttcc	aaatctattc	tcagcaggag	ctcagccaca	169986447
cctgtgtccc	agaactgagg	ccaggcccag	ccttcactcc	acgcccagcc	169986497

FIG. 1.104



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agccccaagg	aaccgactcc	ctgaggctct	atgctccctg	cctccagtgg	169986547
ccccgtgtct	gggaaatagt	ggccctggcc	tgatgccctg	acctgggcaa	169986597
tccatccccct	ggtcctctca	gctcccgggc	ccagggttttc	tgggctactt	169986647
taaccagggc	aaactcattc	ctcgagtaca	aaataaaaga	ttcgaacagc	169986697
ataatcaa	aggatcatacc	cataaatcaa	cacatttgag	cacctatttt	169986747
gttggttcttt	cactaatcca	aaccatattt	attgagcatc	tactatgtgc	169986797
cattctccag	tagccattct	aggatgcagg	gatacagcag	agaccttgaa	169986847
aaaaggaaca	gtctctgatc	ttgctgagct	tagagtcaag	tggagggtgag	169986897
gaggaaggaa	atgaattaac	aactaagtga	agcagaagggt	aaccaattga	169986947
ttgactgacg	aaggggtaca	aacaacaaac	accttccttt	ctccaaactc	169986997
tatctttaac	tgtattctct	cgttttcctt	cctctccatt	ttacaatcat	169987047
tttacaacat	ctctggctat	tctcctatat	ttctgatcac	ttcgggtctc	169987097
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aatgtcaat	ctcacacgca	gtttaaacgt	ttcgccctgcc	cgtgagctca	169987197
gacctgtctt	ggtgcctcag	ttcttggtgtg	gaggggagga	gaggagaggg	169987247
gaggggagga	gaggaaagga	gaccggggag	gtgggggggg	agaggggagg	169987297
ggaggagagg	ggaggggagt	gggggagaag	gggagaaaag	cgcagctggc	169987347
ttcctcactc	tcctttcctt	cctcaccatc	cttaccctgg	cccagggcag	169987397
gaggaggatt	ggcagagtag	aggcagggtc	ttctgtctta	gctgggcctg	169987447
ttggtgactt	tctgttgggc	aacatgggct	gactggaatg	ttctccagca	169987497
tggcacatgg	tcacccagat	gcaggctctt	ccctggggca	ctatagcaga	169987547
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aagcacccaa	cagctctatt	cagaatacag	ggctgcccag	ctacttccca	169988247
ttcattatcc	ccagggttgca	agcttttagtc	aaaaccagga	ggcagcaggg	169988297
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aaacgcggta	aaacatgatg	cttagagatt	aagtgggatg	gggactgggc	169988397
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gagccactga	gcagtgcact	gggggatggg	cattgcaggc	aaggcagaac	169988497
cccaagtggg	aacaacctca	ctgggcttag	caaaactaaa	gaggcccaaa	169988547
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tggaaaccaga	ccctgcaggg	ccttgccagg	gatgggaagg	agttttggaag	169988647
gtgctggaag	gtttgaagca	gaggagggat	atgatcatgc	ctgtagctgc	169988697
tatgtagaac	aactgtatgc	atgccaggcc	tgtgccacgc	atgctcta	169988747
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caaggctccc	cagctgttag	gtgctaaggc	tggattcaat	ccaggacttg	169988897
cagactccag	tatcttggct	tttctaacga	gagtgtgcta	gcttttcta	169988947
gggggtgggg	aaggcagctc	gccccctcc	catggcaccg	tgagcaggtg	169988997
tactgctccc	agccagtacg	cctggacacc	gactaggaag	gagtatgtgc	169989047
tactaggagg	gatggtctgg	gctgactctt	tgaagttgac	aaggagttgc	169989097

FIG. 1.105.

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ataatcccag	ctaataatta	tgctggacca	ggggcagaga	cattactcca	169989147
aggggtgacca	ggtgtggaga	agaggctgct	gactccgggg	ccccaggacc	169989197
tggcccccag	gtctcattgc	ccgagtgtctg	ccccagaagg	agtagaagct	169989247
ggagctgtcc	gggccacagc	cgaggctggg	tgaatgctgc	agtgaggctg	169989297
ccgcacaagt	tgcgtgttgt	gacatttgtc	ttctggaggg	gattgggatg	169989347
ggctacttca	gcatttataa	accctacta	ggtctgagaa	atccctcag	169989397
cttatgagcc	tgggtgggca	gcaggccttc	tcaagaagcc	cagaaggcca	169989447
gatgctcact	tcccaggctc	tcttgcggt	gagctgagag	caggcacctg	169989497
aggcctggca	agtgtgacag	ctggtgacac	agacagacag	ggacagggag	169989547
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catccgtgtc	tttctgtggg	gccagtgggg	gccgtggctc	tgacgatgca	169989647
tccctccccc	acgttttttc	tcttctgttc	ttggactttg	cagggagcac	169989697
tctgcttttg	ggaacaggag	ctgggtctct	ggccattctc	cgcagccct	169989747
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gcctgacccc	acacctgcca	atgccggggc	aagaatgtcc	caggctgccc	169989997
tggttcccag	agctgatgct	tcccacagtg	cccagctgtg	ctggcatgga	169990047
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gcatgagaat	atcgggtgac	ctctctctct	agtaaagtgc	aaaactttta	169990497
acaaaaatgc	cttcatcccc	cagcgccagg	cctgagctaa	tctcataggt	169990547
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attaaccaca	gocggtagcc	agcttttccc	cgcccttctc	ccaggcacac	169990797
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cccacactca	cagtgaatct	tggccattat	gacaactggg	gacactgagg	169990947
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agaatttcaa	cttcatctct	ctaactccaa	agggcgtgtg	tgtgtgtgtg	169991047
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cagcgtggc	cacaagccca	ccctgtgcct	cgtcagcccc	actgagcctc	169991547
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tccgcctctc	cactcccacc	tcgcacatct	atggatttgc	tgttcagaaa	169991647
acatctgttc	cctccttcgc	ccctgacata	cgcacatgac	tcattgctagc	169991697

FIG. 1.106



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ccagctgcct	aagctcacca	ctctgggaga	cagactctca	gtcctcatca	169991747
gacagagatg	tagggggctg	taagggacgg	ggtgcaggta	gggcctgagg	169991797
attccgacaa	ggtgagccat	gggcaggggc	attgttcatg	cagggacctc	169991847
ctggccaagg	tcctacgtca	aggttagaag	gaaagagtaa	atgatcggat	169991897
aggctaagac	agcaactcag	caggccaagg	gactcctccc	ccaggacctg	169991947
ctccaccctt	agaggggtcc	cggacagcca	agccctgatg	gagttgggtca	169991997
gcaaccaacc	agccctgggg	ccaaggcctg	cagaagcaga	gaggaggggt	169992047
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cccagcacac	tgtcctttct	ccaggtgctc	agttagattg	agctgggtcc	169992147
catcttgggc	ctttgctggt	ccctccctag	aaagtctgcc	ccctccccct	169992197
gcagggtggc	atcagcattc	aggcctggcc	ctgacgccct	cctctctggg	169992247
ccaccttcac	ctccacaacc	ccggcaccag	cacccatccc	caccacatcc	169992297
ccagcacgca	gcattctagta	agggcaccaa	atgcatgccc	agacatatga	169992347
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gatacagaga	agatctaggc	acagtctttc	cccaccatgt	cagacaaaaa	169992747
ggttagatac	aggacctgat	atgttataaa	actcaatcaa	tatttactta	169992797
gtgaataaat	ggacggatgg	atggatggat	gcattaggca	gccaagtggg	169992847
cagcaccgat	gacttaatat	actgagtgtc	ccgactccag	caacatgcat	169992897
tcattgttcc	tactgtgtgc	cagtgaacaa	gagcaatgaa	ctcaatgact	169992947
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gcacagcaca	ggtgagaaca	tcaagaccag	gggtcaggga	atctactggt	169993247
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gaaactgagg	ctcagagggg	gactttctga	tgagtgcagc	gtgcagataa	169993447
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ctgataacag	ctgtcagcac	gggacagtgg	agggaaact	aggttaggaa	169993547
taagggtacg	aggcttgagt	acagattgtc	aatgactcag	tgtgtgaact	169993597
tggtcagggtg	actccaacca	gatgacttcc	ttctctgagc	ttctgttccc	169993647
tcctctatga	atggggacaa	tcactcagct	tcacaaaaca	atggctgcga	169993697
aattgcctgg	tacaagagag	agaacttcca	gtgtgtaggg	gctgttgtcc	169993747
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agccaccagg	ccccagactg	ctggcttatg	tatttgtcat	tgtcatcat	169994197
gaatggatgc	caggaaagtc	tctttgtgat	gggggcacaa	ccctcaaat	169994247
ctcctcccct	ccagatgcc	tccactggag	ctgagactcc	caggtcccct	169994297

FIG. 1.107

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agggcttctc	tcccaggggc	ctctgggctc	cccaaggcca	cgtgctgccc	169994347
ccactagaga	cctgggcccag	tcctgaccag	gggaaagagt	agcgccgaca	169994397
acagccccag	atgggtatgtg	cactgggcaca	tactggcagc	tgccttcatg	169994447
acagcaagcc	ataggtccaa	atcccgcccc	ttcacaggga	cattcccaac	169994497
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ctctgagtcc	tgcgaggcca	cagaggacct	tcgtgcctgt	cctctgtcct	169994647
cctgcccagt	ccccaggcca	ggctcagctg	gagttgggga	gcagaaaaac	169994697
acgcatctga	atcaaggctc	tgggagcctt	tgcttctgcc	tccaagaggc	169994747
gaggggaaat	gaatacccag	gcgagcgagc	aagagagacc	ctcagaaaaac	169994797
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acaggctatt	agtcttctctg	taattaggat	tctcgctca	aatcttgtat	169994897
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aggcgggaga	tgaggaggag	cagcgcggt	ctgctgcgtg	gccctgggca	169995097
agcaccacaa	cctctctggg	ccgtttgcac	attcttaccg	ccagggatgt	169995147
gggcggtaaa	tgaaagagac	cagcacaac	cagtgtcagc	tcccttcctc	169995197
gattcctaaa	atgtgatgcc	caaagatggg	ccagcctcct	gctgtgcctt	169995247
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agaagtggct	tggagtaaga	cctgaagtgt	gggactggat	atgcagatgt	169995997
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gaaatatcgg	gaacttatgt	toggacttgt	taagtttgag	atggctggga	169996797
gatatactaag	tggagagggc	aaggaataaa	atgcttccta	aactccagca	169996847
tccattcagt	cccctggaga	gcttggttaa	ccggatggat	gggtgccacg	169996897

FIG. 1.108

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ccccccctg	cacccttgag	ttgcaatagg	cccaaaatga	ttcaataggc	169996947
ccaacatggg	gcccaagggt	ctacatttcc	aacagcttcc	caagtgatgc	169996997
caatgctgcc	agactgagaa	ccacacttcg	agtagcacca	aagtaggcaa	169997047
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actgggatgg	gaaaccactg	aagcaagagg	aaggccaggc	agatgtgtcc	169997297
tgaaagccaa	aaagagaaaag	gtcatcatta	atatgatata	ttttgcaatt	169997347
tgtttatatg	taagaggaga	ttaatagctc	atagcattcc	caggcattgc	169997397
tgtaggaat	tgcagctcca	ggctggcaac	ccttaaatca	caaactagat	169997447
tgtcaagagg	actgcctgga	attccagctc	tgtaagtaat	atgctgtgtg	169997497
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tcctgactag	ctgaaattac	aggcaccac	caccacacc	agctaatttt	169997747
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tgttctaaga	gtctctttca	gttctgaatc	tctttgttat	cttacctgtt	169997947
acccctcag	agatgccttc	cctcactccc	ctgtccaagg	tagctctcca	169997997
cccaagtcag	cagtcatcac	agaaccatca	caacctgaag	ccctgtgcat	169998047
gttgctgttt	atttctgttt	tacatcacaa	cctgaagccc	tgtgcatgta	169998097
gctgtatact	aaacctagag	ttagtatagc	ttagttaaag	tttcatttat	169998147
tgctaaagggt	ttatcactgc	tgtctctatc	agcctccctg	cactgtaagg	169998197
gacaaggggg	caggctccagt	ttctgtcttg	tttcagggtt	tgtctccagc	169998247
caagataagt	atctttgcaa	ggctctgttt	ttattctgaa	aggaaattag	169998297
gagctattgg	agggtatgga	gtggaagggg	acagtcttct	gccttggatg	169998347
tataaaagggt	atgctgggccc	acgctgatgg	gctagaccat	ggcaggcaga	169998397
gaaaacaggc	aggaggccag	gcaggggctg	ccagtgccca	gacacaggcc	169998447
gggagggtgca	ggtggcagtg	gcaggcagtg	gccaggccct	gggtatatatt	169998497
tgaagggtcaa	gccaacagga	cttgccagtg	ggctgggtat	gggcatgaga	169998547
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ctcattttat	taattctgag	agtttgttgt	attagacagt	gaagcggaaa	169998697
tgtcaggaag	tcagctggaa	ataggagtct	ggagtggggg	ggaaagccta	169998747
gccagagaca	ggaattgtgg	cgtcattggc	gtagagacag	cgtttaaagc	169998797
tgtgacgcta	gatgggttca	ccagggggaat	gagagtogaa	agagaagagc	169998847
agagcagagc	tgagccctga	gggggggcaga	aaggcacaca	gggacagtgg	169998897
aggcaggagg	cagaaggcag	aggggtggcgg	gccaacagct	ctgaagggtca	169998947
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gaggcactat	cccaggcctg	ccttctcatg	ccagcagcag	tgatctatcc	169999047
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ggctcaatca	atatgacacg	gccacgcttc	ctgatccgag	ccctctgagc	169999147
aggtattttc	catcctggac	ttatccctgt	ttctcaggag	agggatggac	169999197
ccaagagaca	aatagttccc	ccaagatcgc	acagcaagcc	agtgtaaaac	169999247
aagcatagaa	accagctttt	agggggctca	aggtgggggt	cagaaaatga	169999297
ggtgagagca	agcatttact	gagcacctcc	tgtaaataatc	tcctacatac	169999347
gaagtgtctc	acccacatta	ctgaccaccc	aataaaggca	ggtcctgtaa	169999397
ttcccaattt	gcagatggat	aagcagaggc	ttaggggtgt	gaaacaacct	169999447
cctcaagggtc	atggcttcta	agtgggtggag	ccaggcctgc	aaaccaggct	169999497

FIG. 1.109

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gtctgaatcc	aaaatccacc	tccaagtcca	cagtgggttg	gccccacccc	169999547
caaccatcc	ccatcaccaa	caggacggtg	gtcagagtcc	actgaatgaa	169999597
agcatgcgtg	cattcaaaat	agacagccaa	tcagcagcct	tccatcagaa	169999647
atgtcatctt	tatgacaaca	gcatcgattc	caggcgtacc	ctgcatatgt	169999697
gaaccaaggg	ggatgggtgga	ttgtcctttc	caagcacttc	ccagccccctt	169999747
agagtccac	aggcccagaa	ccacggccct	tgacaccctc	taccaccccc	169999797
tgtccccct	tctcctcaga	ccccgagtg	ctggccaggc	tttctcactg	169999847
ggaagtggcc	actccatcca	aatgaccacc	gcacccctcc	tcaccagctt	169999897
ccctgcttct	gccctggccc	ccactctttg	agtccattct	tcaaccagca	169999947
gacaaagggg	tgctgtacac	gcctctgcac	agaacccctc	caatgccttc	169999997
tgtctcaact	cagagcaaa	ggcagcagct	agcacactcc	aaacactccc	170000047
acccacacct	cagctccctcc	ctctgtccct	ctgctctatt	ccctcagatc	170000097
tgacggctcc	atcccataaa	cgtggcacac	acacacctgc	ctcaaggcct	170000147
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aaatacatgt	gagcgatgct	ggggcaggcc	gactagaaga	agcagactat	170000397
ctgcttcttc	tccaccctta	gaatgggtgt	ggggccagaa	gaggcatgca	170000447
gtcgatattt	gctgaataaa	tgaatgtcag	ataaagtgg	gtggggactc	170000497
caggggaaag	atttgtcatt	ctccaccctc	ccagttcagc	ttaaagcaga	170000547
gaagtgagag	gtgcccacaa	aggggtgtgt	ctgggggggtg	gggggtgggg	170000597
atgttccaag	atctccaagg	cctggatttt	aagcaagggt	tgagatgcc	170000647
gcaagagggc	ctggcattgc	cagattgata	gtctgcattt	cagagaagga	170000697
caacccacc	tctgacctta	gcccagcct	caacagcctg	ctcaaggaga	170000747
tccaccctta	gtaggaggag	gcagccaggc	caggttccag	tccctgccac	170000797
cgcttgccag	gtgtgtcttg	ggcagcagtt	gcctttgtctc	ggtggtcttc	170000847
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catggagtcc	tctcagtcac	ctctgtatgc	cctgcagcat	ccccagttct	170000947
cagtgagaag	agtgtgctct	gaaagttaag	taacttacc	aaggtcacac	170000997
aaggtctgag	tctcaaattgc	atacaatttg	accccatagt	ctaaggtctt	170001047
gaccgcaatg	gaataagaaa	ttattttacc	attctgagtg	gcagtctctg	170001097
aagactacag	caataattga	tgctctcag	ggggataggt	gtgtcactta	170001147
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ctcctaacaa	gtcatgtggc	cattgcccac	actacaacga	cagaggaagc	170001347
ctcaggggaa	ccctcctcct	ctcccgaatc	tccgggcttc	ctgcatccct	170001397
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gcctggggaa	gaccagagg	cccaggccta	ggggagaggc	cggtgtctcc	170001497
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gccttgctct	atttcttcac	aagcttcccc	atgacactga	cccaaggctg	170001647
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cgaaatgcct	tctgcttaga	tcatctttaa	tttccctcc	agaatgacat	170001747
tcgactctgc	ttagagttac	aggcagccca	gcaattactg	agcgcaata	170001797
ccgtgttcac	ccgcctcacc	tcatccacgc	cccacaaca	cccagccctg	170001847
agactggctc	cacgatcacc	tccactttat	aaaataagat	atcaaactct	170001897
gaacagaacg	gacgtctcaa	aaaatgggca	tattacattt	aaacctcaa	170001947
tctgttgggt	atttgagtga	aatggacata	cctccaggga	gtcggtggcg	170001997
agggccggct	ctgaggactt	cctgggttgg	gatcctggct	ctgcaggact	170002047
gcgtgacctt	ggtgagttac	ttcatccctc	caaacgcgct	gttctccttc	170002097

FIG. 1.110

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atagaatgga	gatgaccaca	gggccagatt	cataagggttg	ttccttgtaa	170002147
tacaggtgaa	tatccatacc	cagcaactgc	tggaccacct	gtggtttcaa	170002197
ggataatttc	cctcccacgt	ccccgtggcc	cttggaaacct	tcctctcctc	170002247
ctgtctcccc	ctgcccccat	cactttgtaa	ttgaaaagtc	atgattgctc	170002297
tcccaggtgt	agcactgctc	acagggtcaga	ttgcctgctc	tgacgtagt	170002347
actcagttgg	atgcggttca	gctgtgtatg	atcaactccc	tccccctgac	170002397
aaaaacatta	ttttgcatca	cagagaagtt	gatttctttc	acacataaaa	170002447
gaaggcaaaa	agtgggtgct	aaagggctgg	tacagcagct	tcaagaaatc	170002497
aggaagaacc	tgggctcctt	ctgccttctt	gttctgccaa	tatcacccca	170002547
tggctgccac	ttcatggccc	aagtggaaacc	atggagcacc	acccttcaga	170002597
cccataggtg	acaacagcct	gctctgtgag	agtggcagtg	gcttccagag	170002647
agacttagga	agtagaatca	acaggacttg	gtgacagatt	tgccacagag	170002697
ctggggaaca	gggaggtcca	acgggtgactc	ccaaggagct	gatgtgagaa	170002747
ccagagctgc	tgtgaatatt	gttcccaact	cctgagacag	ggacagtggg	170002797
cccgtggcta	ggaagtggta	ggcagtagag	agtcaaatg	cacattagta	170002847
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gccaatatcc	agagctgggt	taaaatgaag	catttcgagg	aaaaaaatgc	170003097
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ccatccctcc	aaacacacac	tgaggatata	cacttagcca	ggagggaaca	170003197
taaggagggg	tggacaagcc	atgtttacta	aaatctctca	gtgtgtgcc	170003247
ggcatgttca	tgtatattca	ggaagaagt	tcagtattta	agatcctcgg	170003297
cccttgcccc	agtcaccaac	acgccttctt	gtctggagaa	ctgtaaatct	170003347
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ggataaacag	aatcgactcc	tctgcttctt	tctgatgcac	agtgaatggg	170003447
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ctcatcacat	ttctcccagg	ctattgactt	gttcaagggt	aaggatgaa	170003847
gagagtcatg	cagcagccct	acctggctct	gctctgctgg	gggaagcctt	170003897
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ttacctgtgc	gtgtgggagg	ttggattgtg	acatctttgg	agggccgggc	170004647
ttctgaagcg	acatttgatt	tctgggtactg	aaatgtcaaa	gggtcctgag	170004697

FIG. 1.111

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gcacccgcta	gggcagcacg	cggagcatcc	acctgcgtgc	gcatcctggg	170004747
ctctctctgg	gccacttggt	gctggggaca	tgccgggagc	tggtgggtcag	170004797
ccctcctcct	gcctcctcag	tgctgcatct	tcaccttctg	cagctgccta	170004847
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agccgggaggt	aaaggacaga	tgccggggaat	ctggaaggag	attcacttca	170005197
agcaccatcc	cactctattt	gttaaacttg	tgctcctgtg	aaaactgctt	170005247
gtgtctgcat	caaaccagc	tagggaggggc	tgagggctaa	gggtaaacct	170005297
gggagagttg	aattccagtg	ctgtgattaa	aaccaatatt	ccacataatg	170005347
caatgtaact	tgctcacatc	gtcccatgta	atctttaaaag	ccacagccct	170005397
tttgcaattg	ggattattat	ctccatttta	cactggagga	aactgaggct	170005447
ctaagaggtg	aaatgattca	cccagttagg	aagtgatgag	tccagatgtg	170005497
gtagactgaa	taatggccct	cacaatggaa	cctgtgagtg	ttcccttaga	170005547
tgacaaaggg	cctttgcaga	tgtgattaaa	ttcaggatcc	tgagattggg	170005597
agacattatc	ctagattatc	caggtgggtt	ctaaatgtca	tcagaagtgt	170005647
cttcataaga	ggaagacaga	gatttttgcta	cagaagaggg	ggaaacatga	170005697
tgatgagtca	gaggctggag	tgacacctgg	aagggggccat	gagccaaggc	170005747
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caactgactc	cacattttctg	gctccagaac	tgtaagagaa	tacattttgtg	170005897
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caggaaggga	ggggatctgc	aggcagccat	cagggctcta	attgcagctg	170006347
gctggggggac	catgggtcag	ggctgccacc	ccctggctct	gtgccttcac	170006397
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tggggacaag	ggaggggagag	aagaactcaa	aatgactgag	gtttccagct	170007197
accagaaaaa	tggagggacc	ttgaaacaaa	tggggccatca	gcaggggaca	170007247
ctggctggaa	gccagagtc	cagtcagctc	tgtaaggccc	ccagaatagg	170007297

FIG. 1.112



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catttgactt	caagtcacag	gcatttcagc	aaaagcctct	ttgctacagt	170007347
gattatggtg	aagcagatgc	ccacagctga	gatgggcaac	tctcaggcct	170007397
ccagtgggga	cagagaatcc	ctgggcccc	acatagcttg	gcctgaagat	170007447
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caacaagagc	agatatcgta	tttttctcaa	accacatgg	gacgttcacc	170008247
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aaaggaatat	tatgaacacc	tctatgccc	caaatttgac	aacttacatg	170008547
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taatgtaac	catcacatca	acaggctaaa	gaagaaaaat	catataatca	170009047
tataaacaga	tgtggaaaaa	gcatttgaca	aaatctaacc	cccagttgtg	170009097
attaaaactc	tcaaaaaaca	aggaatagag	gggaattttc	tcaccttgat	170009147
aaagaacatc	tacaaaaatc	ctccagctaa	catcatactt	aatgggtgaga	170009197
aactagaagc	tttctacta	aggtacaagg	caaggatgtc	ccctctcact	170009247
cctccttttc	aacatcatat	tgggaagtcct	aggtaatgca	atgagacaac	170009297
aaaaggaaat	aaaagggtata	cacatagggg	agggaaaaat	aaagctgttt	170009347
ttgtttccag	atgacatgat	tatctgtata	gaaaattgaa	aagaatcaac	170009397
aacaaaaaca	aaaacctcat	gtaactaata	agctattata	ctgaggttgc	170009447
aggataagggt	taatatacaa	aagtcgatca	ctttcctata	taccagcaat	170009497
gaacaagtag	aatatgaaat	ttaaaacaca	ctaccattta	cattggtaag	170009547
gtatatccca	aaatgaaata	cttataatct	aaataagtat	aatcaaaata	170009597
acatatgtac	aagatctata	tgaagaaaac	tacaaaactc	tgatgaaaga	170009647
aatcgaagaa	gagccaaata	aatgaagagt	attccatgtt	tgtggatagg	170009697
aaaccttgggt	attgtcagggt	tatcagttct	ttccaacttc	atctatagat	170009747
taaatgcaat	cccagccaaa	attattgggt	attagcaact	attaacaaat	170009797
tatttttatgg	atatcaacaa	agtgatttta	aagtttacag	agagaggcaa	170009847
agactcagaa	tagtcaattt	aatactgaag	aagaagaaaa	aagttggagg	170009897

FIG. 1.113

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attgacacaa	cctgattcaa	gactaactct	aaagccatga	taataaagac	170009947
actgtggtat	gggtgaaaaa	tagacaagta	gatcaatgga	acagaacaga	170009997
aagcccgagaa	atagaccac	atgaatagag	ttgactgac	tttgacaaag	170010047
gaacagaggc	aatacagagg	agcaaagaca	gttttttcaa	caaacagtgc	170010097
tagaacaact	ggccatccac	attaaaaaaa	aaaaagagtc	cacacacaaa	170010147
ccttgacccc	ttcacaataa	ttactaaaaa	atgggtaata	gatctaaata	170010197
taagacacaa	aactataaaa	ctcctagaat	ataacatgga	atcatatcta	170010247
gaagatcctg	agtatggcag	tgactttcta	gatataacac	caaaggcaca	170010297
atctgtgaaa	gaaataattg	agaagttgga	attcattaaa	atttaaacct	170010347
ctggcctgta	aaaggcaatg	ttaagagaat	gagaaaataa	gccacagact	170010397
gggaaaaaat	atttgaaaaa	atatatatct	gataaaggac	tgttattcaa	170010447
agcatacaaa	gaactcttaa	aatcaataa	ttagaaaatt	aaaaatctga	170010497
ttcaaaaata	agcagaagac	ccgaacagac	atttcaccaa	ggaagatata	170010547
cagatggcaa	gtaagcatgt	gaaaaaatgc	tccacatatg	tcattaggga	170010597
attgctaatt	aaaacaatga	tgagatgcca	ctacagaact	catagaatgg	170010647
ccaatatcca	aaacacttaa	caacacaaaa	tgtaggtgag	aatgtggaga	170010697
aacaggaact	ctcatcagt	cttcgtggga	ctgtgcaaaa	cagtacagct	170010747
gctttggaag	acagtttggc	agtttcttac	aaaactaaac	agacccttac	170010797
cataagattc	atcagtcagt	ccctttggta	ttcacccaag	tgaacccaaa	170010847
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cataattgac	aaaacttgta	ggccaccaag	atgtccttca	gtgagcgaat	170010947
ggttaaataa	atgatgggtgc	atcctggcag	tagaatatta	ctcaagacta	170010997
aaaagaaatg	agctatcaag	ccagtagaag	gcatggagga	accgtaagt	170011047
cacattacta	agtgaaaaaa	gccaatcatg	cttccaacca	tgtaacatta	170011097
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gttgtgggga	ggaagggatg	attaggtgga	gcacaaagga	tttttagggc	170011197
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atttgtcaaa	acacagagaa	tgtaccagga	gtgaacccta	atgtaaaacta	170011297
tggactctgg	gtgatagtga	tgtgtcattg	tagattcctc	agtattaca	170011347
aatgcatcat	cctgggtgtg	gatgttgatg	gtgggggaag	ctgtgcatgt	170011397
gcgggagtag	ggagtatatg	ggaactcttc	tacttcccac	ttaattttgc	170011447
agtgagccta	aaactactct	aaaaaataaa	gtttattaat	caacaaagaa	170011497
cacagtgage	tgcaacttca	taaccagtag	attgacaaga	attaagaaat	170011547
ttaataaaga	attgattaga	atatggagca	acaggaaactc	ttacacatta	170011597
ctgatggaaa	agaaaattgg	tatacctact	ttgtaaatag	tttggaatg	170011647
cctagaaaag	ttgaatatga	ccccaaatg	acctaataat	gccactatta	170011697
agtattgacc	ctaaaaaatt	attgttgaac	gcatttttta	agagataaat	170011747
gcaaaaacat	ttgttgcatg	atcatttcaa	cagcaaaaac	tggaatcaat	170011797
ttaaacagct	ctcagtgggt	gaatgaataa	actcatttta	tgcaaaatga	170011847
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caagccatgc	atttggtgct	aggctctgtc	tctaccacaga	gagaggaggc	170012097
atcttttact	tcagatatgt	atgtcatcta	ttccccaaat	ccagtgtcta	170012147
caagtctgga	tctgccctgt	gggaagtatt	tttcaaattc	atctactcag	170012197
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agcactgacc	tgttcaccac	ccagcctatc	catcctggta	caatcctgtt	170012297
gtaaccaagc	aggtacccag	gcctttttta	tgcagcagag	aaataggaag	170012347
tgaggcagga	gggaggcaag	gtgatgtctt	gtcttttctt	tgtcatgaaa	170012397
aggtcaggaa	agggacagat	agagtgaag	aagattggaa	aataagccag	170012447
agaggctcgg	ttgttcttca	taacaaaaag	aagttggggg	taagtaagag	170012497

FIG. 1.114



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aaagagccag	gaaagagagc	cagaaaagtc	ccaaaggagg	ggtgccctgg	170012547
ggagccctct	tgtgctttat	agcatgagtg	gctcctgtgc	agttggggaga	170012597
aggaagaaca	tcagagggga	gagaaaaggg	aatttttaaga	aatattgcta	170012647
agcgttatag	attagatacc	ctttaatgta	aatattcaaa	ttccttttta	170012697
taaaaaaga	tatattgaaa	tataattgaa	atacaaaaaa	attgtacata	170012747
ttaaacaat	ctgattttat	tagtctggac	atatagccag	acctatgaaa	170012797
tcaccacaat	caagatatga	atataactat	caccccccaa	agtttcttca	170012847
tgtccttttt	aatcccacct	tccatccctc	ccaccctgcc	atccccacc	170012897
tcaggtaaca	ctgatctgct	tcccgtcagt	agagagtagt	ttgcattttc	170012947
tacagtttta	tctaaatcag	ccacgcagta	tgcattcttg	tctggcttct	170012997
tttattctgc	attattctgg	gactcattca	cgttggtgtaa	ctgaatactt	170013047
cattcctttt	tattgctaag	tagtattgta	gtatttcttt	gtatggatat	170013097
accacagtag	gcttattcat	tcatctattt	atagacaatt	ccaacttttg	170013147
actattacaa	ataaagctac	tatgccattc	acatacaaat	ctttacgtgg	170013197
aaatgctttc	attcctcttg	ggcaaatacc	tagggggtgga	attgctggat	170013247
cacatgatgg	atgaaacctt	aactttttta	gaaattgcca	atttaggatt	170013297
ttccaaagta	gatgtagcat	tttataccca	ccagctctcc	attaataaat	170013347
tggatttcat	caaaaattta	aacttctgct	ccaaaagaca	ctcttaacaa	170013397
agggaaaaag	caagccacaa	tatgagagga	aatatttgca	aagcatctga	170013447
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actaaggaat	gaatgactgt	acaaggacca	cattctaatt	aggagcttct	170013547
gaacccaaag	gaatttcaga	taaggggaaa	tttaggccca	aagccaggag	170013597
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caactctgga	ctccattgga	agaaccttct	aacagtcagg	gtccccagag	170013747
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ggtgcaaatac	aaagccaagg	cttggagtg	accatttaa	atccatttct	170013847
tatcctgtga	ttcttagagt	cctatctgta	tcaggggaag	gcaggtgggt	170013897
tctagaactt	tctaaatgtg	tccctgtggg	tttttcttcc	tccagctaca	170013947
cacaaacttg	ggcctaataa	gaagtctatg	gcattaaccc	agcaggaatg	170013997
cttaatgctt	atatctgacc	tcaaaccaag	actgtctcca	cagtgaacaa	170014047
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ttacttttaa	atatttgctt	ccgtaaaaaa	acaaatgaat	gcctcggaca	170014247
gattttataaa	gaacattcct	ggagaggcgg	gtggattaat	tattcagcat	170014297
cctctccctt	tgtactatt	tattgtctca	tatgcattta	tatggtacct	170014347
atcactgcag	atctcgctcc	atgctggaga	cataatttcc	agtgactgac	170014397
tacttgtcta	agatatatat	cgtattgcaa	tactatttta	tttctgactg	170014447
taagggcacg	tgccactgtt	gggtaattgt	gttcatgttt	ttaaatgtga	170014497
aaaataatca	aatataactt	gaaagagatt	gtacagtaat	tcaaggggat	170014547
attaaccac	caggaagtta	ctcggcaaat	aaataggcgt	ttgtggctgt	170014597
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gttgtgttgg	gggaaaggag	cttctaattg	ccaagaatag	aagacctgaa	170014747
gttggctagt	gcgtggctag	tgctgtaat	cccagcactg	tgggaggcca	170014797
aggtggatga	ttcgtctgag	cccaggagtt	caagactagc	ctgggcaaca	170014847
tggaaaaacc	ccgtctctac	taaaaataca	aaaagttagc	caagtgtgat	170014897
gacacatgct	tatagtttca	gctactcggg	aggctgaggt	gggaggatag	170014947
cttgagccca	ggaggcagag	gttgcaagtga	gccagattg	aaccactgca	170014997
ctccagcctg	ggcaacagat	tgagacccta	ttaaaaaaaa	aaaaaaaaaa	170015047
ggaaggaagg	aaggaaggag	aaaagaaaaa	agaaaagaaa	agaaaagaaa	170015097

FIG. 1.115

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agaaaaatga	cctgaagtca	ctggatttcc	ttcgaggtag	ccagaaacag	170015147
aggaaagggg	gcattgcccc	cttagggtaa	aaagtagagc	accgaattgt	170015197
ggaaggctgc	aggttttcat	gtgtgcttgc	ccaagtgatg	ttccatgtca	170015247
ggctctaggg	tccctgcagg	gacagagagg	gactaacatt	tacttacatg	170015297
cctatagtat	gtcaggcata	tacttgtgcc	tttatatata	tcagctctgt	170015347
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tacagatggg	gaaacccaag	ctctgagtgg	ttcagcaaac	cctgggtgca	170015447
tacccccacc	ttgcccctgc	aaaaccaaca	aaaaaacgaa	ggccctgcct	170015497
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gtagggggacc	agtctgctgg	acatgcagac	agcgattgga	gaaaagttag	170015697
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tgtcagagtt	gctggatttg	ggattttgca	tcttgccaag	tgtccatgag	170015797
gaattgggga	aactctcccc	ctggctggac	tgaggcttca	gcaagcattg	170015847
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ggtatcacga	acatatcttc	tcctttgctt	ccttctcctc	actcttcac	170015947
atcatcatca	tcacatcat	caaatatgga	tctgtgaggc	tacctctggg	170015997
gttgaaactt	ggttttgggc	aaaatttggt	atgttctctc	tgcccaatcc	170016047
agcctcaggc	tacaaatgaa	tgtaaaaatc	tctaatttag	tgccaagtaa	170016097
cagaaaacag	ctctacttat	cttaagccaa	aaagagggac	ttctcagagg	170016147
catactaattg	gaggatggca	agagggcctc	acgtggaacc	agggcctgga	170016197
gcggcacagc	attcaggaag	ctcagtcctc	ttctctctct	ctctctcatc	170016247
tctgcttggt	tccctttacc	tgtagacatg	ctatcatttt	tccaatatcc	170016297
atggcagaat	gtggccacca	gtaactccag	gtgtataaca	gaagcctggc	170016347
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ccctggggcca	agcaactggg	ggccaggagg	agctcatatt	gcaggaatat	170016447
tgaaattttc	actaaaatca	tttgaatcga	ggagacatt	tcctagaaaa	170016497
aagggtgcta	gtctgacaag	cccacagtgg	tccccttcat	ctggcaattc	170016547
atcttctgca	aaggtcacac	catccttttc	gctttccaac	ctctgcacca	170016597
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gttttccaca	tattgagcat	tgctgagcac	ctattctgtg	ccaggcactg	170016847
tgcttcaggg	ccattggggga	tgctccaagc	ggtaaaatgc	aaccaaagcc	170016897
cogaaggagc	tcacattcta	gtcatgtcca	caaagaggta	ataaatccat	170016947
aaattgtatg	tactattcta	gtcacaataa	aattgtgtcg	tactgtaatg	170016997
ctgggtatcc	attttaaaac	ggggggcctc	ggctgaatct	gggtcattac	170017047
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ccacttataa	aaataaggat	ctgtaagtgt	gctggataaa	atatattaca	170017597
aaataatgac	ttaagtggct	ctggagccag	cacaaaagat	aaaaattggg	170017647
tataactcaa	attaccttca	aaatatctta	agtcattctt	aaaatacatg	170017697

FIG. 1.116

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taaatatgcc	aactcaaaat	acatccaaca	aaactaatat	ttttcccaat	170017747
ttgttggaag	aaattttctct	ttcttttagtt	gtgcattaga	tgaggaagtc	170017797
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cccgccaccg	ttggccaata	gcaattttcta	ggccccacct	caccaaggca	170018097
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gggccccaaa	gggctagtag	gaggttgagg	tgggggagag	caagagagga	170018547
caaaacaggc	tgggtactga	ccttcctcgt	actccatggc	tcagaactct	170018597
gacctcttgc	caacctgcct	tccgcaagca	gcgagagtag	cacggctctg	170018647
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aacctgttcc	taataatagg	caaagcttca	gttgatggag	tgccatatatg	170018747
ggcccagccc	tgtgaacagc	ttcctctcag	ttttcccgaga	atgaagctca	170018797
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tgtttataga	attgocgggag	gggttaagag	aaagacaaga	gagtggtgaaa	170018947
tgccccagaa	ctagtagcag	gaagctacta	ccatccctga	gcctgaagga	170018997
cagaacccag	agagacagac	ctgtgctgta	ggtcaggggcc	ccccagtgtg	170019047
agcctcagct	cccgtgtcca	gtccccaaact	caacaggaga	gagctggaca	170019097
ataaagaccc	tgtgagcacc	cacaacttcc	cattggctgc	atcctgttag	170019147
aatctagagg	tcatgggagc	ctgggagagg	ccacccatga	agatcagctt	170019197
ccaggggcag	agagcagagt	ggacatggag	gggcaaatgg	ggaccgtcca	170019247
gcacagtcac	catctcatag	acatttttct	ccacctccta	cctcgagtag	170019297
ccagtaggg	tccagccgga	ctgtggagca	tcaccccaac	aactgcatgg	170019347
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agcaaggccc	ttggctcccg	ctgtggccct	cacccatgcc	catccccacc	170019447
cgcccccatg	ctcagcacat	cagcttccct	ctggctgacc	atgtgcacag	170019497
acatgactca	gtaagtctgt	cttttctttt	cttttttctt	tctttctttt	170019547
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ttaacccttt	cccaaggata	gacagcttcc	cccatcatte	tagatccctc	170020147
acacttcccc	agctcctacg	gaaataaact	atcccatccc	ctaagatctg	170020197
caactgttga	gggtaagtgt	ttggttaaaa	agagtgcagc	agactttggc	170020247
gctagtgcga	aacaagctgc	tgctgtaaga	gtgcatgtgt	gtacctgcag	170020297

FIG. 1.117

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actggtgcaa	tcagatgacc	ttcccaccag	gctgcacagc	actggatgtc	170020347
ctcacagtca	ctcagccact	cagcaaactt	tgactgcaca	gcaacccatg	170020397
ccagacctgc	tgctggactc	caggcatggt	gagaaatgaa	tataataccc	170020447
aggctatggc	ctcaaaacct	tcaaaaccca	gggcaggaca	cagacaggga	170020497
cacagatgtg	atacctgctg	ggatacagtc	ctcatgaggc	tctctaagag	170020547
gtatctaagc	agggacctag	agggaggagg	tattacctga	gttgaaccta	170020597
atggaaaggc	attgcaggca	gagggatcag	tataagcaaa	tactcagacc	170020647
aaaaacaatg	gcatggggga	ctccacccaa	gaagtaaaag	agaatagggt	170020697
gctacatggg	gtctcagtcc	cttttctgtt	gcttagaaca	ctgaaactag	170020747
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agtcccagggt	tgaggggagca	catctgggtga	gcccttcttg	ctggggggcag	170020847
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gctgagtgca	ctagctcagg	tttctcctaa	aaacccacca	gtcccactcc	170020947
ccaaataatc	cattaattca	ttcacccaca	aattttattaa	cctcttaaag	170020997
gtcctaacctc	gcaatactgc	cacattggag	attgagtttc	aacatgagtt	170021047
tttgagggga	aaagtattca	aactatagct	cacagagatc	gcttttccta	170021097
gagatggcag	atgaattttg	gaggtagagg	gagaggggca	gatcacacag	170021147
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ggaaggggtct	gtctcatgaa	ccattaaggc	tgagaggtct	agcacagcat	170021247
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ggaagaagaa	atcaatggag	ccaaatgact	ccaccagatt	tgcatthttag	170021347
acgggtcactg	caagactgca	ccagtcacca	attcccaaga	cagcaatgtt	170021397
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acttcttgcc	tgcgttcctt	taatgcttgc	ctaataatgag	ctagtcttct	170021697
ctgatcactt	tttttttttaa	tccaaagtag	gtgggcattg	tcccaagagc	170021747
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tgctctcttt	gtgggttaaaa	ttaccttcca	ttcgtgggtg	gtgtatgtca	170021847
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gggactaatg	acaaaggcat	gggtgggagt	agaggggaat	acaagggaga	170021947
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aaatttgggg	aaaaaagcaa	actagaaaga	agaaaaacca	cattgcctga	170022047
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ttcttctctt	ctccctttct	ccttctttgt	atagagaggt	ctttcctgag	170022147
gacttcccag	aactctgcag	atccaaaatc	ttaagaattt	gcagaggcag	170022197
tgaggagtta	acatgcacag	ctcagggaat	attctgcttt	ttatctggaa	170022247
ccaggctcgg	aacaagactc	cttgcttttc	tgctctgtgt	tttcatcttc	170022297
tctcagaacc	ctaactttga	gataagatct	ttgactatta	ttaggcgggt	170022347
gcaaaaagtaa	ttgtagtttt	tggcattatt	tttaatagaa	ctgcttctgt	170022397
gtcctcagat	ctccatcggt	catctcctga	taagtccctg	aaaatttcct	170022447
ggccctttgg	agctccttcc	aggagtagaa	tgatcacaa	agctgccatg	170022497
tattgcttat	tctggcctat	ttccttaggc	acattagccc	atctaaccgt	170022547
ttccatggcc	cacagagggt	ggaggagcat	gaagaaaaat	gcaaggaaat	170022597
aagctcatct	caaggatatc	ctggctccca	aagaacatag	gacattacca	170022647
acttgaagtt	agcttctcag	gaaactaaga	cccagctgct	tttcaaatac	170022697
tcaaaatatt	agtatgaatt	atagatatag	ttatagcctt	cagaacttct	170022747
ggcacagccc	aaaactgttg	gctgtaaaac	catgtttcct	aaattcaatc	170022797
atgtttctca	ttgattttcca	ttttgaaatt	ggaagtcttt	gccctcaaga	170022847
tataataaaa	accataccaa	agaaaatgga	aaacttttcc	cccttaatat	170022897

FIG. 1.118

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ttaaaggaga	atgatttttta	taaaaaaa	aaaaaacatt	catttgtcta	170022947
cttaaagtaa	atcacagtgc	agtgccagtc	tgggtttgga	gcataacact	170022997
ttttttgatt	tatggtttct	gccaggagac	acccagctaa	tgatatttgt	170023047
tcctatgtcc	ttctctgact	agctgggtgg	cagctaaaga	gctaggggtga	170023097
ggggagacca	gaactccagg	cctgtcccat	gttcctgtct	cacccatattg	170023147
tggatttcaa	ccctgggctt	agtgtctgcc	tctagcgaca	tgggaagaga	170023197
gggatgggtc	ctctccttct	tcttgtcaaa	tggcccccag	agtcccacca	170023247
aggtggagct	ccaggctcct	gaccagcggg	gctccccaac	cctcctgctg	170023297
tgccagctct	atccctcctt	ccacgcccag	cagagctcag	cagacttgcc	170023347
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gtgggcttgc	tgatcacaga	gaaagctcac	gtggcaaaa	aaccagtgag	170023447
attaacaagt	cgaggtttgg	gatatatctt	agagatggag	ccaatggggc	170023497
ctgcagagga	tttccctggg	gactggaagg	gtgaggaagg	agaatgctct	170023547
cagatgacac	ctaggtggct	gatgtgatag	aatgggcatt	ttctggaaga	170023597
tctgttcagg	ggcattttgt	gagacagaaa	tcaagggttt	ggcttgggac	170023647
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cacaggggtc	tgtgtgttcc	cctgtggtgt	gtgtggggac	acgtgagtat	170023847
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acaatttctt	gtctgacctt	ggctgaggta	tgtctgagtt	ttaatggcct	170023947
gtaaaatgag	ggggtgatat	tagatggcat	ctgagaccct	tgccaactcc	170023997
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atgcgagttc	tgcacctccc	ctggggcctt	cagcagctgc	attcttggcc	170024147
cagcagagga	cttgccctgat	ctccaggata	gcaaaggagc	tgaggccaaa	170024197
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gctgcaattc	aacataaaat	catatcatto	acacctaccc	actcatgcat	170024297
tcattcagca	catgtctatt	tttgaaccgg	caaatatata	ttagatatcg	170024347
atgctgtgct	gaatgccaca	gattgcaaca	ggaatcagac	gccaacctgt	170024397
cccggaggag	ctcacacatc	tttccaaaac	caatttctac	ttcttgggtc	170024447
ccctctcaat	gtgtacaaca	tagagctttc	cttgcaaggc	tcgagcacia	170024497
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ataactgaac	ttgacttctt	tcttgggtcc	tcattctgct	gggcatggat	170024747
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cagtctaggt	agggtgttct	ttcccttctc	ttcccactag	agaattttata	170024847
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tcctccactc	cctggagaaa	aacctatccc	acacaccctc	acataattctt	170025397
caagatctat	tgggttaaggc	atccaactta	ttgcttaagc	atttcaagga	170025447
ctggactttg	gaaagccaag	aatctgagtt	gcaaagtctt	ccttaaaact	170025497

FIG. 1.119

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caaaaactgg	gctcataggt	gctcttctct	ttttcttggc	atttgcctaa	170025547
aagccaccct	gaggacacct	aggagaggcc	acctcaccac	ttcttgaacc	170025597
aggcatgggg	gatggggaag	aagacactgg	ggaaaagctc	tgagtgggtac	170025647
ttcagatcat	cctgcctcag	gtgttggttc	tgatcctctc	aacgactccc	170025697
aagggaatat	gtcagctcca	ttttgcagac	tgaaacccga	gtctcggaat	170025747
gacttgtcca	tggtcacaca	gttgctaaac	atctgagcca	gagtgaact	170025797
ctgggggtatt	tgactttaaa	gtcccagcct	ttaaatactc	ccacacttgc	170025847
ttattccaac	ttggacttgc	cggagtccca	tagacagagg	ctactctccc	170025897
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cctgggcttc	gtctccaccc	aggtgcctct	ccccagcag	ctgcaccagg	170025997
ccagctgagg	gggatttttag	cccgaatcca	gggtttctcc	tacagaagac	170026047
aaggagtttg	ggcactgcca	gaattagaag	aacagaaaga	aaatgttctg	170026097
gatttctcat	caaatacccc	tagcctgaga	aatataacta	aattcaccct	170026147
taggtcatct	tacaatctgt	cctgccccag	tggtccccac	tcagggaact	170026197
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ggcctgtgcy	ttcactcctg	ccccctcctc	cagccctgtg	tacactccct	170026447
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ctcttaggaa	ggctttccta	acctccaaaa	caggctcagt	tcccctcttc	170026897
aattctcact	gagcctcctc	cctagcatctt	ccctctctgc	attataattc	170026947
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tattggctag	atttcgggga	tgaaaaaggc	agacaaggcg	ccctgccttc	170027247
aaggggtttt	cagtttagtg	gggagcaaaag	caaaaagaca	aacaaacagt	170027297
taaatataac	atctagtagt	gataaatact	ccaaagaaaa	ctaaagcagg	170027347
ggccagagag	catgggggca	ttgatgtttt	agacaagggtg	gtaaaggggag	170027397
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ttccaagtca	caagcatcag	gcttggaaga	cctgtgtggg	agagtaatta	170027597
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aatggggcaa	ttgatttaaa	gaacagaccc	agtggcttat	tgatcagtgt	170027747
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gatcatocca	agccttttgta	atacgctgt	ctctcctgcc	atgctctgtt	170027997
cctatctagc	ttttcaaaac	aaactcttca	ttttagaata	gttttaaaatt	170028047
atagtttagag	aaaaacttca	aagatagtaa	gagagttccc	atatcctgca	170028097

FIG. 1.120



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caoctggtga	gccccattgg	taacagctta	ggttaacact	gtcaccacta	170028147
atggacaaat	gttgcaatat	tattatttgc	tcaagtccat	acttaactca	170028197
gacttcctta	gttttttaoct	gaagtccttt	ttctagttca	ggatcccaca	170028247
ttccatttcg	taggcatgtc	tccttagact	cttcttggt	gtgacagttt	170028297
cttaggcttc	cctctgtttt	gataaccttg	acaatattaa	ggagatattg	170028347
ggcagatgac	tgtagaatgt	ccctcaactg	ggtcttatct	gaagtttttc	170028397
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gctgatggtg	acctcgatca	cctggctaag	attgtgtttg	tcaggtttct	170028547
ctgctgtgaa	gtcattttcc	tccttcccct	cttacacact	gggctccttg	170028597
gaaggaaagt	actgtgtgca	actcacactg	aaggagtggg	aagtttagaga	170028647
tcctccttga	gcgtgggcca	tcttcatgaa	ttattgggaa	ttattctgca	170028697
taagagattt	gtttatatta	atatgagctc	atggatattt	atggtgacac	170028747
tttgggttat	aatccaatag	tattttactt	cttttcttgc	tcaaattact	170028797
ccacctttgg	gtactggggc	tcttgagttt	ggctcctatg	tccccgtcat	170028847
tgaggggttt	gggttttgtg	tgtgtttgcg	tgtgtgtgtg	tttgagcact	170028897
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gocctggccc	tggagccact	ccaaggaacc	tccaagaacg	cctgattcct	170028997
tttattactg	gctcctatta	taattttcat	aatgggctgt	cattttgttt	170029047
tgtctggttt	tgtttataat	tataagggtg	agtcaagctc	ttgcataaaa	170029097
tatagcaaag	atataaaaaga	ataagaatga	aaataagtat	cccaaataat	170029147
ccaagcagca	aagaaatcca	gcgttaacat	tttgggggtat	tttcatctgg	170029197
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ctctgccaga	ccaagggata	tcattggccc	tggtttacct	ccctgtccca	170029297
gcattctgtg	ttggagcagc	ttccatttgg	ccattcctcag	gtgggtctgct	170029347
cgctgggccc	ctgcccactt	ctccctccag	cagaccgcag	gccaagaggc	170029397
caggagccag	ggtgtgtcct	ccagcagact	ctgaggaagt	gaatacatca	170029447
ctgttctgtg	acttccaacg	tgatagttgg	cctcattttc	ctcttcttta	170029497
cgaagtaaat	gcgataatat	atacaaagtg	ctcagagaaa	ggcctggtaa	170029547
gaaacaggta	ttttaaaaag	taaaaactgt	cggctgggcg	tgggtggctca	170029597
cgcctataat	cccaacactt	tgagaggccg	agggtgggcg	atcacgaggt	170029647
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cccagctcca	tcacttacct	gctgggcagc	agcctgagtt	atttaaacct	170030247
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tttacagaat	ctcattgggt	ccaatgggct	catacgtcca	tccccaacc	170030547
aatcacagtg	actgagggat	tatccaagga	tcacactggc	cactttcaca	170030597
ggttttatcc	ctaaaggaaa	tcacaggtaa	tagatgtggg	gctgcagaaa	170030647
tgaacatgco	acttttcctt	gaaactgcat	cccttttccc	tgaagatgaa	170030697

FIG. 1.121

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gcttgaaaga	actctaagag	gttaagcatg	gagctgatgg	gcaagccaca	170030747
ggcagaaaga	gtagctgtgc	agccaggctc	ctggccaggg	agggcagata	170030797
aggaggggag	gcaaagtttg	gtaaacagga	agctaatacta	tgggcaagaa	170030847
tcatttttctt	cagcatcctg	acctctccta	aaatgtttctc	cactgggtccc	170030897
tgctaggaca	aaggaattac	caccagacta	gagtcaggag	tcctgggctg	170030947
gttctgctgt	atgacacagg	acaggtggct	tgcttgggtct	gggccacagc	170030997
ctcctccccct	gttgatgagc	atgttgggtg	ttccagcacc	atgtcagccc	170031047
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cttttccttc	aaataaagag	attggcatac	aggggaggag	cccagtacag	170031147
acggcatgct	tggctcaggt	tccagaaccc	agaaaccaga	caagagttgg	170031197
gaaacatga	tggtggagga	gggtgtgcc	ctccttacta	gtgcctaata	170031247
tcttcgagac	actaatgttt	cagtattatc	cacagattct	gatgccaggc	170031297
agcccagatg	actaggggtca	gttattagca	tgcttctctg	aggtgggtcc	170031347
caggtgcagg	ctacctgcag	tctggctgga	tgggccctgc	accacacttg	170031397
cttctgggaa	gctgggttttg	gggttgccac	aatctctgaa	agaatcacta	170031447
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cactagtctt	accttcttgg	ggaacccttc	ctggattccc	aggctgggct	170031547
gggtgtccct	gcagcctagc	cccacagccc	tcctgcttct	ctttctcatc	170031597
acagtcttgt	tatctctacc	aactgtaggc	ctgccccact	gatggtgtga	170031647
ataaagggac	tgggtctctc	tagcacctag	catagatctg	atacatagtg	170031697
ggtgatctct	attgaatgaa	cgatgaatga	atgaatgaat	gaatacattt	170031747
agataattca	gattactctt	tctagctcag	cagtgtaaag	caggaagaca	170031797
tgctgtcaat	atgatttagg	gcaagtttct	aaatctctct	ggacctcagt	170031847
tttacctctt	gaaaaataaa	tataataatt	tgctcttact	tcattgagact	170031897
attttgaaga	ttaaatgaga	taatgtatac	actactactc	actgtcctta	170031947
cttgaatatt	cctaggtcct	tggtgctaca	ttaggctaca	tagaatgtat	170031997
ttaaagtaat	agagtgggat	ttataaata	ttcattttct	ttccccagaa	170032047
ctaccttaaa	ttaatattgt	gaaaggacag	atggatggat	ggttgatgga	170032097
agtagcaggc	ttccagcagc	aggggatgga	gtgagtgtgt	ggataccgct	170032147
ggatcagcag	aagggtatac	catttttagag	taactatctc	ggacttcgga	170032197
gagttcctgg	gtatgaaggt	ttggctttta	ttaaagtctc	agcacagtgt	170032247
taaatgccat	tttatttttag	gtcataatta	acactaatga	gatgagtgga	170032297
ttacaaagag	cacacatttt	gagaaagtga	aaaacaacat	ctgagcttgg	170032347
tggtttccat	tttcgctttt	ccccctccca	tgctctgttc	aattaaaagt	170032397
tttgagaaaa	tattacaacc	atactccttg	tctttgtggg	aatgaagcat	170032447
attaatttga	atgtgatgaa	tacaatatcc	cactgacttt	tttattccct	170032497
tatctacaaa	agtttaaaat	aatggaccaa	ttaaaccagg	agagaagaat	170032547
gcaggggttg	cctggggatc	caattcagca	accagagaac	tgaaagaaca	170032597
aaattttttg	acggagtctg	ggccagactt	catcccttac	ctatagctga	170032647
caaacagtaa	gtcaaatttg	gcagatgtgg	accagcgcag	aacacatact	170032697
atattgagga	tcgaaaggcc	aggttccaga	ccgtcctcta	atattttctt	170032747
agtgaatatt	tgttggtatga	atgcatggat	gggtggatga	atagatggat	170032797
ggatggacag	atggacggag	agagagatgg	atgaatggat	tggtggatga	170032847
agttgaaaga	tgaaggtaga	tgacctccca	tggtctgatt	cttcctaagg	170032897
tagcaaatta	agcctaggat	gggctgacct	aacccttcca	aggacttaga	170032947
agtcagggca	agaacttaca	gggaagggtt	cagttctctg	acctcactac	170032997
cctagaggca	taaactataa	attatagagt	tggtctgagc	tcagtttccc	170033047
tgggagctct	gctctaaagc	agagcccctt	gaccctgcac	caatttggtt	170033097
aacccgagta	aggctgagct	tccccagca	ggagctcctg	ctttggaaga	170033147
gaacatcctg	ggccaggcgc	agtggctcac	gcctgtaate	ccagcacttt	170033197
gggaggctga	agcgggtgga	ccgcctgagc	tcaggagttc	aagaccaccc	170033247
tgggcaacat	ggtgaaaccc	catctctact	aaaatacaaa	aatttagcca	170033297

FIG. 1.122



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ggtgtggtga	tgcagcacac	ctgcagtc	agctactcag	gagactgagg	170033347
caggagaatt	gcttgagcct	gggaggtgga	ggttgagctg	agctgagatc	170033397
acaccactgc	actccagcct	gggcgacaga	gtgagactct	gtctcaaaaa	170033447
acaaaaaaaa	aaataaaaaa	aaaagaagag	gacatctgga	gcaggcctgt	170033497
gaacctgaca	catgggtccag	gtgtctccct	gaggacttct	ggaagtctcc	170033547
ccacctctct	gtggtccttt	aggcattaac	accaccttgt	cactgtgtct	170033597
tctgaggcag	tctggaagtt	catacccac	aatctctgtg	taccttgtcc	170033647
cccattctgt	tctctgcatt	gcagatgggt	taaaacacac	acacatacac	170033697
gcgcaaaatg	ttgttccttt	tcttaaaacc	catttgtggc	aggctagaca	170033747
aatccttaac	acgggtctaca	atattctgca	tggcatggcc	cctgggtgcc	170033797
tcccaacctg	atctgtcaca	caccacctcc	acctttgcct	gttccctggg	170033847
ccctagcact	aacctttggg	tcattcctag	acaccttttc	agcacttagg	170033897
ccccacacgc	cctcagaacc	tttacacttg	ctgtctcttt	tgctttaaat	170033947
gttcttgccc	cacctaccac	ctagttaatg	ccttttcctc	cttcagctct	170033997
tagttgaagc	atcacttcct	caaggagggg	agccctgatg	aaactcatta	170034047
tgcaaaactc	agcctggggt	gggccttatc	tttatgctgt	catggccctg	170034097
agtattcttc	ctttatggca	ccaatcacgg	cttatatgat	atacttatgc	170034147
tattatttga	gttatgtctg	tctccccag	tatgccacta	gtattagaat	170034197
cattgattht	taatcattgt	atccctagt	cttagcacag	agcctggctc	170034247
ataatagatg	cttaataaat	atthgttgaa	taaatgaatg	agtgaatgaa	170034297
taaatgcctc	attcaagagc	tttggctctt	tctgtactac	tacattactt	170034347
ctatttttta	gctcttaatt	ctcaaagcac	tttctttgtg	ctgggcttat	170034397
gctgggagct	tagacagtaa	agcttagatg	gtaaaactaca	gttgctctca	170034447
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agtgtgtcga	gtgctacaat	agatggaggg	gtgcagthtt	atggatgtgg	170034547
agaagaaatc	cttctattcc	tcactggagg	cttcactaag	gagatattcc	170034597
ctaagctgct	tctggaagga	aaaggthttg	gccaaagaaa	taagggtgga	170034647
ggcagaatth	cagggtgaaa	gaccagcata	tgcaaaggct	cagagggcag	170034697
agcctggcac	tggaaacaaa	atgcaagtca	cttcgtggac	tgagacctgg	170034747
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agatcacaga	ggcctthcaa	tgacagcaac	atatggcagc	tgacagagaca	170034847
gcatggaagg	gactggcatg	gtgagacctg	tgataggag	aactccctct	170034897
cgaaggggtt	cagaaaagag	atgtccatat	ttcaagtga	ggacttcctc	170034947
ccctggagaa	actgaggctc	tgccccaggg	ctgtccatca	gactccttcc	170034997
cagaatccaa	acgcttccaa	aggatgttca	gtgtggctga	ccttgcttat	170035047
tcattgtggg	gagaattaat	ttcagggtgg	agaatthtaa	aaaaatataa	170035097
gattaagcag	tgtaatcagc	tgctgctgag	agttgcaaat	gcaataaata	170035147
ataatagcat	tgagagctgt	thttaataac	tcaccagtgt	aatttagcct	170035197
cggcttctta	gagcatattt	aaaatatgtc	atagtgtgtc	taatggcaaa	170035247
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gcagaaaata	gaggagaaat	tggaggatth	gattgcaaac	aggggtgtagg	170035347
aaggcaagca	ttgttcattc	tgacaccact	aattcaaaat	ctgtgatctt	170035397
tgcttaggca	ataggthtta	gttggthttg	cttcaagggt	gaaacagatg	170035447
gatagcaata	atatggtaaa	ggagatattt	ataatthtga	agagaagagg	170035497
thgtthttcag	aatctataga	atcaccattt	tcatgcagtc	catattctaa	170035547
ttacagatca	tcttgacta	tctattatag	caggthccca	ggcaactgat	170035597
atcttgacaa	cattthgttht	acttagttga	gttactaaat	attcatgata	170035647
ccatgaaaat	gtgtthattta	aaagtgttcg	atgaattctg	agththtagta	170035697
attcatatgt	gctgtccccg	cccaaccccc	attagtctaa	actggtgaga	170035747
tggggctagg	agthctcccc	tcttgggtaa	cagacttgac	acagthaaag	170035797
tgagacaaac	thtggagtca	gacagacctg	agthtcaaatt	ctagthctac	170035847
cacttactag	ctgtgacctt	thgcagctta	aacactgagg	ctctattccc	170035897

FIG. 1.123

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gatctgttaa	gtgagagtgg	tgatgatgac	gaccatgaca	gctaataattt	170035947
atggatcgcc	tattgtgtta	tctccaacac	aacgatacag	tgacgtagggt	170035997
ctaccatggg	tcctgtttca	cagatgagga	aacttgaagc	ttagcgagct	170036047
caagtaactt	tcctgaggca	cagggctagt	gaataaccac	tctgggacct	170036097
agtatctgtt	ctagctgggt	tcaaagccta	tgctgttaag	tgggctctga	170036147
tactatcttg	tacagttggg	ggaagatttg	agaagacatg	tgtaagggtat	170036197
agttcctggg	atgtaattag	gactttataa	atatctctta	tatggaagga	170036247
ctgaatgtat	cttcctgggc	tgtgtcctcg	cagggagata	taacatctat	170036297
gtcactctca	acgctttatt	aatgtccctg	tcactctata	cccttgtcca	170036347
agttactcca	caccctccaa	agcctcaagt	ttttaatctg	taaaatgggtg	170036397
gtgggocggag	gtggggagtg	agcgtctcta	cacatactac	taggttgggg	170036447
gtaaattagt	aaaacaactt	tgggaaacaa	tttggcaaga	cttagtaaaa	170036497
ggtgcataga	tcctgtgaca	cagcagtttt	attcctggga	taaatgctaa	170036547
agcaggttgt	ctccatctct	gcactactga	catcctggga	cagatatttc	170036597
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ggaaggaagg	aaggaaggaa	ggaaggaagg	aagggaggga	gggaggagg	170036747
gagggaggga	aggaggga	tatttaataag	ttaagttaca	tccacagggt	170036797
tgattataaa	tgtgtgtatt	gaattggaat	ttctgttgaa	attctgatcc	170036847
cttctagaca	aagaaggtaa	aaattgaaac	atgtcaatgg	atatctaaat	170036897
atcattactc	actggcttta	tttgcaaattg	gctttccatt	gacaacagtt	170036947
acattttgtt	caaagcaaca	aatgattggc	gctgacaatc	cacaggaaca	170036997
tggtgcagtc	attaatgaat	gtgctcatta	ttcctccctg	ccgggaggga	170037047
tcgactcccg	ttctccagcc	tgttttaagc	agacagacct	acatctgcac	170037097
ctgtcagctt	ggaaccctag	taggggaggg	ggatgctgat	gtgatggaga	170037147
atgaagaatg	ggccctgcag	gctgacattt	tgggagagta	ggttctgaaa	170037197
tttatcccaa	aggacatgga	atcctggaag	cagggttcaa	gacccctcca	170037247
aaattgatct	cccaggatgc	ttggaatgat	tgttccgagg	gttttgtaaa	170037297
atgccagggg	aaaaccagga	agcttctctc	cagttgtctt	gcctccttcc	170037347
tctccagtct	ccatggagct	gactttgaga	attaactcct	gagggacaga	170037397
gaccctggga	tggagagcca	gccctgctgg	attccacaag	gtgctgctta	170037447
aagcacaaca	cctcttccca	atgacaggtt	ctgaaagaag	gcctttagag	170037497
tagatgcaca	gagggttttg	ttttgttttt	ttttttttaa	cctttcagca	170037547
tctgtctaaa	attgctctgg	gctgggtaca	gtggctccca	cctgtaatcc	170037597
caacactttg	agagctgagg	caggagatc	gcttgagccc	aggcgttcta	170037647
gaccagcctg	ggcaatatag	tgagatctct	atgtctagaa	tgttttttaa	170037697
ttagctgggc	ttgctgcctg	cacctgtaat	tccagctact	tgggaggcta	170037747
agggtggggg	atcactcgag	cccagggggc	tgaggctgca	gtgaaccatg	170037797
attacaccac	tgaactccag	cctgggcaac	agagtgagac	cctgtctcaa	170037847
aaaatatata	tatataaata	aataaataaa	aataaatggc	caggtgcagt	170037897
agttcatgcc	tgtaatcctg	gcactttggg	aggccaaggc	aggcggatca	170037947
cgaggtcagg	agatcaagac	caccctggcc	aacacggtga	aaccctgtct	170037997
ctoctaaaaa	atacaaaaat	attagccggg	catggtggca	cgcacctgta	170038047
gtcccagcta	ctcaggaggc	tgaggcaggg	gaatcacttg	aaccagggag	170038097
goggaggttg	cagtgcagccg	agattgtgcc	actgcactcc	agcctggcaa	170038147
cagagcaagc	ccccatctct	aaaataaaaat	aaattgctct	gtaagttgac	170038197
accactaaaa	acatcattag	tagttgtaat	aattaagata	aaggagaaaa	170038247
ctgtgcagag	cccagcacag	tgctgtctcc	atggaaaatc	ctaatagacat	170038297
ttagtttccc	tctctttgcc	cccattttct	tatctataaa	acagaaataa	170038347
tgctgtatcc	taactcaaaa	gttgattatg	gagagtggca	tagtattggt	170038397
tcaacaaata	tttattgaga	aactgcaaca	cgcaaataga	tgtaaaagggt	170038447
tgaacagaac	tttgcaaatt	aaaaatccta	aaggacattt	tagaccttat	170038497

FIG. 1.124

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gaacttccta	ataggtaaga	ctttttaatc	tatctgcagt	gtccaacagg	170038547
tgcaagagct	tgggcggact	gtgaatatct	aagaaaagag	agagagcaga	170038597
aaggagggag	gaagatgaaa	gaaggaaggg	aggaagatga	aagaagggaag	170038647
ggaggaagaa	gggagggagg	gagcgagggg	ggcgggggag	ggagagaagg	170038697
gggaggtagg	gagggaaaga	aggaaggaaa	ggaaaggaaa	ggaaaggaaa	170038747
ggaaaggaaa	ggaaaggaaa	ggattacagg	tgggagggag	ggaggaaggg	170038797
agatatcatt	attattgtgc	aattgtttatc	attatataac	taattttaaac	170038847
aaacccatcc	tgtgcccaca	aaagggcacc	aagataaagg	ctaagataaa	170038897
gaacacacga	atcatttttcc	catttttcgtc	agtgatggga	atggtaaatga	170038947
ttttctctct	gaaccataac	catcttgcag	ttaaataatt	gctttctgat	170038997
agaatcagga	gctctgagat	ggtgctctga	ggagttcttt	cattttctttc	170039047
gcacctttta	aagaaaagaa	aacttcaagt	gcaattattg	gcattattttt	170039097
aataccgact	gcagcagaac	attctggaaa	atgaggcccc	tatcaaatta	170039147
gtttttccaa	atgaggttta	gacagtacct	taccaggaga	accactcaga	170039197
aagcccccat	ggcagcagca	agccctgttg	agtcaagggc	acatggatgt	170039247
cacactgcac	atgtgttttc	agataactaa	gtgaactgct	ccgatcttgt	170039297
gggtcattgc	accacggggc	ctctccattt	acttcaggtt	acacagcaac	170039347
aagcaagctg	agagcagcag	aagtagctag	ctaaaattgc	atttgattttt	170039397
gtgactgcta	gaggccaata	ctcaagtga	gtttaagcaa	aaacaaatca	170039447
tactcagctg	aaaacatttg	cctggaagaa	agatctgtgg	ctggagaatt	170039497
ggagttcatg	cacccagcaa	tttccagagg	aagtctgatt	cccctacctg	170039547
aagtaacact	ccttcctctc	cccagatcca	gatctccaga	ctatacgtac	170039597
tcaatatatg	acttgtccat	ggggcccaga	tgagcattat	tgctcttagc	170039647
ttatggttaa	taataacagt	aataattata	ctaattattat	tctttctatg	170039697
cataattact	aattcatctt	aatctcacia	ctctatgaag	tacatactgt	170039747
gaatgtctct	gttttacagg	tgagaaaact	taggcacaga	gaagttaagt	170039797
aactcatcat	agtcacagag	ctaagtagga	ggcagagtta	agagtcaatg	170039847
taggcttctg	accagagat	tgtgctctgg	acctctgtgc	cacactccca	170039897
cttactgggt	atcagggact	gtgctgagca	gtttatggca	tcatctcatt	170039947
ttgttattgt	aacaacccta	tgctatgggt	atcagtatta	ttcccaggta	170039997
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tagtaagtgg	cagagataaa	attgaaaccc	agagctaaaa	ttgtttggca	170040097
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ggactctgca	gaccatggcc	agtattcatt	tgtcaagatg	caaggaccta	170040197
aactggaatc	cagtctttta	tgatgtctgg	atcatacaaa	aagtcaggta	170040247
tctgtcccat	gaggccagct	aatcccccca	caaccccaaa	tccccctgac	170040297
acacatcatc	ctcacctaga	gaaacctttt	cacaaataat	caaacctttg	170040347
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ataaaaatagt	aatttgggac	aaatttagta	agagaaatat	cagaatctat	170040497
gcaggctcac	atctccaata	caaacatatt	caccttacac	tctatatgga	170040547
aatagtaaag	agcaatttgt	gaaatagatt	ccatgagtgc	cccaattagg	170040597
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caccatttct	aggaaatagt	aggtaagtct	ttctggttgc	cactgaggtg	170040947
actcacctga	gacacagttg	ctcctaaagt	tcaaggttag	gagacaatcc	170040997
agaaggggag	ctgtctgtga	agtcagaatt	cttggaagaa	tgtaagtctt	170041047
tacacagtaa	cagcaaagca	gacagtggga	accactactc	tgctttcttg	170041097

FIG. 1.125

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catcattctt	tcctagaaat	accagaaagc	agtgagggat	taagtcta	170041147
tcctggcacc	tgaccttata	tctaacagat	gctcagtatt	acctgttgat	170041197
gggacctcac	tgggaatggt	ttgtgtgcag	tacaaaaggg	caatagatga	170041247
aactttggga	cgggagccca	ggaaaatggc	tgagaggaga	gcttatgcct	170041297
agcttatgca	tgagcttgca	aaaagggaga	atacacggga	gggaagatca	170041347
gcaacagcat	gagttttata	aggcagagag	ttgttgggaa	ggaagcagca	170041397
gggagagggg	aaggagtaag	tagaaacct	gaagagatac	agctaagata	170041447
agccaagaga	acaaagtatt	gacttaccag	aaacatggaa	gtcttcctgc	170041497
ttctaattta	gttccgcata	tctggatatg	tgaatgccta	aaatcccatt	170041547
aagcccagtg	ggtaatttat	tacacttgct	agggccccag	aggagaggaa	170041597
acacagtaag	tcagaaaaac	ctctgggcag	gtgaatttct	cagggtttct	170041647
tctgggcaga	tgggatctgg	aatggtagcg	tggcatcctg	gtaattcaga	170041697
gacagtgggg	agggtgaaga	aacactgatg	tgtagcattt	ctgtgggtgc	170041747
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tgctgatttc	ctgaaaattt	aacaattagt	tttcatgaga	tgcaagtggg	170041847
tgaccccagg	acatcactgc	ctacacgcca	atgagaatgg	agattgacac	170041897
aaagaacaga	gtggagagac	acagagcagg	gaagacaaga	ttttcccgag	170041947
tctcaatcca	atatgtagac	tatgtctccc	ttttcacaaa	gaagggaagg	170041997
gaggagagac	cagcattcac	attcagttat	tggtgtttta	aatccattac	170042047
gcacatacat	aggagaaaat	ttcagcaaca	gtcaccctct	gaaccagtt	170042097
cctcagttct	ctccagaggc	aactaaaatg	ctcaattatt	agtgtatcct	170042147
tttggaata	ttttatgtat	atgacagtgt	gtgtgtgtgt	gtgtgtgtgt	170042197
gtgtgtgtgt	gttcctttcc	aatattaaaa	taatattaac	attggtaata	170042247
gtggtactaa	acaacttagg	gtgttttttt	tttcatttaa	tagtatattt	170042297
ttagtatctt	tccaggaaaa	gatacatgga	tgtgccacat	tattttta	170042347
ggctcacatg	gtactccttt	tatgtatgca	ctataattta	tgggaaccag	170042397
tttctcaccg	atgagcatgt	aagttctttc	agtcttttac	tggtataaac	170042447
gaatgatgca	atgaatatcc	ttgtacatat	atatttgtgc	gcatatgtag	170042497
gtatccttac	aagtgggaatt	tctgaataaa	tggatatata	caattttatt	170042547
atgaattttac	cttcctacaa	gtgattcaag	agagtgtctt	tgctccacag	170042597
tggtgtcaat	atagtgtatt	ctcaaaatct	gacaccaata	tgtgtgaagt	170042647
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tatttaagaa	gaggaaactg	ggcctcatgg	agatctagga	acttgcccaa	170042747
ggacaggtct	ctgtgactct	aagagtgcaa	tcttcccttt	tcccatgtc	170042797
aagcaccttt	ccccaccagg	ctcactgctg	acaatccagt	gtacgaagaa	170042847
gggaaattac	ccccacagag	cccaaaagtt	taggacatgc	cgacagcatc	170042897
actcttttgc	ctcctcattc	tctctttcat	ttccagaaca	tttgctcact	170042947
cagtgtctgcc	cagtgatact	tagccagcct	gattacccat	ctaataattt	170042997
ctgatactaa	tataaaacct	tcccaaagac	aaatataact	gagacgcact	170043047
ccagcttacc	atagctttcc	tggtgggtaca	gtttccaggg	acatttcact	170043097
gtgtcaaagc	agggaccaca	tatgttccag	accagcttgt	tgggtttttc	170043147
actgggaagt	gaagacaaat	tgttgtccct	ttgaaaaagc	atctttcatc	170043197
tctccatcta	tctgcgatct	aaagcaatgg	ggctctttct	gtatgtcttt	170043247
caaatggtct	acactgacac	acgttttctc	tgagctgccg	agagaatatg	170043297
ccatgagatg	ttgccagtga	tggttacact	cagctagcag	aagattaggg	170043347
actgggttaa	cctttggaga	aattgccttg	ggaaaagagg	aaataaaagc	170043397
aaatattact	atgaaacata	gagattacca	ggtaggagga	ggagagaggt	170043447
ggagggaggg	gtaggagtgg	aaggaaggga	gggaggcaga	aagaggaagg	170043497
cagactgggtg	gaaaataaac	cgtgcacttt	agaacagcag	gaaggagggc	170043547
ttggaagcct	ggttttctgg	ctttgaatga	ccgcctagcg	cttgccgggtg	170043597
cgccagggtg	ctgtgaggat	gtgggcagag	ggcgagtcgg	aagggtcca	170043647
gacactggga	atagtgggtg	tcgtgtgctc	ctccctgaaa	cttttgcact	170043697

FIG. 1.126

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acctcggact	gattgacttg	tcagacggta	agcgaaccct	ggagcttccc	170043747
cgttttctgt	gaatgtgttt	ttgtggcttc	ggttgctgtg	acagtcgttt	170043797
cgaaaatgca	cggaaatgag	ggcggagacc	cgagagattt	gaaaaagccg	170043847
ggctgaaaca	gcgtgggtatt	ggcccccgcc	tccccagtcg	cgccccagtg	170043897
ctgcgctgtc	cgtcgtgctg	aaatgtgggtg	cgcctgggga	gtgcggggagc	170043947
caggaagtta	gggtctcctg	ctccggccct	atgagcatgt	gagtcttgat	170043997
ggattattag	ctatgggtga	ggccagcaca	acacatcaca	attctctctg	170044047
aagctgtctg	gtaactacgt	atattgttga	tggaaagccag	tgacttttaa	170044097
aagccattat	gttgattaac	tttttttaaag	aagttagga	gattatatgg	170044147
aggtaaaaac	ctttgtaaaa	tgctaatacac	agtgtctgac	aattagaaca	170044197
catttaataa	atgtcagttt	ctttgctcaa	cccttataag	aacccttatt	170044247
ccaaagccac	ctcctcagct	ctgacttcag	ctccattcct	tagtgagaat	170044297
ggggttataa	atccagggtta	acccgattgt	ttaggattag	aaagtgattt	170044347
ggtttccaac	gttgaaggag	ttcaagaaac	aaagagtttt	atttttcctc	170044397
cttatgagat	attgttccaa	atagaacaca	gtttgtctag	atgatttttg	170044447
tcacttaaaa	ttaggtctca	ggaaagattc	caaatttcac	gagcaattgg	170044497
gctcataaaa	caagatcaaa	ctccaatagt	gtatatccaa	agtatgtata	170044547
atgtgtattc	ggtgtatatt	cttcaccac	tgcatggtgt	agacagaatt	170044597
tctcttccaa	ggggcaccac	atgacaaaac	cgtacataat	aatgaaatgc	170044647
attttagtag	aaaggactag	ctaaaatacc	aactgaaagt	gggaagacca	170044697
gaaactgaag	tgtaagatga	ggtaagccct	ggagtaagag	tcaagaaatc	170044747
cactttctat	ccataatctg	tctcggttta	atggttggtca	agtcattttt	170044797
taaaaaatte	taggtcttgg	tttccttatg	atgactttag	atctctgttc	170044847
cttggaaatc	tagagtgate	caaagggttc	tttgaattca	gttttgtggg	170044897
ttgagacggg	cagccagact	gtgagtcctt	cagctctgct	tcaaccagaa	170044947
cagctccact	ttactgttca	gcatgttagc	cctgtatgta	aggatgtttt	170044997
ttagcttttag	ctaaaattta	gtgactctat	gaccctaagg	ccctgcttcc	170045047
ctgagatttt	gaaagctgaa	gcacattcgg	aaaacttttt	cttccttaaa	170045097
aatcacctga	aatctgacaa	tctggaagac	tagttctgtc	tgctccagcc	170045147
cttggtccct	tagatgtgct	tttctgaaga	tccaaactca	acctgccagt	170045197
caatatacca	actgagcaga	gccctgttcc	tccaccagat	ttcaagagaa	170045247
catgttccat	tcctgttcag	agcttcagag	cagcttccgc	taagattgca	170045297
cattaatgca	acagegtcct	attttctttg	tttctttttt	tttttttttt	170045347
tttttttttg	atgagacagg	gtttcaccat	gttggccagg	ctgggtctcaa	170045397
actcctgacc	tcaggtcatc	cacctgcctt	ggcctcccaa	agtgtctggga	170045447
ttacaggcgt	gagccaccgc	atctggccaa	gcttcctact	ttcttataag	170045497
gctaaagtgt	cagtagaaat	attcccctgc	tcttcctttc	catatcataa	170045547
gtatccatct	tccttccctt	gctttaactt	ctcatgattg	cagtttttgt	170045597
tttattacaa	taaaggatat	caatcattca	tctaagtgtta	tagcaatgag	170045647
gggattttaag	gtgaaaggta	gagaacatat	gttgagaact	gtttctggaa	170045697
actctagggt	aagaaaaaga	agggaaattaa	cattttattca	acacctacaa	170045747
tgtgccagggt	acagtgtctaa	gtgcctttat	atacatgagt	taatataaac	170045797
ctcaaaaataa	tgctctaagg	aaaacatttt	aaataatgct	gaagttaaata	170045847
atcatgattc	cttttatata	aggaagaaga	cagatttaga	gaagttaaata	170045897
aaaattttcca	aaaatgcagc	aatagcaagg	tggagggtatt	tgtctctaaa	170045947
atttcaccct	ctgttctgtg	caccaagtac	ctcagcaagt	aatccagttc	170045997
cagatgggat	ctgcagtctg	ccattaaagtc	tttaccacac	ataggctctt	170046047
atgctagagc	ccttaccata	tgggtccaaa	tgccattttt	aatgtgtatt	170046097
tgatatggag	actctgttca	caatttgagt	actaaagaga	gaataccacc	170046147
tcctagtaga	tacaccagga	ccaatgtaat	gctgtcattc	taaggagagc	170046197
agtggaaacat	ctccaaagaa	cccactctgta	gtcttccttc	ggcccttgat	170046247
cttattccta	ttttattttt	aagggtttttt	tttttttctt	cgagactaaa	170046297

FIG. 1.127

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tctcactcta	tcacccaage	tggagtgag	tggcatgata	tcagttcatt	170046347
gcaacctctg	cctcccggac	tcaagcgatt	ctcctcactc	agcatcccaa	170046397
gtatctggga	ctacaggcat	acaccactat	gccagctag	tgtatgtgtg	170046447
tgtgtgtgtg	tgtgtgtgtg	tgtgtgtgtg	tgtgttagta	gagacagggt	170046497
ttcaccatgt	tgcccagggt	ggtcctgaac	tccagagctc	aggcgatcca	170046547
cctgccgagg	cctcccaaag	tgctgggatt	acaggcatga	gccacagcgc	170046597
ctggccaatc	tttttagggat	aatttttagaa	cagtatacag	atattgagcc	170046647
aagagtcaaa	agagctgggt	tgcaattctg	gttggtgccat	ttatcagttg	170046697
tgtgaggtgg	gacaagtctc	tttttctccc	tagctttctc	tttcctcatt	170046747
tataaaataa	agaaatgaga	atgatagtgtg	tattaatttc	tgaggactgc	170046797
cagaacaaat	tactacaaac	tgggtggctt	aaaacaacaa	acattttatc	170046847
tcacatagtt	caggaggcta	gcagtttgaa	atcaagttct	tgacaaactc	170046897
ccctagagtc	taaagtctct	agagaaggat	tcctccttgc	ctcttccagc	170046947
ttttggtagc	tccagtgttc	tttggcttgt	ggcagcatca	ctccaatctc	170046997
agcctctagt	ttgtggtaat	gtattatgac	agtcttagga	aaataatata	170047047
tcagtatttg	gaaatgtttc	ttcatttgcc	acaatatgat	atcaaataaa	170047097
atacatccac	ttaaaagtcc	aggtatggat	acaccatttg	atttggaatg	170047147
ctagtgaatg	taaaggctta	ggtcaacttc	tctctgcagt	tccaaggagg	170047197
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tccctgggtca	ctggccacac	aaggacctgg	catctcccag	taaatgtgtt	170047297
cctctgcaac	ctgagccaca	aacctctctc	tcttttatct	ctttcctctt	170047347
tctaccttca	tatttggttg	gctattttta	gttcttctgc	agatatagtt	170047397
acactttaaa	tgacacacag	cctttaatta	cttacatgtt	gacttgaagc	170047447
aatgtctgtt	gctcaccttc	ttggaaatat	cagaagacaa	gaacactttt	170047497
acttctctct	ccttctccca	tccttctctc	tgtctactta	atctgtttat	170047547
catattctca	tttttacacc	atcaaggttt	ataatgctcc	cagaacatac	170047597
ctccttcaag	gtaaatggga	atggtaacct	ttggcctctc	cttgcccata	170047647
aggacaaccc	agtctcctgc	tctgcgtggg	ttcccaattt	ggccctaaga	170047697
cttttctgtt	tgtatgatca	gcaaaaggac	atcaaatact	ttccatcctc	170047747
caatgagcag	aacacattct	gtggtcagaa	gccttctcat	tacttctgat	170047797
ctcaaaggga	catccagagt	tgcccaaacc	caggccaacc	acccttccat	170047847
ttagccacag	cctgaagatc	ccaactatga	tcaacaaata	agactgactc	170047897
cagatcccac	tctgccaact	gcctaccta	taccagact	cttgagctg	170047947
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cagaatatct	tgtattttgt	agtctattat	agcaagcata	ataaacttat	170048047
ttgtttgaga	ccgagtctca	ctctgtcgcc	caggctgaag	tacagtggca	170048097
cgatctcagc	tactgaaac	ctctgcctcc	cgggtttaag	cgattctact	170048147
gcctcagcct	cctgagtagc	tgggattaca	ggcatgtgcc	accgtgcctg	170048197
gctaattttt	gtatttttag	ttgagacatg	gcttcccat	gttgaccagg	170048247
ctagcctoga	actcctgacc	tcaggtgatc	caccacctc	ggcctcccaa	170048297
agtgtctggga	ttacagggtg	gagccactgc	ccagccgata	aactttaaaa	170048347
ttactttttc	tattccatat	catagattct	gggaggaaac	aaggcccaat	170048397
ttgagtaaaa	gcaactgcat	ttagctggct	tgaacttctt	cagagaaaga	170048447
acaacataaa	atattcagct	catctgattt	tttaatgaca	tttccttttt	170048497
atttatattc	aattacacaa	gtaatacatg	aacagattct	ccctttttta	170048547
aaccatccct	tattctacag	atcaggtgaa	agtacttgtt	gctggcctgt	170048597
acttcccac	cccacttttg	tcccaggac	aaagtactat	caggatacta	170048647
gcattcagag	tgagcagatt	cctagtactg	acataaggag	gatcaccatc	170048697
taatttttaa	attttaaaaa	atgaacacaa	agtctattag	aggaatgaaa	170048747
tgaacctgct	ttgtaggtac	ataatatttc	tctctccaga	gagaaaggag	170048797
gagagcacac	ataagatagg	aagatgagag	ctacaataaa	tgagagaaga	170048847
gagaaactgt	cagaaatagc	agggcagaaa	gagggaaga	ggtgagaatg	170048897

FIG. 1.128



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agagagaggg	ggaggggagga	acagaggaag	atgcgaacaa	ggagagtcac	170048947
tcagttctga	ggcaagcact	tgattctccg	tggttcattt	gggtatccaa	170048997
gtaagttatt	tcctataatc	attggccttt	aggagtctgc	ttagctaatt	170049047
aacagtttgc	aaattgccaa	ttgttttttg	ccccgcattc	tccagagact	170049097
ttacactgca	aaggcagacc	acagcagccc	accttacact	tgagttgtgg	170049147
ccaaagcacc	atccccacca	gacaaagcca	gccccacagc	tgaccccggc	170049197
ctgtgagtgt	ctgaaaactg	gctgtaaaga	acattctgtc	tagttacttc	170049247
ctcagtaaac	tctggggctg	ggcactggag	gttttctgaa	aggaagtgtt	170049297
tggtgtctca	cacagccatg	tgcttagtat	attccatgca	gcactccact	170049347
gagccagtgc	ccttgaaatg	agcaagcact	gcagccatcc	tcctttattt	170049397
ccctcaaggc	aatatccaag	gattaaaaag	tcagagccgt	ctgcagattc	170049447
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ccagccccaa	acctctctcc	tgatccacgg	tactcctcct	gggatgtcca	170049547
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gtctccagca	aaattaacct	agcctatgtc	ccatgccctc	tggaactctgg	170049647
ctgctcgtca	atcactctta	aaaatccggg	ttctccttag	gcaatcattt	170049697
tgttttgatt	ttatgtgtaa	aaaaacctga	gtaaattttt	tttttttttg	170049747
agatggagtc	ttgctctgtt	gctcaggcta	gagtacagtg	gcatgatttc	170049797
tgctcactgc	aacctccgcc	ccccgggttc	aagcgattct	cctgcctcag	170049847
cctcttgagt	agctgggact	acaggtgccc	accaccatgc	ctggctaatt	170049897
tttgtatttt	tggtagagac	agggtttcat	catactggcc	aggctgggtc	170049947
caaactcctg	accttgatgat	ccacgcactt	cggcctccca	aagtaatcac	170049997
tgctgggatt	acagaagtga	gccaccgtgc	ctggccaaac	ctaagtaaat	170050047
gttttaaaat	tatactacta	acatagcata	caggctttag	actgttgggt	170050097
gcttttaagt	ttgcttactt	taaaagctag	agagaagatg	gttgaggtga	170050147
tcttgtctcc	ttcagtattc	actctgagcc	atgcctcctg	aggaagtttg	170050197
cttttagggga	ggcattgcta	tgttatacac	tctacgatgc	accagccctt	170050247
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ccttaggaaa	tagattttat	ctccttaact	cactttttac	atttgcaaaa	170050347
tggttaaatt	gtgactacct	cacatggatg	tcacatgatg	aaatgtaaga	170050397
atgtgtgtcc	ctggcatata	gtaaccactt	tcgccaaaga	ctgagttatc	170050447
caactacaga	cagagaacag	ctgggtggcct	aatcaaaggg	agatacaaaa	170050497
taacaatgcc	aagactggaa	aaggaagtgc	atcttaggat	ttccaagaga	170050547
aaaagaaata	tgactgtatt	ataataggta	tatttattaa	gctcttacca	170050597
tgtgccaaag	aaagtctctt	atatacatga	tatacttcat	atacattatt	170050647
tcatttagtc	ctcatggcta	ccaggtgagc	accattattt	ttccatttta	170050697
cagatgaggg	acagagaagt	taagccactt	acctaggaag	ggcagtccta	170050747
gttaagaagc	tgggattcaa	atccaagagg	ctggattcca	gacctcaggg	170050797
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cccaactaag	ggcaagactg	tgacacagag	gtcactaatc	agaatgaaag	170050897
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cacagctgca	attctcaaag	gatggactaa	gccatgtcac	ccctccagat	170051197
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tccagggcta	accagttagc	atggaaatgg	gacacccaag	aacaagagga	170051497

FIG. 1.129

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tagaaagaag	ggaaggggtgg	aaagaaggaa	ggaagaaagg	gtgggagggga	170051547
gggaagagtg	gtagtttttg	aaggaaggag	ggaatcagag	ctaaagataa	170051597
tacatgatat	gagtcagtgt	tcaatgtccc	tgaagattag	gggaatcaag	170051647
ctttgcttcc	aggagaatta	acacaggaga	gccaacagag	atgtggaaat	170051697
ttaggaagtc	agaggagaca	ttctttcatt	cattcattcg	ttcattcatt	170051747
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gtgttcagcc	tgacacaaat	actctgtatg	catgggtcata	tgtcccttga	170051947
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aaactgaggc	ttagggaggt	caaataactt	gcccagtaa	aacaactagt	170052047
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agagaagagg	aaaaaagtca	tttcaaacag	aaagaacagg	ttgtgcattc	170052247
aaaggtgaat	tgagaggaga	gaaaagcatg	ttcaggaaaa	gacaagacat	170052297
ttgtggccct	gggagctgag	atatgccctc	gggaaggctg	gagatgatgt	170052347
caaagacgaa	gattggacaa	taatgcccct	caggccagga	gcccccttcc	170052397
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tcaaatacagg	ccccctctt	attaaacatt	tcaaagggtt	tctgttctac	170052497
ttaaaaccta	aaacccttct	tttgtatgca	aggcctgaac	agcctgcctt	170052547
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gtgggttatgt	ctgctctact	cacacacatc	cctactgcc	cgcacgggtgc	170052647
ccagcacata	gtaggtcctc	agtaggggtg	tgaatgaatg	aacaaatcac	170052697
tgatgaatga	cggccctaag	cagggatttt	tctccaaagc	ttcctcacac	170052747
cttggaaatgc	atttgggggc	ccaacacaaa	ggtttccaac	ttcaacagca	170052797
aaaactccac	ctcccacaca	atgtagagtt	acttcttgct	catttccagt	170052847
gggtttctgt	ctttctccac	agcctgactc	cttctcaaaa	tctctctatt	170052897
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gaaatctcct	gatatttcag	agaatatccc	agaatatagat	aaagttccat	170053047
ctgacaaata	gatgctcagt	aaaatctggg	gagtgaatgg	attaatgcaa	170053097
aaactaatta	tcatgctggt	catggcaagg	gatatgataa	ttttttcaag	170053147
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ccaggtggca	ttcagtagac	atagactaag	cctcaacccc	agccctcagg	170053247
cacatcagtg	ccctctctag	gctctctctc	accaacttta	gaattgaatt	170053297
acatcagttg	tttccagatg	gtgatctgca	gaattccttt	aaagaccacc	170053347
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ccaagcatct	gattgctttc	atctgtttta	catacttagc	ttctgtgcac	170053447
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tctctgttcc	catagctgcc	acaggctaaa	taagttgagg	gggtattgta	170053847
aaaccaaga	tgagatcact	gagcctctgg	tatcaaaaag	gtgtatttca	170053897
cagaatgttt	agttggacga	gagcttgaag	agcatggaaa	cgatctggta	170053947
tcattctggg	caaagaccag	aatttagacc	ccagttctgc	catttgctga	170053997
ctaatagact	tgggcaaaat	acttaacttt	cctgagagtt	agtttcctca	170054047
tctataaagt	ggggtaatat	aaccacactt	gcaggatact	ggtaggatta	170054097

FIG. 1.130



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gttgaaataa	attgtaggag	aacatttggc	tcagtgcata	gcctatataa	170054147
atactccaca	agggcacaga	gagggaaatga	cttgccctagg	atctcctcct	170054197
ggaaatcaca	caacaattcc	actagtatca	tgtggccccc	aggcagctgg	170054247
tgggcacaa	cacactgggt	cagcattgcc	atgggtccaag	aggcttctgg	170054297
tgcccagggg	accagcaggg	tcccctgagc	gttcctcctc	agctcccaac	170054347
acttccctcc	aggcaccagt	atgcagggca	aggtcctgga	gggggcgccg	170054397
aaacaccact	cgagatcctc	actctcagga	attcaatata	gaaaacacat	170054447
taagacctgt	ttacatggaa	ctgctgttta	taattattgt	tccctatggg	170054497
atattcccca	ctgcttcctc	caatcctcct	ttaaactgct	caactaatag	170054547
agttttcctg	gcttccccag	ggagacattc	acagatgcta	atagagacat	170054597
aattcaaaaa	ttgcttgata	tacatgccct	caattttccc	caagaaccac	170054647
ctaagtaaag	agccccagac	atgcaacaca	ttcattggcc	agatgcaatt	170054697
taacatgcgt	gggattaaat	atacaggcta	ctacagccag	gttgtcatca	170054747
agcagcagca	ggcatggcat	tttatcctaa	ggtaccacca	cggccaaatg	170054797
caacaggaaa	gaagcaggct	gctgggtggg	acccctggaa	gatccccctc	170054847
tctgtaattt	ccactgcaag	cttttcccag	gccttttcag	gcaaagcggg	170054897
gagttttgaa	aataaatccc	ccaggcttgg	agaagcaaag	aatcaatgct	170054947
aagcagctcc	ggaaataata	gcttccatct	ctctgatata	taaagaggat	170054997
aaggaaggca	gaaagaaggg	gcatgatatt	atgagattgc	aacaatacat	170055047
tgcaacatta	cattaaagaa	ttacagaaag	caagatctag	cttcagatgc	170055097
cagttcatgc	acttactccc	tgtgtgaccc	tgggaatcac	ttaagctgtc	170055147
tgagacttag	cttgtcta	gacaaaactg	ggataactaa	atcacctccc	170055197
aggattgttg	ggaaggtaaa	tggagattga	caaagtgtga	cacacttagt	170055247
atgtctttac	atagtaggta	ttcaataaac	cttctatat	atcttctcct	170055297
tctgaaaatc	tgaatatggg	gagcatggat	atgcttatat	gttggttaaa	170055347
caaatgcatg	aatgttgagc	aaatcagaaa	atactaaaat	tagaagacta	170055397
aaaggagtaa	actaggaccg	attaaaagaa	gtttgccttc	ccaaaaactc	170055447
ataaaacttaa	tgaaacttgc	tatctccaga	ggaaattaat	ataaatttaa	170055497
aatagcatag	gtttgagatg	actttagcgg	agtttctgga	gaatagatcc	170055547
atcactgggt	aataaactaa	aaatatagag	agaactgccc	aaggttacac	170055597
gagtagaata	ttgggtgtccc	caccactcct	ttttattgca	gaggggaattg	170055647
acattcaggg	aatggaaatg	cccagcccag	aattggggat	gtgggtctggg	170055697
aaccaggtc	tcccatccca	ctccctcgcc	ctctcacccc	ctcccgtctg	170055747
tcagtgttct	ttgtcctctg	ctggcatccc	tggggacggg	ccagccccca	170055797
tccccccgac	acacacacat	tgtcccttca	agatggagcc	aggctgacac	170055847
cacgtagaat	gacctggaag	ccccactca	gtctaccagt	cctccctcct	170055897
cacacaggaa	tagatgggag	ggaaatgaaa	taagctgcca	tctgctgtgc	170055947
atcctctgtg	tgccatgctc	tgggtaccca	tctaactcct	gtgaagaccc	170055997
tgagaagtga	gtgttcttca	cagactaggg	aacaccagaa	ggcaggtgaa	170056047
gaacgtacag	aagctacaga	gtgcacaggt	gacaggtatg	agagccaagc	170056097
cattcaaact	ccctgggtat	aggacccagc	tcttcccacg	tctctgcctt	170056147
taccgaatca	aacacctgag	cacggaagac	cctccatcaa	catgaactgc	170056197
tttgaattga	catgaacaag	cttcaatcaa	actataaatg	ctgaaatttt	170056247
tcaattatag	aaagtatttg	aaagatccca	taaattcccc	tgtcatatca	170056297
cgtgagctgc	atttactgca	gcagacactt	tttatctcgg	gotttgaggga	170056347
aggattagca	agaagaaagt	ggaggggggtc	tgaggaaggg	ctggcagcct	170056397
agaggaggac	agcagcaaga	agcaggctgg	aggcagttct	gtgctgccgg	170056447
ccttcatggg	tgtggccttt	ggacagcacc	ttagcaggaa	tgtggtggag	170056497
agcagcccca	ttcactccag	aggagagcct	caaactcttc	aggcagatct	170056547
agcctaggta	gaatcttggc	ctggcccttc	cgggatgaca	ggtgccattg	170056597
cccaagaatg	gggaaaaggc	tgaagtgtc	cagccaaaga	ccccaattta	170056647
tcttcaggac	aattttcact	ggaaaccttg	cctcaccact	gccacttttt	170056697

FIG. 1.131

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tcagaagtaa	ttagaatgct	aatctataag	aaagatgact	attaaaaata	170056747
aattaataat	agataataca	ttttggctta	caattttgaa	taatatagcc	170056797
atcccatctt	aaagtaaaaa	ttcatatatt	tttaataagc	ctgagacatg	170056847
ttttccaatg	aaccacagat	ggttcatttt	tattatccta	taaagagaca	170056897
ttatgggcaa	gtgtttttta	aaatggtaaa	acagaacctt	agagcagctc	170056947
tcttttgaag	atctctaagc	actttctaag	catcaggacc	cccttctgtc	170056997
atcacagaga	ctgaaatgag	gagatggctc	ctgtcacccc	ctcactcacc	170057047
agtgagcccc	agaccttcac	ccctgatcag	atggaagcag	tgtggcatga	170057097
ttacagttca	tatttcaact	ctgccactca	atgactaata	gccaagcact	170057147
aataatgcag	aaaatgtaaa	tttaaaaaat	aatcttcctg	agattgggtta	170057197
tgaaatgcac	tcaacacagc	accatccaca	gagaggttct	ttttaattgc	170057247
tcttttcttt	cctctcgaca	cccagaatca	caaagcatgc	ctgaaagcgt	170057297
cacacatata	tgtctgtgac	cataacatgg	cattgcacat	gcaaaggaaa	170057347
taaatagggtg	ttacccatgt	gacaaagggtc	catgagctct	gtccgcaaaa	170057397
agctgttgag	tttaaagaac	aaataattct	gaaaaatctt	ccaggagatg	170057447
aaatttgtag	aactcaaggg	cagtaaacta	gtgtctttcc	aaggacttgt	170057497
catagcttta	ttgacttaca	atagccaaag	ataagtcagt	attaatcaaa	170057547
ccatttctct	agaaaaacct	catcatcact	ggggccaggg	cagagaagtg	170057597
tgacacagct	ctctccagct	tcccacttcc	acagcatggg	tccaccatcc	170057647
acccaattgc	taaagcctgg	atagtcttcc	ttgtcacctc	ccgatcccct	170057697
tctctaacac	ccatcccccg	gccacccaac	atcagcaagt	ctgggtggttt	170057747
ctctctgtca	cagagattca	agatcttccc	ctcatctgtc	tgtttcaaag	170057797
ttaacatcat	ctctcatcca	gacagttgca	acactctcct	agcaggctcct	170057847
tctgcatcta	ttttttaatt	aaatttttaa	agataaaaac	attcctctaa	170057897
atagaatctg	ctccagaacc	cagattaaaa	aagaacgaga	aggggggaaag	170057947
aagattaggg	catcccagaa	gctccctatt	tgccccattt	gattcattac	170057997
tccccaagg	taactgctat	cctgacttct	agcaacactg	gttaatttcc	170058047
gttgattttg	cactgtatat	tcatccgtgc	tggttgacac	tgtcatactt	170058097
gattcattca	cattgctgtg	taacatttca	ttgtgtgact	attttaacat	170058147
ccattttact	gttgaacact	tgggtaaact	tctgctttga	ggctattata	170058197
aacttgacac	ttctgcttcc	cattgcttta	aagataagag	cccaagtcct	170058247
tgtcagacag	gtgaatgggtc	cacacagtta	gcacccatag	ctgggcgcgg	170058297
tagctcacgc	ctgtaatccc	agcactttgg	gaggccaagg	cgggtggatc	170058347
atgaggtcag	gagatcgaga	ccatcctggc	caacatgatg	aaaccccgtc	170058397
tctactaaaa	atacaaaaat	tagccagggtg	tggtggcatg	cgcctgtaat	170058447
cccagctact	tggaaggctg	aggcaggaga	attgttcgaa	ccagggatcc	170058497
gaaggttgca	gtgagccgag	attgcaccac	tacactccag	cctgggacag	170058547
agcaagactc	tgtctcaaaa	aaaaaaaaaa	aagccaggct	ttttctcatc	170058597
tcataatctt	tgcgcatgct	gttccctctt	cctgaaactg	ctttcctacc	170058647
acttctcacc	tttatgcttc	acctcgtagt	gttcatagac	tctccttccct	170058697
tcctaactta	aaagaggctc	cttctgggtt	ttccttcata	cacttccctc	170058747
actcttttcc	ttcactgcac	taaagatgat	ttctaattgc	atagtcattg	170058797
atgccagtat	ttgtttattg	tgtcattcct	gctgaacaga	ggatgggcct	170058847
gacttatttg	ggaccatggt	gctgatgcct	ggacctaagc	ctggcacaga	170058897
gtaggagctc	aacaaatttg	ttaaatgagt	ggctgaatgg	ccatactctc	170058947
aaaggaccca	cagtctagga	gagacagaag	aatctttgtc	tttttgtctt	170058997
gcagtgggat	ggaagctgca	gggaggggtc	ttgtcacatt	gatactgtct	170059047
ggggaagaca	gaaaaacttc	agtttcagag	gaggtagccc	ttgaaacgag	170059097
atgtgagaga	gggcagcaca	ttgtacaact	ccatgggcac	catgcacatt	170059147
gtagtccaga	taaacagagc	cccttgagga	tatgtgaggc	atgggataga	170059197
ctcagagaaa	cccaggaaat	aacccttcca	ggcatctgac	atgcaaagat	170059247
gtggaagtgt	caaccaggaa	gtcatgttgg	gggaacagca	agtatttaca	170059297

FIG. 1.132

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gaaagtgact	gtgtgtgtct	gtgtaggagg	gtgactttgt	ataggagaga	170059347
taaaacctgt	gagctaataca	aggagaagat	cataaaaagac	cttcataaag	170059397
agcatggcct	ttttcctgca	agcagtgagg	agccattgaa	ggcttttagca	170059447
taaggacagt	cagatgtact	tccctagaat	gcacatttcc	ttctgctcca	170059497
gaacttctgc	acaggaggct	cctaaaagct	ctccccatcc	tcctgtaca	170059547
cgtagaatct	gcctctgtct	ctctttctct	ctcctcctcc	tcctccatct	170059597
cctcctcctc	ctcctctccc	tctctctcgc	tgtctcacac	acacatacac	170059647
acacactcct	tccttcctat	ctagtccagat	tcactcctt	gggatttcag	170059697
gcccaccgtc	actcctcagg	gaagcctgcc	ctgaatgcct	gcactacacc	170059747
agggccctt	tcccctgccc	ccatcccaga	gcaccaaata	gctttccctt	170059797
gcagcacttc	tcacagctgt	catttttatgt	ttgtgtctgt	gattcttagg	170059847
ttaagtccct	catgcaccaa	atcataagat	ctgggaacaa	ggaccacacc	170059897
tgtcctgttc	atcactgtaa	tcatacact	gcctgccaaa	gtgccttgca	170059947
catattagat	acttagtagt	tatgtgttcc	atgaatgact	ctttaagaga	170059997
tcttctagct	gttcttgcaa	agaaccatt	ggtaagggtg	aacctacagg	170060047
ctgatacttt	gcactagtct	caggaagaga	tggtagtac	atgaaattga	170060097
gtcccccaga	ggttaatgcc	cagtgcocca	gctaggaaac	gtccaaggag	170060147
gcaatttgaa	ccccatctgt	ctggctgcag	agcctagccc	tctaattgcat	170060197
tcaggggtcc	tagctcctcg	aggatgccac	tgtgccgtga	acttctttct	170060247
gacctcatg	gctcccagca	cagcatccac	actcagaagt	gcaagatgaa	170060297
tgtttgcaga	taatgaacat	aaagctctca	ggaaccctca	tctcctgaga	170060347
atctgctttg	gccccacag	caggtctggg	tgtggacctt	ccccaatggc	170060397
cttgggaaat	tatcaacatc	tccccattag	ctgttgcaat	attaaattgt	170060447
gtgactggaa	atgaatgaat	aatcccatgg	gcaagtgagg	gagaccaagc	170060497
agcagggatt	taataacaag	tctgcccctt	tctccaagca	gaaggtcttc	170060547
ctaattaaat	attaaaaatc	tatccataca	agcaagagcg	aaaaattgca	170060597
ttttcagcag	tgcagctttg	agatgctgcc	tcagaagacc	caagagctgt	170060647
gggaatgccc	tctccaggac	ctagaagagg	gggccagaaa	accgccatgt	170060697
ggtaagcact	gocgggtacc	cgggtatcac	aggccttgcc	acattcaatc	170060747
ctcatgggga	caatgagaca	ggggtagat	cacagccact	gtctaaatga	170060797
gcaaactgag	gcttagagag	ggtagtgac	ttaccaagg	ccaccaggta	170060847
tcaagtggca	aagttgggat	cttaaccag	ttctatgtgg	ctataaagtt	170060897
catggaatag	aatgctgcag	ttaagaacat	gggctttggc	atcaagcaga	170060947
cctgtatttg	agccccacct	ctgctgttta	ttaactgtgg	ccctgggcag	170060997
atgaccttac	atccttaagt	ctctagttct	ttgtctttaa	aagggtggca	170061047
gaatgtacct	cactggtttt	aggaaggta	catgagatag	tgcacatgaa	170061097
gccctaggca	tgggaaaatt	cttctaaaat	gtcagctgcc	attctgatca	170061147
ctgcaagacc	cccacccccca	atactcccaa	ttgtaccacc	ccacccact	170061197
caccagtgtc	tcagaaatgc	ctcctccaga	aggaaggcat	cctgtctaac	170061247
ccactgcttc	tagccaagct	gtctttcttc	agaaggtaga	aaaagattgt	170061297
tagtcattgt	ttaatcttta	ttgagtatat	accgccacac	caattgcact	170061347
gccattcatt	atctcattta	aatctgacaa	gagccttgta	aagtagggat	170061397
tattcccacc	atttcccaga	tgttgaaact	gaaattgata	aacacgacat	170061447
gttgccatgg	ctacatgaag	atctccaage	cggaggatct	ccaccctcac	170061497
ctgcctagct	tcccagacct	ctctgcagaa	aagggactga	ccccaagac	170061547
agccctggcc	tctgggctcc	accccttcca	cattcatccc	agggccgctg	170061597
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ctttatgaat	ttcttcatat	acaaaaattg	tacttactca	ttgcagcaaa	170061697
tttagaaaat	acacataagc	aaaaaagaac	gtaacagcca	tccataaacc	170061747
taactctcag	agatcaccac	tattaaaatg	tttattatct	aagagagaga	170061797
tgatatagac	aaagatgaga	cagattgaca	cagagaagat	gggtacatga	170061847
tagatatattt	ctgtttttata	acccttgctt	tttcttgcac	ttctaggaat	170061897

FIG. 1.133

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ttttctgaga	actaatctga	aatctgcaca	gggtccccac	gtctcggatc	170061947
ctcatcccat	tgctctccac	cttcttgaac	tttgcttcaa	taattatcac	170061997
acctcctttg	catgtttaat	cttccccctt	ttaatgacaa	ctaccaagac	170062047
ctgtttccta	gtgcagggtc	atgaggtaac	taaaataaga	attaaattgc	170062097
tctgtgaaaa	aaaaaaaaaa	aaaaaaaaag	tttacagtcc	caggagattt	170062147
tctccagcct	tatcatattg	ttgataccat	agggtcagtt	ctgaagctga	170062197
gccccactca	gccctaagct	ttctaaaggg	gaattgccag	gtccccctgg	170062247
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aaggagaaac	acacttcctt	ccccttccca	tgacttgtag	ggagtctagg	170062347
gtctcaggcc	tatgtcacag	gccctcgatt	gccatgagtc	agcaaggaga	170062397
ggaaggacac	gaagccagca	ggcagagagc	tggccccaca	gagccatcct	170062447
ccgtgaagcc	ccagcaaacg	ggagggacca	agtttgtttc	agttttccta	170062497
aaaataacaa	gactgtattt	tctttgctgt	tggctgtccc	taaaactggt	170062547
aacatgggtt	cccagcctgg	cacaatgtgg	tccatgcctg	cctcccatat	170062597
acctgcctcc	cacccctctg	ggccttgttc	ccttcatccc	agcctccaga	170062647
cacacctgcc	tccgtgtcatc	tctagagcag	gcttatcttg	ttctcctgtg	170062697
ggctccttgt	agaggatggt	ccctctgccc	agaacgctct	ccctcactca	170062747
tcacctgttg	gtcccccttc	cctccttcca	ggctctgtgt	caaggccacc	170062797
acagagaagc	cttgcggtta	tgtttagttc	ttcctgccta	agttcgcctg	170062847
gtaaccata	cctttcctcc	atcataattt	gctcaactgt	aatcaaaccat	170062897
tattttttaa	aaatcattcc	agcctgggaa	acagtggaga	acccatctct	170062947
acaaaataaa	aaataaaaat	tagcttggca	ttgtggcatc	tgcccggtgt	170062997
ccctgctact	caggaggctg	agatgaaagg	atcacttgag	cctgggaggt	170063047
tggggctgtg	gtaagccgtg	attgccccat	tgactcccat	tctaggcaac	170063097
agagtggagc	cctgtctcaa	aaaaaatatt	attcatttaa	tatctgttgc	170063147
caccacagga	ctgatccctc	tgtgaggggca	gagattgttc	atgcatggaa	170063197
ttgtgattta	taagcactgg	ctctggagcc	agggtgcctg	agcacggagc	170063247
cagctgtgcc	ctgcgggaca	cctgtggcac	acttcactcc	tgggacacct	170063297
gggacacgca	cacaatagaa	atgttcacat	tttactaggc	aatgccagtc	170063347
acatagtcc	acctaatttc	aaaagggtaa	aaggtaacac	caacacgcac	170063397
caggaaggag	gaggaccaga	aattgttggt	gacaagcaca	aatgaccacc	170063447
ccaatataat	attttgtttg	gaaggcattt	tattccacaa	aaacaacatt	170063497
acaataaaca	aaacaacaaa	acactgggtg	cagtagaacc	aactttccag	170063547
acctatctgc	acagcacaac	cattatccca	ctcaaatgt	catgttttta	170063597
ccaaaacat	taaaatttta	aaagcaattc	aaaccatag	cttaaaaaat	170063647
gttccaacca	gtaataaaaag	gaaaagtgtg	cctcctcctc	ccaacttccc	170063697
tacccacaaa	tcgcaagata	ttatccttat	aggcgaaaag	ggtttcagga	170063747
tttgagatgc	aggctgggag	gtctgagaag	acttcctata	gaagacatga	170063797
cttcaaactc	tttcttgtat	gtgagattta	attttcaaag	actcctctga	170063847
tccaacttaa	gctttatggt	aaatcacctt	gggacttaaa	tgatgagaag	170063897
cactgctatc	tcacagttag	aaattcagaa	gggctgggag	ttccaagtca	170063947
gagctctgat	ctggaaagtt	ccatcaaagc	gtcactccag	gcttagcggt	170063997
tgccacccac	cactcgtcag	actaaacagc	ctcagagccc	tgtgacctgc	170064047
taatgtattc	acaaactaac	tcagctaatt	aatcccagct	cattcatcct	170064097
ctcaaactat	gcaagtcttc	cagctggccc	tccggcttgc	tgccctggct	170064147
aatggagtgt	tacgtggact	ctctgtagg	tgcaccttac	tgcagccaa	170064197
gcaaaggcac	tcattaagaa	gctgagcccc	agggtcctcc	catgagtggg	170064247
gaggaaactc	atgagtgcct	tctatatgcc	agcgctctat	ctgcaggggt	170064297
tcttttgata	gcagcagact	gagagatgat	gttactgtcc	cctttttcct	170064347
gttggttgga	actgagactc	agaggatgga	agtgacttgc	tcaggtccac	170064397
cacctcttca	gctgtggagc	tgcgacagga	gcctttgttt	gacttcaaag	170064447
ctcaccatca	ctcctctctc	actgatgctc	aagtgggcta	tcacctcgcc	170064497

FIG. 1.134

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tttcctgagc	cttccttcgc	tatcctaaaa	cagcgctccc	cgaaatcacc	170064547
actaaagaac	ttattcatgt	aaccaaacac	cagcgggtcc	cctaaaaacc	170064597
tatggaaata	aaaattaaaa	ataaaaaacag	tgccctcccat	gacccatgtc	170064647
tctccagtcc	cataactctg	ctctatcttc	attcacagct	ccatccccac	170064697
ctttatgtct	tttgttcact	gctttatccc	cagtgcctag	aagagtgtct	170064747
ggcacctagt	agacactcag	taagtatttg	tcgaatgagt	taataagggt	170064797
gtgaaaagaa	cgtagatta	ctggaaggat	tcatctgagt	ttaattctgc	170064847
tatgctggga	atccagtgtg	cggccttgga	tgaagccagt	tcctccctg	170064897
ggccccagta	gccacatctg	tacatttaga	gggcaggaga	aaagccacac	170064947
gctctgtgac	ttatacaact	tggtgcccag	agtggagggt	gctttgatgc	170064997
tcagaaaaaa	gaaacaaaca	tggaaatgct	aaatgggtgg	cagagagctt	170065047
gagggaggaa	ggagatgggg	aggggtactct	tgaaactgtt	tggtgtcttc	170065097
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tgtattagt	gaatttggtc	cctgacttgt	tatagagaca	caattacaaa	170065197
gacacaagag	tgggcccagc	agagaccott	aggggtggtcc	cttgagggttc	170065247
caaagcatct	gcccatacaag	cagatgatgt	gattagtctc	tgtgaccca	170065297
aggatgctc	ctgaaattgc	tgattcaatt	tctcctaata	aaataggaac	170065347
aataattagc	taataagaaa	tcaacaatta	aagctatgag	agaattaagt	170065397
gagatcatgt	aagcaaagta	catgtcacag	tgctctgcaa	ataggcagtg	170065447
ctcagaagt	tcaccttttc	tctttcttct	ctgagcctcc	gtcttctctt	170065497
cggtaaaatg	agaataatat	tatgcatacc	tcacaggggt	taagcaatgt	170065547
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gggactgcgg	tttaattggt	gccgtgtggg	aatgtggggc	tggcatggcc	170065947
ataatttcag	atttctaaag	gaaagccaaa	agttcatatt	tttatgtgaa	170065997
ataaatgttg	ataaagttca	cacttaaatg	aagtgaacaa	gaccagggct	170066047
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tcacttgagg	ccaggagtcc	aaggctagtc	tgggcaacac	agtgagaccc	170066147
catctctacc	aaaaaaaaat	taatttataa	aataaaaagaa	gtgaaacaac	170066197
agtaccctgt	gggctgccag	attgtgattt	ctgaactaaa	ctgtcagatt	170066247
acaaagttac	ccgctaaatt	agccaaatac	ttccagata	ttccctgggc	170066297
cactgtctcg	ggactcttaa	tatatcttcc	aattagttcc	ttttagtgtc	170066347
acatacacac	ttttagcaaa	taatgagcac	ttactagtca	ctttctatgt	170066397
gcaaagcaga	tattagacat	cacagaggga	gtgagatacc	gaaaacaaaa	170066447
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atatgaaaac	tgtgacaccc	aaaggtagat	tttgatacct	gctgggtgat	170066547
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gtgctctgca	aataggcagt	gtcagaagt	gtcacctttt	ctctttcttc	170066947
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ctcacagggg	ttaagcaatg	tgaaagtact	ctgtaaaagta	taaggctgaa	170067047
atgtactggg	ctcagaattg	gggaatcgtc	tggaaaggta	gaccagggcc	170067097

FIG. 1.135

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ctagcgtgga	ctcttcagcg	ccagcaggaa	aatctagget	ctgtcttgaa	170067147
ggttcctcag	caggaagggtg	gggggttgtt	gtgggggtgaa	tctgatggaa	170067197
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tctcctgccca	tacaaccttc	ttttttattta	aaatagattt	aagcaggata	170067347
gagccccctc	ccccaccatc	aaggctgttt	ccttgtaggt	gggggggatgc	170067397
cttcatggta	atgatgtaga	ccctgagaca	atatagagag	gcagcagggc	170067447
ttggaaacag	gcagtatttc	ctctttttat	gatggtttca	ttttacattt	170067497
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tgtctgattt	gcttctaaat	gagacagaac	tattatcgcc	ataaagttgc	170067647
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tcagttgtta	tgtctgttca	ctaattgttc	aggccctatg	cttctgggtg	170068097
ccaccaccca	cagacccctt	gttctgttcc	acggactgag	atgatcaaca	170068147
gtctttcatc	cagagggttg	tgtttgctgg	tggccattac	ctttaacata	170068197
aaacgatcat	atttacttta	tcctattcat	gtccaacctc	aactgacaat	170068247
tgagttgtgt	ctctgacaat	aaatagcaga	aaaaggaaat	cttcctatac	170068297
tgaagagaaa	cacaattaat	taactagatc	catcaggaaa	ggtacaatca	170068347
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tttgagcacc	tactatgcat	gtagagcatc	ttacatacct	tatctcactt	170068497
agattttacag	ctgcaagggtg	ggtatgattc	tagcttgaat	tagtctaata	170068547
accatatacc	tcctaggggc	agttagatga	ttagatcaat	tctaaaacta	170068597
ttaccatgct	ctctgagctc	accaagacag	gcagttaata	caaggataca	170068647
ttaataccga	atccagcaaa	agctcacatg	gccagcttcc	attatgttcc	170068697
tattttgtgat	tattctgtat	caagcacaga	aatgtatgtt	cacacgaaca	170068747
acaaagaagg	ggtttatttag	tgtggattac	agggcctaag	cctaccctct	170068797
gaaactgggt	ttggagtctt	tagcacgctt	gtttgggaca	gttaaacatg	170068847
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cgtgcttccc	aaagtatgat	cacttcattt	caacaacttc	acactaacag	170068947
cctgaactgg	gctgtgaagg	gaatatttag	accaaggaaa	ctggaaaact	170068997
gtatcaatca	ggcttttcca	ccctccccaa	gagccagttg	tcagatatct	170069047
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caaaggagaa	acagtgggaa	gtttctccac	tgccacctga	attagatgag	170069597
aaagagttgt	ctactgaaat	acactagctg	gtggcaggat	tgggacgtca	170069647
tttgactaat	tgccctcctag	agctgcagag	actgctggaa	ctacctaagt	170069697

FIG. 1.136

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aaatcatcaa	aaaaaaaaaa	aaaaaaaaatc	atcccagggc	actttttcca	170069747
gacaaaaagg	tccacttaaa	acatcctcta	gagatctgtg	cctgaagctg	170069797
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ttctctagt	ctggaatcta	gataattcct	ttcccagccg	tttgtttctt	170069997
caatcttgga	aaatatctgg	atgaatgtaa	cactgtcaca	cacaaacaga	170070047
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ttgatataatt	tcactcattt	ttthaaaatg	ttcatttatt	agctctthtaa	170072297

FIG. 1.137



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atatacgttcc	attatcatta	tttatctctt	tcttttctga	gactccaatt	170072347
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cagataaatc	caaacaggga	ctgagctgtt	ttcatgcagg	ctgccttggt	170073197
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tatatatggg	acatgctgta	tgtgctaaac	accaaattca	ttgataacag	170073597
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cttttctttt	tctgcatctg	gttactaata	aagcttaatg	ggggaagaaa	170074847
gaatcaaaaa	ctttagtagt	gtaagctcca	agagaacaga	gaacagagct	170074897

FIG. 1.138



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gttttattca	ctgacttgta	cctagtagat	acttcattga	cagttattgg	170074947
gtggagtgag	caaacaaata	atcctacaag	atatgcagtt	tccaatcaca	170074997
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caagctcatg	ttttgtaatt	agtcttctca	tgaccagct	ttctgtgtcc	170075547
tttgtaaca	agccccacat	atatagaaac	agttggaaat	gttcttttag	170075597
agacaagtta	caggaaaagc	tttgctcccc	gtaagaaatg	gttacgtttt	170075647
ccttttacag	acatttgtaa	aaactcagag	cccatttgca	gctcaagtgt	170075697
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ccaggggtga	acaacaggac	atcctagagg	ctgtggctgc	ccagagggga	170076047
cagccggtgt	tcagctctag	caggctgctg	aagtgtctga	atttgagacc	170076097
aaaattgtca	gataatccca	ttttccaaga	caaatcagac	atccagattt	170076147
gtacatggat	ctctcatctt	ttaacatgga	caactaatte	caaaataatt	170076197
aagatacatt	ttacaggtca	aacaagacct	atctttgggc	cacactcaag	170076247
ccgaggatca	ctattttgta	acctcaaagc	tagacggatg	gccgggtgca	170076297
gtggctcatg	tctgtaattc	cagcactttg	gaaggccaag	gtgggcagat	170076347
cacctgaggt	cagaaacttg	agaccagcct	ggctaacgtg	gtgaaaaccc	170076397
gtttctacta	aaaataaaaa	aaaattagcc	gggcatggtg	gggcacacct	170076447
gtaatcccag	ctactcagga	ggctgaggca	ggagaattgc	ttgaaccogg	170076497
gaggtggagg	ttgcagttag	ccgagatcac	accattgcac	tccagcttgg	170076547
gcaacaagag	caaaaatcca	tcttaaaaaa	aaaaaaaaagc	tagatgggta	170076597
agtataaagt	ccaaatcaga	gacaccatga	gggaggcact	attggccagt	170076647
ccagggagga	gatggtcatg	gtcacgggtcc	tgagcctgac	agaggggtca	170076697
cctcactggc	gagaagaccc	aaggtgtgag	tcctcccact	gctcacagtc	170076747
caggtctaac	tggtacacaa	gcacacagct	tcgtaggagc	atgtgtgctg	170076797
caaggctggc	tacaagcgag	tttgcaattt	gtgcttgagg	aaagcagaat	170076847
ccactgtggg	gacatgtgga	aaccagatat	gatgaaaggg	gcctggactg	170076897
gctggattct	aggtccagat	atgtcaccca	ttgctcaacg	acttaggact	170076947
cagacaaagc	cagttagtga	gaaggtttag	aagagatctc	ctatgctaga	170076997
atagcttagc	attggctgga	tgtgtttaac	agatacagaa	accactgaa	170077047
agtagctaga	tgctctgcat	aatgacgttt	ccatcagcaa	cacaacatac	170077097
acaattgtgg	tcccataaga	ttataacaga	gctaaaaaat	tcctattgcc	170077147
cagtgcattc	ttgaggttcc	tgaccctgtg	tgggctcagg	ctaactgtgtg	170077197
tggttgtgtc	ttcatttgta	attttaaaaa	aagggtttta	aaagaaaaga	170077247
aatgaaaata	aaaaattttt	aaatagagaa	aaagcttata	aaataagaaa	170077297
ataaagaaaa	atatttttgt	acagctaggc	agtgtgaatt	ttaagctaag	170077347
cgttatcaca	aaagagtcca	aaagtttgaa	aaaaaaccaa	atagtttgta	170077397
aaataaagtt	agagtaagct	aaggtttaatt	tcttattgaa	aaaaaaattt	170077447
attaatttag	tatagcccta	agcataaagt	atgtataaag	cctacctcat	170077497

FIG. 1.139

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gttttagtaat	atcccaggcc	ttcacactca	ctcaccatca	ctcactgact	170077547
cacccagagc	aacttccagt	cctgtaactt	ccattcatgg	taagtgcctt	170077597
aatagttgta	ccatttttta	tttttttacac	cttagtttta	ttgtaccttc	170077647
tctaaattta	gtatgtttgg	acacacaaat	acttaaaata	cttaccattg	170077697
tgttacaatt	gcctacagta	ttcagtacaa	taacacactg	tacaggttta	170077747
tagcctagga	gcaaaaggcc	ataccataca	gcctaggtgt	gtagcagggc	170077797
taccccatct	aggtttgct	gagtatactc	cacgatgttc	acacgatgac	170077847
aaaactgcct	aacaacacat	ttctcagagc	gtatccctgt	tggttaagcga	170077897
cacatgactg	aataagcaaa	tgtgcagtga	ttgtgcattt	tttttctctga	170077947
gagagtctaa	acccctcatt	ccacactcag	aagagtctat	gatcccaaaa	170077997
cattaaggat	cacttaatca	aaatcatcta	ctattcaatc	tgagaatttc	170078047
ctgtgtagca	tcctctagag	ttgggtgattc	catctctctt	tgcccttagt	170078097
gataggtatt	catcactgtg	tgaggcactc	acagttagaa	aatcacttct	170078147
taatatacaca	tgcgaggggc	aatgggtccc	tcactccctt	cacacgtaag	170078197
gttatggaac	aacaggcatg	agaacgctga	atggcttaaa	agtactttac	170078247
aaacaaaagg	tgctctaatt	tattcttggt	atgtcattat	tgccatagta	170078297
ttacatctca	agttaatttt	tatctcaacc	attcaaactt	aagtctgact	170078347
tagtaactag	ctcatcatta	ttttttataa	caaagtaatg	actagcaaca	170078397
tctggcatca	gactttgaac	aaacctcaga	aggaactgtc	aaggaggctc	170078447
cccacgggtt	cacgctcttc	tctcctcctg	cacacagggg	acagggccat	170078497
tctccttctt	ttactgggac	tacctgggct	tcattccagg	aatccccagg	170078547
tggcaacagg	agggtgggtga	aaaccgctgc	ccgtcacctg	taaagtttcc	170078597
tgtgaatgtg	tctacagcgg	ccagcaccac	aaggcataca	aagaaaggga	170078647
aggagagact	gatgtgagag	cggcagcgtg	ggcactcctg	tgagggtgccc	170078697
acagctgtag	acaagttaaa	tcagtgcagt	tcaatcaaaa	gtcatgacct	170078747
atgagcgtca	caaccagcac	gagtctacaa	aggaatacat	taaaactaag	170078797
accagagcac	agctcacatt	agtgaaggat	gggatcattt	catggagttt	170078847
ttgtttcaaa	atatttcatt	aacattttcac	ttatatacat	gtgtgtatac	170078897
tgggttgtag	tttaaattac	aattcttact	ataaaataca	gcaaaagaaa	170078947
gaagaaacaa	agagagggcc	actgggtttac	ctaacatcca	caggcaggct	170078997
acttcccagc	atcttgagcc	ccaaagaagt	aaatttctct	ccacaaccga	170079047
tggtaccaca	gcctgacact	tagccaatga	tgaaaacgaa	aaacaaaaca	170079097
aaagcttggc	agtcagtatc	caaatatgca	gatactacag	aatctgtttg	170079147
atgtagaagt	tgatcctgct	accagacag	caaacaactc	atattattaat	170079197
aaagtcaggt	tcctccttaa	tgaagtgggt	ttaatagttg	atatctcaat	170079247
aattacttag	tgcatTTTTT	atgaaggtga	tgggaaacaa	gtgctgtttc	170079297
ttgagtcgga	aagagtctct	caagctccca	caaagaaatt	tcccagagctt	170079347
gtgaggaatt	cagtcacagg	aagatcaagg	aattaagtgt	actgcaaaaa	170079397
acccttcatg	cttctggcta	agataaatct	aacagtgtac	tggatgtctt	170079447
caagaatacc	tcattttactc	aaaaaataca	atattcccat	tttctttatt	170079497
tgcattttta	tgtgattttt	gcttcatctc	ctttcttcac	tcaagccacc	170079547
tgggcccgtac	ccaggggaatt	cctaaggggc	aaaaggaggg	atgtgaaaac	170079597
ctctgcagcc	ccttcggaag	tttcttgtag	atatatgcac	agataaacag	170079647
atgtgcattt	taaaaataaa	aatgctttta	gatctaattg	taggagattc	170079697
aaaccaacaa	ttaattttctc	tgttaaaatg	ggttaaaata	gatgtaaaat	170079747
attaatatgt	atataagcat	tctgaattag	acttatgtga	atTTTTctcc	170079797
ttttctttct	ttctttttga	gaataagccc	tttcattttac	gtagaaatgc	170079847
ttcagcgttt	agataattgc	tacttatctt	gttagctaca	aacacaacca	170079897
taattaaagg	ctctgtaaga	attatgaatt	ctgggggaaat	tggccacttg	170079947
tctctgtggc	gtaaacagta	tctaatttat	aacaaatcat	ctgccttagt	170079997
cccagcagga	taagggtgata	tgtattgccc	agcacatgag	aaagatggca	170080047
attaggaatt	gttaccaagt	tacgggagcc	tcacacgaac	atccatcacc	170080097

FIG. 1.140

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tttggggata	tgtacaagat	acaaacttaa	tttgatggat	tccttttcta	170080147
ttgggatcaa	agtctcaaaa	gggaaagtga	caatttcagg	gaaaatctgg	170080197
tgcaatgaga	ccaacactga	tgagagaaat	gcacacaatt	taatacacct	170080247
gctcacctga	tgtggcaact	cagcctgtgc	ttgctgtggg	ttgcccacagg	170080297
atgagacatg	gtctgtgcat	attcccagca	gccacccatc	tcatacactat	170080347
tcttgccagc	ccagattttac	agttgttcaa	tagatggatt	tggtaaatatc	170080397
tgcatagaaa	caacaggcag	agaagggttag	atggcaattg	attccttgatt	170080447
ggtgtaagtt	tatagaacac	attctggcag	ggcccaaagg	aatcactca	170080497
cctacccctc	tgtgatggta	aaacggtgaa	aattccacgg	acttggacct	170080547
tgtgatcctt	cagtgggaaga	tgggcagatt	ccttgcttta	attgacagac	170080597
actttctaaa	taactaatgc	aatcttatat	tacattatag	tccataaggg	170080647
agacatactt	aaactactac	ttacaacaac	tgtttttaga	gcctttcaaa	170080697
tggtttctac	aaagtagctc	ccatttaaga	tattttccta	gtatttaagg	170080747
ctatctagta	gacattacaa	aacaatacgc	tgtaaataca	ttcagatttt	170080797
tatcagtaat	acttaacatg	ccgtaatttg	aactttctgc	taaatcatgc	170080847
tatccattcc	tagttggccc	caatggtgag	agtttactgt	ttcctttaa	170080897
aattttgttt	ccctttgctg	tctagaggtg	tttatcattc	tgccttactg	170080947
cctgtgtctc	tgggaatattc	agaagggtcc	atgggaaaca	atttgaatat	170080997
gcaaagaagt	tattttttaa	gcaaggaaaa	tgttttcata	tggattttat	170081047
ttgagcactt	ctgcctttgc	ctccactggg	aacatgtttc	tctccaacgc	170081097
cgaagccccc	tcctgtgtgt	gtgtttgacg	cagaggtga	cagggcaggg	170081147
aagtgggggt	caagatagga	aggccattgg	cagtgtgacc	ccagcccaca	170081197
gtcctagatc	ccaggtcgtg	acaccactct	tttgacagcc	cagattgtta	170081247
cctaacaaga	atgactocca	agctcaacca	ttccaatgcc	atctcctctg	170081297
gttccAGATA	AGATTGAAGA	TGAGCTGGAG	ATGACCATGG	TTTGCCATCG	170081347
GCCCCAGGGA	CTGGAGCAGC	TCGAGGCCCA	GACCAACTTC	ACCAAGAGGG	170081397
AGCTGCAGGT	CCTTTATCGA	GGCTTCAAAA	ATgtaagacc	cgtgcacgct	170081447
ctgaaggcct	gggggggggt	cccacgtgag	gctacactct	ccccaatgcc	170081497
aagggagctc	ataaggcggt	tcccatatgt	gaggctgtac	aaggaaggcc	170081547
agctctataa	agggggcatg	agagggagat	cacctggcta	gaaaggaagg	170081597
ctccaggcga	ggatggagca	acctcaggag	acagtaaacg	gccaactgcc	170081647
cagaaatttc	acaggggtggc	acatcctcaa	ggaattcacc	ctggcccagg	170081697
gtcaagcctt	agcccttaac	ataatcatac	cttccaacct	ggtgggtgcc	170081747
ccacaataat	gggatttggc	cctgtgtgact	tatgctaacc	aggctcaccg	170081797
agactgatgt	gtaagccgaa	tgtcgggtga	ttaatttacc	ttgggaaatg	170081847
gaactgacag	tggaaacaga	cactcctctc	ccttcgctgg	gacctgctct	170081897
ccttgggaagc	cacatggaag	ccaggttaca	atcaaaagtg	gagtcagagg	170081947
acgggagttc	cttgttttagt	tgttacttta	aatacattaa	tgtgttcctg	170081997
cagtctcagg	ccagtttgag	agctctcaga	tacaatcctg	gatattaatt	170082047
tatttttttaa	gtttaactct	cagagtgcga	tcttattccc	aaatcctgga	170082097
gtggtgtgga	gtgggggtggg	ctacagcgac	atgcacctgg	tcacctctcc	170082147
tccaggtgca	gtctgtaggt	agagctgagc	tgggtcagtt	ccaaactgac	170082197
cacagcctca	atgttctcca	aactgctgac	ccacagggat	tccagccctt	170082247
cctgggagtt	atctgacagg	tgttgggatg	cctcttctct	ccacactagc	170082297
cttgactgca	catgccaaagt	gccagtttc	ctaccattag	ggcttctttc	170082347
cttcgatggc	agcattagca	gtgggcagcc	gagttggaga	aggatcctgt	170082397
gggaaagttt	tccaggcagg	cactgggctc	agagggaaca	gcatccagaa	170082447
aagagaagaa	atctacactg	cttggcatct	accatggact	caataccacc	170082497
taacataggt	tcataagata	cccttgggga	agttattgtt	acccccattt	170082547
tacaggttaag	gatattgagg	atcagagact	ggcttggcca	aagtcacaaa	170082597
gcttagtatt	ggctgagcca	ggatttaaac	ccaggttttt	ctgatcttaa	170082647
agccccaat	ctctccacct	cacagtgcgc	attctctgac	aatgtctcat	170082697

FIG. 1.141

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cattttgcaa	agcagctcca	gtcctgagat	ggcactactt	gggagaagtg	170082747
gaaatgcaca	gggccctgtc	cctggggatc	atgaggaacc	ccagacacca	170082797
aggctgggccc	cagtcttctc	ctagtgtgtg	ccctcaaagt	cctcccgctg	170082847
actctctccc	cttcccacag	GAGTGCCCCA	GTGGTGTGGT	CAACGAAGAC	170082897
ACATTCAAGC	AGATCTATGC	TCAGTTTTTC	CCTCATGGAG	gtgagtctga	170082947
ccttgaaatc	tatcttgccc	agctccctct	ctggtaagca	gccttccctt	170082997
cctccaagtc	ctctcttcc	tgccatttgc	ttccttctcg	aggaagagac	170083047
aaactcaggg	caggacacct	ccctcatcgt	gagaggtggg	agtctccaaa	170083097
gcttttagcag	gaaagaactc	tgaaaatgaa	cccaccctgg	aaggggaaga	170083147
agggtctgata	atgcaacatc	acaacgtctc	agaacagctc	tagaaagcag	170083197
gtattataat	cccagatgga	gtaactgagt	ttcggggaag	ataagcagtg	170083247
tactcaagat	tgcacagctg	gtgagttagca	aaccaggatt	agattccata	170083297
agggtctgaa	acagggttttg	ccatgctggc	accaccattg	tgcagggcac	170083347
ttttgaatct	tttccttaaa	atagctgaga	caagctggaa	ttttgtaaaa	170083397
gaacttcagt	aaataccgaa	gactataaaa	ataaactaat	tgaaaaagag	170083447
gcaggaaaca	taaagtgtg	cttattaagc	cagtttacia	gtgtgccagg	170083497
cccacaacag	ctgctctgtt	gccctgcccc	actcctgtgg	gaaccagctg	170083547
tgccccatg	ggcctgggac	cacatcggtg	actcctcctg	tggcctccat	170083597
gtgtcacatg	ccactttgca	tcctgtcacc	aagagctgtc	tcctgcaaga	170083647
catcttccct	ggatcctgac	aaaatgcaaa	tccaagtatt	ccaaacactt	170083697
cttggggccct	gtttctcatg	ggcctttttg	gcagcagaca	gatgccttcc	170083747
ttgggtgtgtg	gggcccctac	ccagatcagg	tgggggaggg	agttttgtcc	170083797
catgcaggcc	ccagaattgc	agtttgctga	gttccactga	gccactgttt	170083847
attgagttct	cactgtatgc	caggcacagc	tgtagttaa	aatacttttt	170083897
aaaaaatctc	aagagatagg	tcttgctaca	tcccattgta	gagaggtagg	170083947
aaaggggaagc	tcagagaggt	cgtgcttgat	gcccacagtc	acatagctta	170083997
tgtagtacag	cggcatccaa	gttcagggtc	ctctactctg	gagtgagtgc	170084047
tcaccccagg	cattcatggc	cgttcagaag	aacattgtca	tgcagtcact	170084097
gtgccattca	tacaccaacg	actccatgca	tagacaggca	ggagaatgg	170084147
tttctcatga	tggttagagg	gaggggcaag	ggctcatctc	actttttgct	170084197
agatctaact	tcacacccaa	acccaaagag	ttgagtcaat	gggccccact	170084247
ccataatctt	ctcctttcca	tcaccctagc	atcactctcc	tctctttctt	170084297
gtcgaagccc	tgccttggtt	ggaaggttct	ccctgtgtgg	aattcctgcc	170084347
cccacacct	gccctccttt	tctgccttgt	agATGCCAGC	ACGTATGCCC	170084397
ATTACCTCTT	CAATGCCTTC	GACACCACTC	AGACAGGCTC	CGTGAAGTTC	170084447
GAGgtacgct	catctggggg	ccactctagg	ggctctctgg	ttctgcatca	170084497
cctccccctc	taaatctcaa	ggcattgggg	gaaggtctgg	accatcaaaa	170084547
gctctcagtc	agaccaaaga	catgtttatc	catttgtaag	catttcctaa	170084597
agatggggaa	aagcagcagc	aactttccct	ggcctgcagg	aactcagggg	170084647
ctcaggggac	taataacaac	agtgtatgag	cttccgggca	cactgcttcc	170084697
cagtggcagc	ccctgtactt	agggccttgt	atgtattaat	tcattttactc	170084747
caattcccac	aataacccta	tagggtaggg	ttttattatt	gattaccttt	170084797
ttacagaaga	ggagagtaag	gcaaagagag	atagagtagt	tttcccaagg	170084847
tcaaagagca	cataaatgat	aaaggatgga	tttgaatgta	ggcagaatga	170084897
ccctcaatac	agactgttcc	tacagtcac	gtcctcagcc	actagaccat	170084947
acggccactg	ggatgataga	cagaccactg	cagccatgga	taaggcaaaa	170084997
acagggctgg	ctgtgttgat	ctgtgtctct	cagagctcca	ttcttctctca	170085047
agggggcacc	ttgcaaaaaa	aaacaaaaaa	atgggggcagg	gtaggggaact	170085097
gaaggcagga	gctcttcaca	gagcatagcc	acatcctcca	ggcagacaag	170085147
aggacgcagg	aggcaccatt	ctgtgagagt	atcacagtct	gacccaaaga	170085197
cacagcttca	cactgtctga	tggcttgatg	gttaatgtca	ctctgccttt	170085247
tccccttctc	agGACTTTGT	AACCGCTCTG	TCGATTTTAT	TGAGAGGAAC	170085297

FIG. 1.142

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TGTCACGAG	AACTAAGGT	GGACATTTAA	TTTGTATGAC	ATCAACAAGG	170085347
ACGGATACAT	AAACAAAGAG	gtaagtgagc	tggggccagg	ggtgtgagag	170085397
ggctccagtg	aaggtaacta	acccaacaga	aaacagcccc	aggcatgagg	170085447
atagcactgt	ctgaatgagg	caggctctgc	tttggggcta	acagagctgg	170085497
tccctggcaa	aataaagaag	gcctccctca	ttgccctacc	ctgccctggt	170085547
cccaagcgcc	cagaaaggat	taaacagatt	cattctcact	gggtcaccta	170085597
gattcagtag	atattacaca	gtggataaaa	atgacttggt	tcagtgtgaa	170085647
gagttactct	tccctagggg	acctgcattt	gggaagggtta	ggagccacaa	170085697
gtcaaagcta	aaagttgaaa	tgggtggaatt	gtaggcgagca	cctagaatag	170085747
aaaagaaaga	tttttaagga	agaggaacct	acaattgggt	catattggcc	170085797
ttaaactatt	ttgcctatta	atacaaccgc	caagggggta	atggaaggta	170085847
cagctgtctt	tacagaaatt	atcacaaata	atctctgaat	cttcactgct	170085897
ttgcactttt	agaacctcag	aggacatgtc	tctagccagt	gaaataccct	170085947
caggtctatc	tcaaaaactca	cttttggtatc	cactgtatcc	tggtatctca	170085997
gtggaagctg	gaaattggca	tcctgtaaca	ctccacttgc	tgagctcctg	170086047
tgtgccaggc	acggtgcctg	gaggtataga	tatcagcacc	aatcttcacc	170086097
tcaaccggc	aagcttctct	ctgtaagctc	agagagttta	tccaactttc	170086147
attcctcatt	catttagtca	tgtttttaat	taacacagat	ttgaaggctt	170086197
attaggtggt	ctaggtgctg	gaggtaaaga	ggtgaacaat	cagactaggc	170086247
cccacactgg	agcagcatag	agagatggac	aataaacagg	ccaaaaagga	170086297
atcagcaggt	agaagatatt	ttggcaggga	agggttagcaa	aggcctctcc	170086347
aaggaggtgt	cgtcatactg	gaaccagtta	tacaaaaagc	caggaaaagt	170086397
gttccaggca	gaaggaacag	ccactagaga	ggctttgagg	caagatagag	170086447
cttcatgtgt	ttcaaaaaca	gaaaggcttc	agatggctgc	agatgaagg	170086497
atgaagctga	agactagtgc	aggatgagcc	tgacagggtca	gcagagtcag	170086547
atggtggagg	gctagggtaa	ggggcccatc	catattcccc	tgggaagctc	170086597
ttagatgaac	atgttttttg	aaagacacaa	aaggcaaaaa	cagacttaaa	170086647
aagaatcaga	aatcttgact	agctctgtat	tatttagaga	aatttatattc	170086697
acagttaaaa	accattccca	aataaaaatta	taggcccaga	tggtggactg	170086747
gtgaattcta	atatcaatcc	tacaaaaaaa	ttttagaaaa	tagaggagga	170086797
tggaaacattt	cccagcttgt	tttataagtc	caatagtacc	ctgataccca	170086847
aaccaaagaa	aaaaagggtct	tatgaaagga	aacaactaca	aaacagtcctc	170086897
cctcgtgagc	acagataaaa	aagctttcac	taaatattag	caaattgaat	170086947
tcagcaatat	ataaaaagga	tgatacaata	caactatgtg	agttttattc	170086997
taggaaggca	agggttggtt	aacattcaaa	aaccaatcaa	tataattcac	170087047
tatatttaaa	gaaaccaaag	ggatatagac	tggaaaggaa	gaattaacac	170087097
tgtctttatt	tgtacatggt	ataattgtat	taatagaaaa	ccctaagagt	170087147
ctacaaataa	actgctaaaa	ataataagt	aatttaacaa	agtgaagaca	170087197
tgagttctat	ttacaaaaat	cattttataat	tctacatcca	acaagcaacc	170087247
agaaaattaa	attaagaaaa	atagcatcaa	aaagcacaaa	atacttttag	170087297
aaaaattcaa	caaacacagg	gcaagactca	tacactgaaa	actataaaat	170087347
attgctgaaa	taaagtaaag	aactaaataa	acacagagat	aaatcatgct	170087397
catgggttgg	aaggcccaat	atagttaaga	tgtggattct	ccaaatttga	170087447
tttatagatt	tagtgtgatc	tcaatcaaaa	tcccagcagg	tattttgtag	170087497
cagttgatat	gggaatgcaa	aaaacctaaa	ataacaaaaa	catctgaaaa	170087547
agaacaaagt	tgaaggacta	aacctacctt	acttcaagac	ttaatgaaaa	170087597
tgtgcagtag	tcaagatggt	agggaattgg	cataaggata	gacatataga	170087647
tcaatggatc	aaaatagaga	gtcaaaaaaa	ctaaaagtag	agctaccata	170087697
tgatccaaca	atcccactgc	tggctatata	ccccatgtaa	aggaaaccag	170087747
tatatcaaag	agatatctgc	actcccatgt	tttttgcaga	tctgttcata	170087797
atagccaaga	tttgggaagca	acctaagtgt	ccatcaacag	atgaatggat	170087847
aaagaaaatc	tggtacttat	acacaatgga	gtactttctgc	cataaaaatag	170087897

FIG. 1.143

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aatgagattt	aatcatctac	aacgtggatg	gaattggagg	tcattacatt	170087947
aagtgaatg	aaccaggcac	agaaagacaa	acatcccatg	ttctctctta	170087997
tttgttggat	ctaaaaatca	aaacaatatg	aagatagagg	gcagaaggac	170088047
ggttaccaga	ggctgggaag	gatatgagg	gggctgtggg	ggaagttagg	170088097
atagtcaatg	ggtacaaaaa	aaatagaatg	aatgaataag	gcctggtatt	170088147
tggtagcaca	acaaggtgac	tgtagtcaat	aatttaattg	aacattttta	170088197
ctaaaagagt	gtaattgggt	tgtttgtaac	acaaaggata	aatgcttgaa	170088247
gggatggata	cccatttttc	atgatgtggt	tattacacat	tgtatgcctg	170088297
tatcaaaact	tgtcatgtac	cccataaata	tatacaccta	ctatgtgccc	170088347
acaaaaatta	aaaataaaaa	ataaatat	tttaaaaaata	gagatagacc	170088397
cacccatatg	tcaatgcaac	agatgccaaa	aagatcaaag	gggaaagaac	170088447
cgtgttttca	cagctgtata	tcattttgga	aacaaaaatg	gacattaacc	170088497
ttaacctcat	gccaaacata	aacatcaact	tggaatggat	tatagactta	170088547
aatattaaaa	caaaagctgt	tttcttaagg	aatacatagg	agaaacattc	170088597
ttacaacttt	ggagtaggaa	aggataagga	atcattttct	aaagtagata	170088647
aatttgactt	tatcaaagtt	aaaaattttg	tgttttagaa	gacaccttta	170088697
agaaaatgga	aatgcaagcc	atggacttgg	aaaaaatgtt	tgcaaatatt	170088747
ataccagata	tataaagata	ccaggatacc	aaaccaatat	aaagactggc	170088797
atccaaaata	tataagggac	at ttataatt	taatacaaaag	ataaacaact	170088847
tcatataaaa	taggcaaaaag	at ttgatgag	atatttaaga	aaagaagata	170088897
tatgaatggc	cagtaaaacc	atgaaaggtt	gctctatatc	actggtcttc	170088947
aaagaaatgc	aaattataac	tataatgaaa	tacaattgca	cagaatggcc	170088997
acaattaaaa	agactgataa	taccaagcat	tggcaaagat	gtggagcaat	170089047
agaaactctc	atagatagct	ggcagaaatg	taaatgggtac	aaacacgttg	170089097
ggaaacattt	tggcatcttt	gataaagctc	agcacacact	taacatacaa	170089147
cccagaaatc	ccattccagt	caggcatggt	ggcttacgcc	tataatccca	170089197
gtactttggg	aggctgaggg	aggcggatca	cttgagctca	ggtgttcaag	170089247
accgactggg	gcaacatggc	gagacactgt	ctctactaaa	aatacaaaaa	170089297
aaaaaaaaaa	aaaagccaga	catggttggt	agcacctgtg	gtcccagcta	170089347
ctaggggagg	tgaggtggga	gaattgctta	accctgggga	gtggaggttg	170089397
cagtggagctg	agattgcacc	actgcactcc	agcctgggtg	acagagcaag	170089447
accctgtctc	aaaaaaagaa	aaaaagaaga	agaaaagaag	tcccactcct	170089497
ggatattttac	ccccaaaaga	aaaatatgta	attccataaa	gacttgtaca	170089547
aagatgtttca	tagcagcttt	attcatagta	atctcaaaac	ttaaatgacc	170089597
caaatgtctg	tcaacaggac	aatgggtaaa	tacatcatag	tctgttcac	170089647
caatggaata	ttactcagca	gtaaaaagga	atgttatagt	tgcattgcagc	170089697
aatgtgtatg	aagctcataa	acctcatgct	gagtaaatga	agccagacgc	170089747
aaatgagttt	acactgtttt	actccattta	catgagattt	tagaaaatac	170089797
aaactaatct	atagtaacag	aaattagatc	tgtgggtgcc	tggtgtcaaa	170089847
gcttgagagg	cactcactgc	gaagaagtgt	gaagggtgtg	cttttggttg	170089897
tgaaaatgtt	ctatatcttg	agtgtggtgg	aggttacatg	ggtggataca	170089947
tttgtcaaca	ttcatcaaac	agtacactta	aaatgggtga	atttggtata	170089997
agtaaaattat	gctccaataa	at ttgattta	tttgttgaaa	aacttggtgt	170090047
aagggggaag	tgccctaacca	atagaagaca	ctcaaaaaat	gtgttggaag	170090097
aaaaaaatcc	tgtgaaataa	agcaggtaag	agaaaataag	aactcaatat	170090147
catccaaaat	atagattaca	aatcctaata	gagataatag	gaaattaatc	170090197
ccagtgtctc	gtttaaaggc	tcatacctgt	aatcccaaca	ctttgggaga	170090247
ctgaggcagg	aggatgggtt	gagcccagga	gttcaagacc	agcctggtca	170090297
acatagggag	agcctgtctc	ttcaaaaaca	aaatttaaaa	attacctggg	170090347
tgtagtggca	cgtgcctgtg	ctcccagcta	ctccagaggc	tgaggcagga	170090397
ggatagcttg	agcccaggag	ttcaagcctg	ccctgagcca	taatcactgc	170090447
accacactcc	agcctgggca	acagaacaag	acccttcctc	aaaaaagcaa	170090497

FIG. 1.144



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taaaataaaa	taaagaaatg	cacatgacta	acatagggtt	tattccagga	170090547
atgcaggaat	agcccagtag	cagagaaagc	ctattaaata	atztatcaca	170090597
ttaatatatc	aaaagatcaa	accattttgat	gctaaaatca	catttgatat	170090647
aattttaccat	ttattcataa	taatttttcag	gattcaatta	attaggaata	170090697
aaatacttct	tcagcataat	agaaaatacc	ccagcctggt	acacagcttc	170090747
atacttttatg	gtaacacgcg	gagattctca	ctgaagaaaa	gatgaggcaa	170090797
gaaaagatga	tgaagaaaag	atgaggcaag	aaaagatgat	gtctgcacac	170090847
tgtcagacat	caccactgtt	taacattttcc	tgaaagctct	tcaaacacag	170090897
tgaaacagaa	aaggaaatgc	gatctaaata	ggaaaaatta	caacattcct	170090947
tgттаатgac	atgatttttct	atctgagaaa	aaagacagca	agaaaaatcaa	170090997
cttaaaaacaa	ctagaacttt	taaaaagctg	gcaaaagtgc	tggttaataaa	170091047
atacatatgc	aaaaagaaat	tgtgtagcca	atatatcagt	tgtgactagc	170091097
tagaaaattg	taatacaaat	attctcattg	tgatcacaat	aaaattttaa	170091147
gcacatgggc	attttttaaat	atccataatt	tagatgaaga	gaaagaaaat	170091197
tttgataagt	agagaaacat	accatcttct	gaaaggatgt	atattataaa	170091247
gatagcaata	ttataatgac	agcaattctt	ctctaattaa	atttatttta	170091297
ttttgaatca	aaatgggaag	gttattttggg	aaggaaattt	ggcacaattg	170091347
ttataaagtt	acattggaag	attaatcaga	tgaaaatagc	aaagataatt	170091397
ttcaaaaaga	agaaaaatgg	tgggatttgt	tctaccagat	actgaaatat	170091447
attataaagc	tgaaactatt	aaaatattat	aatatcagag	aaggaacagg	170091497
tagatcaatg	gaacaaaata	gaaatcccag	gtacaaatac	catcttggtt	170091547
cataataaag	ggagcatatt	gaatagagag	gtaatgaatc	attaaatgat	170091597
tcttggaaaa	ctgggttaact	atttttggcaa	taagtaagta	aatattctta	170091647
ctcggtacca	taaacacaaa	atcactatag	atatgtacag	ttgcttttta	170091697
actaaaaaag	aactaaaaat	catatgtgaa	tatctgatca	aagaatggaa	170091747
aaagcataaa	atcaaagtta	gaaacaattt	tttaaattat	tgatggcttt	170091797
acactgtaaa	tatttttaaaa	ttctgcatat	caaaaaatac	cataaacaaa	170091847
gttgaaaagt	aagtgacaaa	cttggttttta	aaaatctgca	atztatgatg	170091897
acagaaagga	ttgatattcc	tcagtagaca	ttcatcttaa	caaaggcaag	170091947
agtcatattc	atcgtgctta	tctttgtatt	tctttgacac	aatatctagc	170091997
acatggtaga	tgcgtaaaaa	taccttttaa	taaattaaaa	atctattaag	170092047
atatttttaac	aattttaata	atctacacga	atatataaag	agctctcaca	170092097
atccagtcag	aaataggtga	acacaatgag	caaagcagat	gaaaaaatag	170092147
ttcatgggaa	aataaataaa	aatagtcaat	acatatatta	gagacctcac	170092197
taagaaagta	atgtatatct	ttaaaaacaa	tgaattatca	cttatctatt	170092247
aaattgcaaa	ggttttgtaa	agtcttttgt	gaaggttggt	ggaaagtggg	170092297
ttttcataca	tagttgctga	aagtgttctg	ataataaact	ttctaaaagg	170092347
tatttgagga	atatgtatca	aaagcattga	aagttatgca	tcccattctc	170092397
cttataaaaac	cacaccttgg	tatatgtccc	aaggaaataa	agaatagaca	170092447
caaagactta	aaagcaagaa	gagtcttcag	gtaatagtgc	cccagaatgt	170092497
gatagccatg	atatccacta	acagcagatt	tgtaaaatga	attacagtaa	170092547
atacatataa	tggaatagcc	agtggccact	taaaatcatg	aaagagtaat	170092597
ataaaaataaa	cattagtatg	atatattaaa	tttttaataa	tattacattt	170092647
taaattgata	aagtgggatg	tatgatattc	caattttata	aacaactaaa	170092697
tgcttatata	cacatgcaaa	tatatgatac	tctaaaatat	tcaaatacta	170092747
ccttgcaaaa	catataaaga	aaaaaatata	gaaataggat	ttagttgggc	170092797
ttcaactttg	gttcactcat	tattccatca	ctgaataaac	ttactagtgc	170092847
ctactccctt	tttgtaattt	gcaaactagg	cagaattctc	cccattaatc	170092897
tatcagacct	ctctggaggg	cagagttaat	aaagtacccc	ttaaaagaaa	170092947
aagaaagtgt	ggataagtag	cttctcagaa	aagatagcag	gatcttcccc	170092997
tggcaatcat	ttggagataa	cctcatccaa	gttgtaggct	atgaaaatcc	170093047
tgagagagca	acaaaattgc	tctttctgtg	attaaaaaaa	aatatcagac	170093097

FIG. 1.145

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aggaaaagca	tcaatggcca	tgtagatgtg	aagggttgt	aaagcacaca	170093147
tttaaaaata	aacacatgga	tagagacatc	tatttcctcg	ttctatctgt	170093197
tgagggcacc	tcagagcaat	gacatccctg	tagcagttag	catactagta	170093247
cctagacttt	gatttctaaa	taccattctt	cgataaacag	aaccagtctt	170093297
cttgaagaat	agttgattct	aagattggga	aagagaaaat	acaagatgag	170093347
cctggagtag	tttattatgc	tgaagggtata	aaagtgtcta	aaaaaaaaaa	170093397
actgcaggag	tcaacctgaa	ggagttccca	atagtcagaa	tgaaagcaat	170093447
ttgagcaaaa	ttaaaaatta	ttaagtactg	gattataacc	tgtaaaatat	170093497
ggtaaatgcc	cacaagtcca	tgctaattgta	aataaacaac	tgaatacata	170093547
aataaatgca	ggagagaagg	tagctcttcc	ttacagaaga	attgtaatta	170093597
ataagtatag	aaggaataaa	ggaaatacaa	aattaccatc	aggcaaacac	170093647
tacagtaata	atttttgcag	gcaagatcca	ctgaaagata	ctaaatcagt	170093697
aaggaaactt	gacagacacc	accttaatca	agtgatcaag	gttaacatta	170093747
tcagtaataa	gacatctcaa	cactatgtaa	ctccctgata	tgacgcactg	170093797
agaaggttat	accatcactt	ctgtggtatt	cttgccagaa	atgcataact	170093847
tcaatctaata	cataactaaa	ccagggatta	actcaaattg	agagacattc	170093897
tacaaaacaa	ctgacctgta	ctcatatcaa	aagtgtgagg	tcctgaaaga	170093947
caaggaaaca	aagaaactca	ggctgggcat	gggtggctcat	gcctataatc	170093997
ccagcacttt	gggaggcaga	ggcaggaaga	tcacttgagt	ccaagagttt	170094047
gagaccagcc	tgggcaacat	ggcaaaaacc	catctctaca	aaaaattagc	170094097
caggtgtggt	ggcacttgcc	tgtagtccca	gctacttgag	aggctgaggc	170094147
gggaggatca	cttgaacccg	ggaggtcgag	gctgcagtga	cggggattgt	170094197
gccactgcac	tcagcctgg	gtgacagagc	aagaacctgt	ctcaaaaaaa	170094247
aaaaaaaaaga	aaaaagaaaa	aaagaatgag	aaactcatat	agattagaag	170094297
agactaagga	gacacaacaa	ataaatgcaa	tgtagaatca	ttgaagggaa	170094347
aaaaatatta	gttgaaaagc	tgagatcccc	ccactgcact	ccagcctggg	170094397
ccacagagcg	agactccgtc	tcaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	170094447
aagaaaagct	gataaaaatt	gaataagccc	tgtagtttag	ttaataatag	170094497
tgaagccatg	ttaatttcct	gggtttgggt	attgtgctct	ggttatgcaa	170094547
gttggttaaca	ttagaggaga	ctgagtgaag	ggtagcatg	aactctctgt	170094597
actaattttg	taaattttct	gtaagtctaa	aattattcat	aatatgcaaa	170094647
aattaaacaa	aaaataaaat	aaaataagca	catggaatga	gactgtcccc	170094697
tgggtctctg	tagaaaccag	gtcaaacatc	ccaaatgctc	ttttaccccc	170094747
attctgagtt	gggccagaat	ggtcagaata	atgggtccca	atgtaccttg	170094797
ataaacacgg	aaactctcag	gaccgagtc	taagggtctc	tgattcaata	170094847
ggtttgaggt	ggacttgaga	actgatcttt	ttaataaggg	cctcagtctg	170094897
tggaaactatt	ggcctcatgt	gccctgtgga	taatcttggt	tggttggttca	170094947
tttttcttaa	ctgaaaacag	tggcagaaac	tatggggatt	tttaaactct	170094997
taggctagaa	cattaacttt	ttaaaaattc	agaatagtat	tttatttgcc	170095047
tcaagcctgt	gaatggggat	cccacaaatc	acccccact	gaagacaatg	170095097
cccataacaa	ggtaacctac	ccatgagctt	ctgagggatt	taggaattgt	170095147
ctaccatctc	ctctctaaga	agggtcccca	caatatatcc	ccttctgctt	170095197
gcttctaact	ccctatcacc	tgctaaagaa	ggacctcacc	ttttaatcac	170095247
tttcattgco	aaggggcaca	aggagcccca	aactctgtca	cctaggaaga	170095297
gcttgacctc	atggtttcca	cactgtgtgc	ttttatgtcc	ctgctccagG	170095347
AGATGATGGA	CATTGTCAAA	GCCATCTATG	ACATGATGGG	GAAATACACA	170095397
TATCCTGTGC	TCAAAGAGGA	CACTCCAAGG	CAGCATGTGG	ACGTCTTCTT	170095447
CCAGGtaagt	gcacacaccc	tgacacatgag	ctgtaagccc	agcctagatc	170095497
aagtcaaccc	acgagcatct	gagcaaatga	tttgtgtcca	accctgtact	170095547
aagcatgggt	ggtaacagaa	aagaattata	agatacattg	tcctcaagaa	170095597
acagatgata	tccttaagct	gcaagtgtac	atgacagaag	agaacaagaa	170095647
agtatattat	taaacgctag	tggtatagta	tgaactctaa	atccataaaa	170095697

FIG. 1.146



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at tt t g g g g a t	c a g g g t a a a c	a c g a a a g a c t	t c a t t a a t t a	c a a c t g t g g a	170095747
g g t g t t a a g c	a t t t g t g t c t	g g g a a g t a a g	g g g a a a t a a g	a t t g g a a a c t	170095797
a g g a t a g g g c	c a g a t t a t g a	g a c c t t t t a a a	t g g a a g a g t t	t g g c c t t g c t	170095847
c t g g t a c a g g	a t g g g c a g c t	a g t g c t g a t c	c t t g a c t a a g	g g a g t g g t a t	170095897
a a t c a t t g g g	g c a t t t t t a g g	a a a a a a t t a a	t c t a g c g g t g	g a g t a t c a g a	170095947
g a a t a t c a a g	a g t t c a c t c t	a g t t c a a c c t	c c c a c t t t t g c	a g a t g g g a a a	170095997
a g a g a g t c c t	c t c t g g c c t t	g t g c a a g t t t	g t a c a g c a a g	t a a c a g g c c a	170096047
g a a t c a g a a c	c t c t t t t t g c c	c a g t g t t c t g	c c a g a t g g a c	a g g g t a g c a g	170096097
g g a g t c t a c a	g a a g a a g c a g	a a t a a g c c a g	c a g t g a g g t g	a t g a g t g t c c	170096147
a g a g c a a g t c	t t t t g a t t t a	a g g a a g c t c a	t g g g g c t c a a	a g t g t t g t a a	170096197
t c a g g a c c t a	a t t g g a g t t g	t c t g g c c a g t	g a a a g a c a a c	t c t c a t t t c t c	170096247
a g g g c a a a g t	t g g t t a a t g a	a a t g a a t g a a	a t g a g c t c c a	g c t c g t t a c t	170096297
c t g a g c t c c a	g c a a g a a a g c	a g g g g a g t a a	g c t t t g g a a t	g g a g a t c a c c	170096347
a g a t t c t g t a	a a g t g c t t t c	t g t t a t g t c t	t t c a g A A A A T	G G A C A A A A A T	170096397
A A A G A T G G C A	T C G T A A C T T T	A G A T G A A T T T	C T T G A A T C A T	G T C A G G A G g t	170096447
a a g g a g a g a t	c t c a g g g c a c	a a t a a c t c t a	c a t c t g g g a a	a g g a a a c c t g	170096497
g g g c c t g g g g	a c c t g c a g a a	g g a a g g t g a t	g a g a a a c c t g	c a c a t a c c t g	170096547
c a a c c c c t c c	c a t c a g a g c c	a a c a a c a c c a	g c a a c a a c t g	t g a a g t c c a c	170096597
a g t t c c a c t c	c t c a a c c t g a	c c t g c a g t t g	g t c t t g g c t a	a g c a c a a g a c	170096647
t g a a c a g a g a	g c c t a a g t a g	g g g t c t g g g g	g c a t g t g a a a	a c t c a g a g g g	170096697
g g t c t c t g t g	a a a a t a g a c t	t c c c g a g a g g	g c a a c a c c a t	t a t t t t t t t a g	170096747
c c t g c c t c t g	g c t t g a t g a c	c c a t t t c c c a	g a c t a c a a g g	a a g c a g c t g g	170096797
g g g g a a a a a a	a c c t a c a a t t	g t g t g a t t c t	c a a a c c a c a g	t g t g c a t a a a	170096847
a a t t g c c t g g	a a t g a t t c t g	a a a a t g c a t a	t t t c c a g g c c	t c a a t c c c a g	170096897
a g a c t c t a g a	t c t g g g t c a c	t t t a a c a c a a	a t g t c c t g g a	c c a a t g c t t c	170096947
t a a c a c t t t a	a t g t g t g a a a	c a a t a t c c t t	g a t g a t t t t g	t t a a a a t g c a	170096997
g a t t c t a a t t	c c a t a g g t c t	g g g g t a g g g c	c t g a g a t g t t	a c t t t t t c t c a	170097047
c a t t c t c c c c	a g t c a c a c t g	g t g a t g c t g a	t c c t g g g a a c	a c a a c t t t t c a	170097097
t t a a g t c t a a	c c a a t a g a c c	a g c c c c a g a g	t c c a c c a g a g	a c t g a a c t g g	170097147
a a a t a a t t g c	t t c a t c t a c t	t t t g a g a a a t	c c a t t t g t a c	c c c c a c a t t a	170097197
t t t t a g a a a t	g t t c a g a g t t	a c t c t g a g c t	c c a g c c a a g a	a g a a t a g c a a	170097247
a t g t a a g a a a	g c c g g g g a g a	a g t t c c t a g c	a g a t a c t g a g	c c c c c a t c a a	170097297
g t t t c a a g c a	c a t a c a t a a a	c a t c a c a g c c	a c c c t g t t a t	g t a g a t g t c c	170097347
t a t g t g c a g g	g t g a t a t c c a	a g a t a t t t a a	c a a c t a g a a t	g g a a t g a a c a	170097397
c t g a c c c c c t	t g g g g g t g a g	t t c t c a c t g t	t a a t t c c c t t	g a g a g c t g g t	170097447
t g t a a a a c a g	c c t g g c a c c t	t c c c c a c c t c	c a a c c t t g a t	t c c t c t c c c a	170097497
c c a t g g g a t c	t c t g c a c a c c	c a g c t t c c c t	t c a c a t t c c a	c t g t g a g t g g	170097547
a a g c a g c c t g	a a a c c c t c a c	c a g a t g c a g a	t g c c c a g c t g	a a c t t t t c c a g	170097597
c t g c c a g a a t	a a t g a g c c a a	a t a a g c c t a t	a c t g a c a t t a	a c c t t t t c a t	170097647
t t c t g a t a t t	g a t a a t t t g a	a a a g c a g t c t	t a a t a a g c a t	t t a t c t a c t t	170097697
t a t t g a t t t t	t t t g a a a g a g	a g c g c t t t t g g	g g g g t t t t c t	t a c t g t a t g t	170097747
c t c t a t t g c a	t g t t c t g t a t	t t t a c a t t t t	t c t a t t a t t t	c t t c t c t g a g	170097797
g t a t a g t a t t	g a a t g t a g a a	a a a t c c t c a a	a t g t t c g g t a	t t a a g c a a t a	170097847
c a c t t c t a a t	t c a t g g t t c a	g a g a a g a a a a	t a t c t c g a a t	a a a a a t a a a a	170097897
t a a a a a t a t g	a c t t a t c a a a	a t t t g t a g g a	t c t a a a g c a g	t a t t c c a g g a	170097947
a t g c a a g g t t	g g t t t a a c a t	t c a a t a a t t g	g t c a g t g t a a	t t a a t c a c a t	170097997
t a a t a g a a t a	a a a a g a g a a a	a a a t a t a a t c	a t t t c a g t g g	a t g t a a t t g t	170098047
t c a g a g c t t c	t t a a a a g a a g	c a a c t c a c t a	t t t t a c t a g a	t g a t t t g t t t	170098097
c t t c t g a a t t	c c t c t t t a a g	g c t a c a g g t g	g t g c t t c t t a	c t t t g a a c t g	170098147
a t c a c t t t c t	a g g t c c c c a c	c c t t a c t t c t	t g t t t t t c a t	a c c c t t g t a g	170098197
a g t t t t c t c c	a t a t a g g a a a	c c c a t g c t t g	a c a t t t g c t c	a c c a g a g t t a	170098247
c a g a g c t c t c	a g g g a g g a g a	c t c a g a g t t c	t a a c c c t c t t	g c c c t c c t t t	170098297

FIG. 1.147

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tttcccagGA	CGACAACATC	ATGAGGTCTC	TCCAGCTGTT	TCAAAATGTC	170098347
ATGTAActgg	tgacactcag	ccattcagct	ctcagagaca	ttgtactaaa	170098397
caaccacctt	aacaccctga	tctgcccttg	ttctgatttt	acacaccaac	170098447
tcttgg					

FIG. 1.148

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## Amino acid sequence of KChIP1

MGAVMGTFSSLQTKQRRPSKDKIEDELEMTMVCHRPEGLEQLE  
AQTNFTKRELQVLYRGFKNECPSGVVNEDTFKQIYAQFFPHGDASTYA  
HYLFNAFDTTQTGSVKFEDFVTALSILLRGTVHEKLRWTFNLYDINKD  
GYINKEEMMDIVKAIYDMMGKYTYPVLKEDTPRQHVDVFFQKMDKN  
KDGIVTLDEFLESCQEDDNIMRSLQLFQNVN (SEQ ID NO: 2)

FIG. 2

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Nucleic acid sequence encoding the amino acid sequence of KChIP1

ATGGGGGCGCGTCATGGGCGACCTTCTCATCTCTGCAAACCAAA  
CAAAGGCGACCCCTCGAAAGATAAGATTGAAGATGAGCTGGA  
GATGACCATGGTTTGCCATCGGCCCCGAGGGACTGGAGCAGC  
TCGAGGCCCCAGACCAACTTCACCAAGAGGGAGCTGCAGGTC  
CTTTATCGAGGCTTCAAAAATGAGTGCCCCAGTGGTGTGGTC  
AACGAAGACACATTCAAGCAGATCTATGCTCAGTTTTTCCCT  
CATGGAGATGCCAGCACGTATGCCCATACCTCTTCAATGCC  
TTCGACACCACTCAGACAGGCTCCGTGAAGTTCGAGGACTTT  
GTAACCGCTCTGTTCGATTTTATTGAGAGGAACTGTCCACGAG  
AAACTAAGGTGGACATTTAATTTGTATGACATCAACAAGGA  
CGGATACATAAACAAGAGGAGATGATGGACATTGTCAAAG  
CCATCTATGACATGATGGGGAAATACACATATCCTGTGCTCA  
AAGAGGACACTCCAAGGCAGCATGTGGACGTCTTCTTCCAG  
AAAATGGACAAAAATAAAGATGGCATCGTAACTTTAGATGA  
ATTTCTTGAATCATGTCAGGAGGACGACAACATCATGAGGT  
CTCTCCAGCTGTTTCAAAATGTCATG  
(SEQ ID NO:3)

FIG. 3

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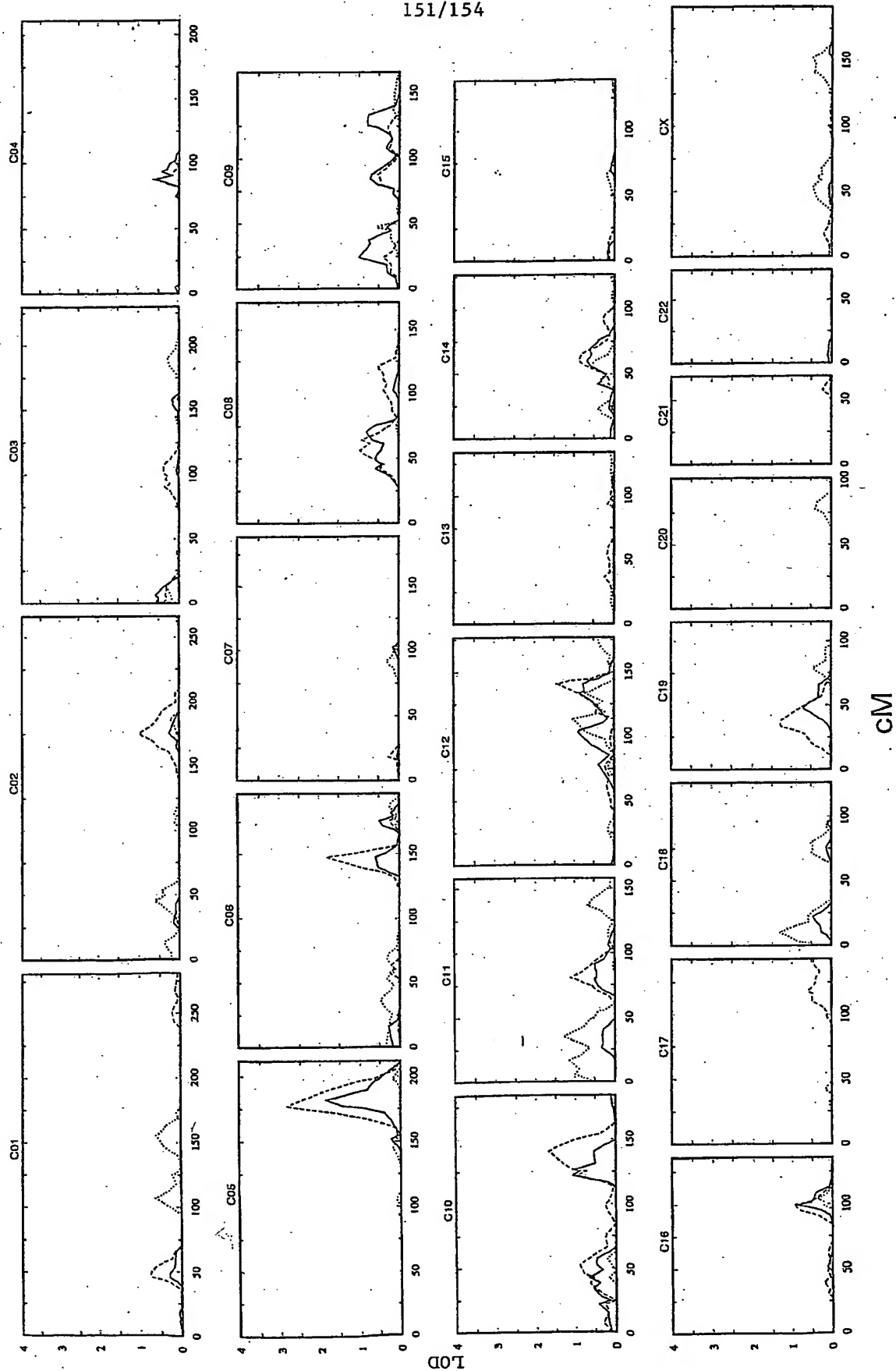


FIG. 4

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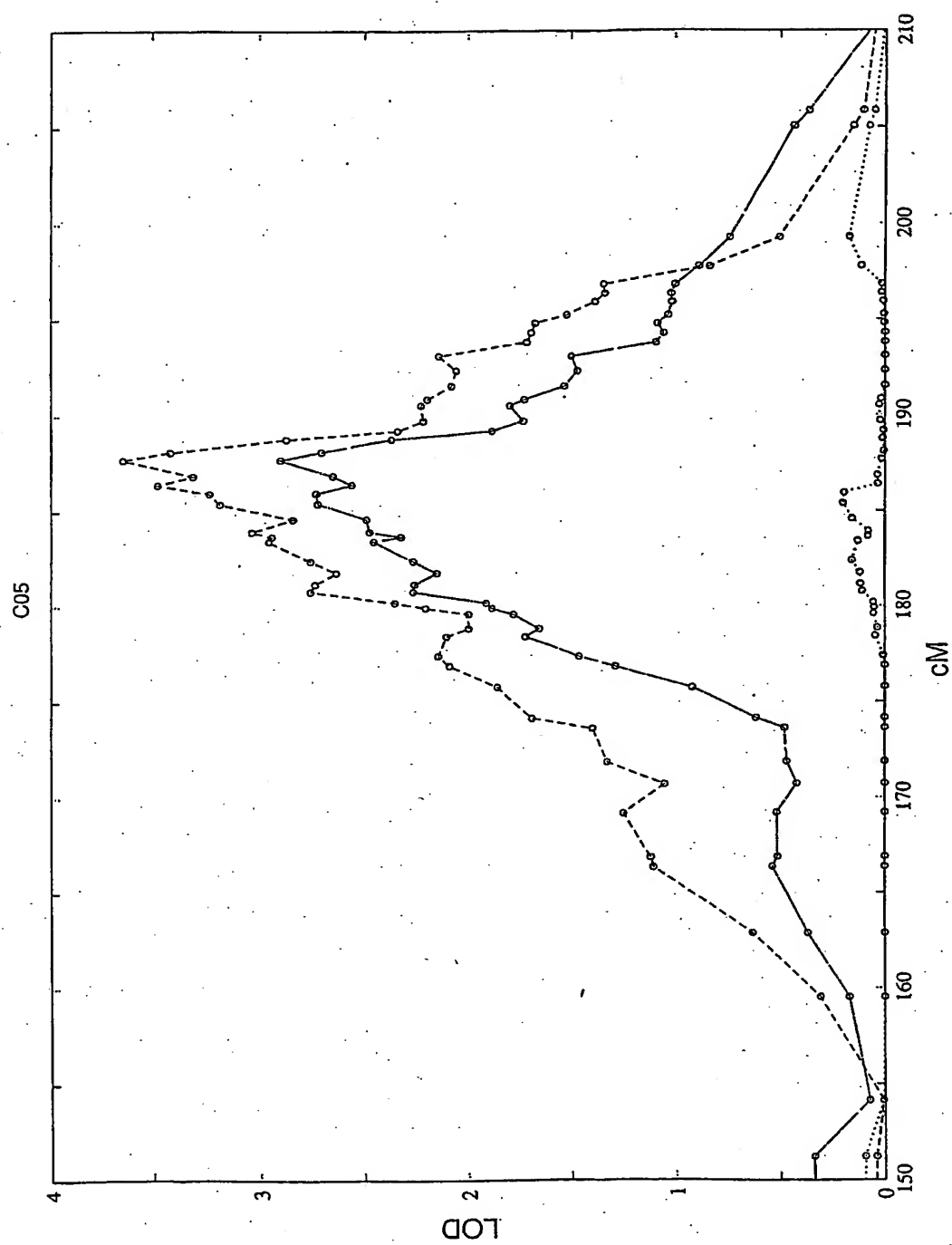


FIG. 5

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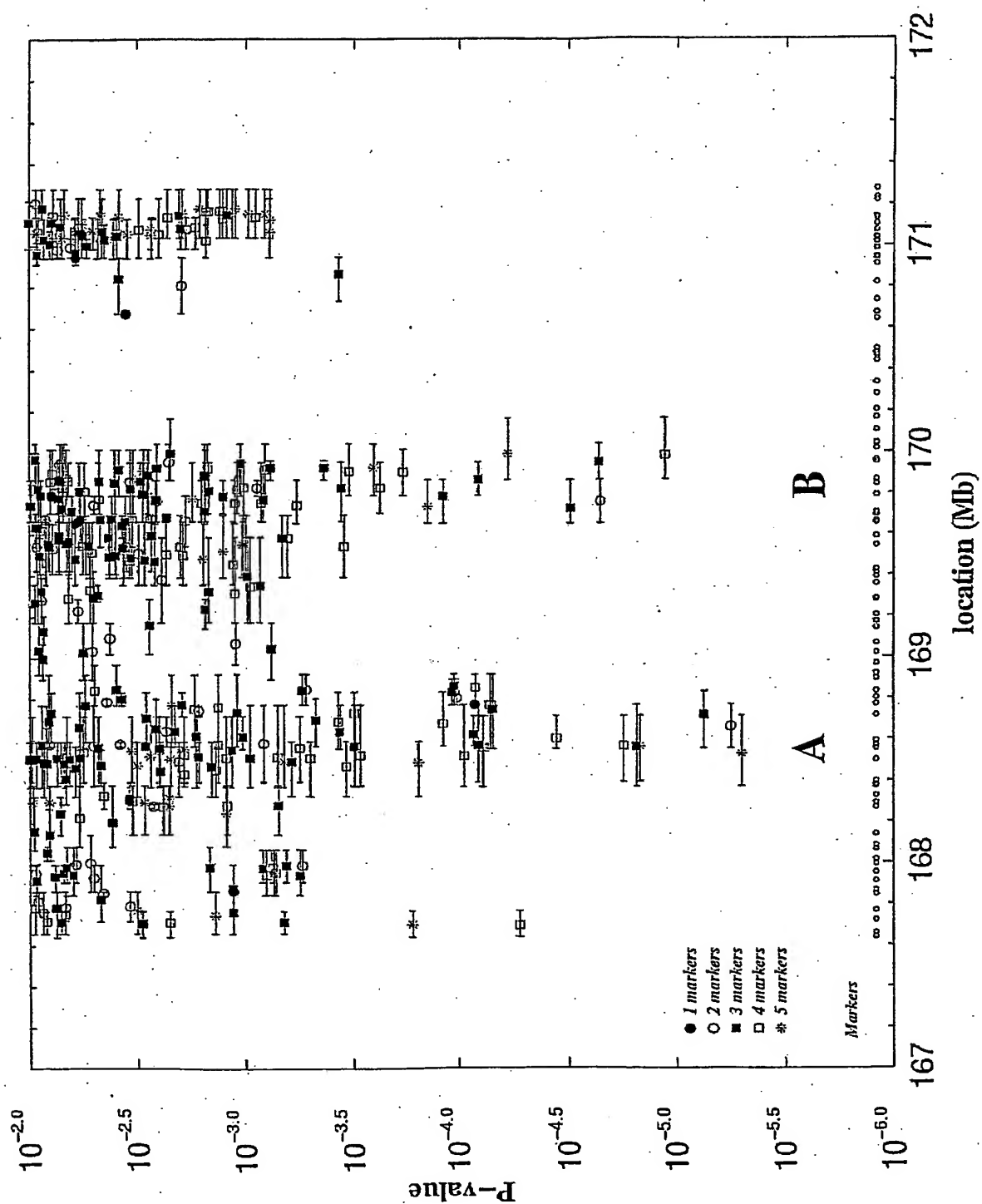


FIG. 6

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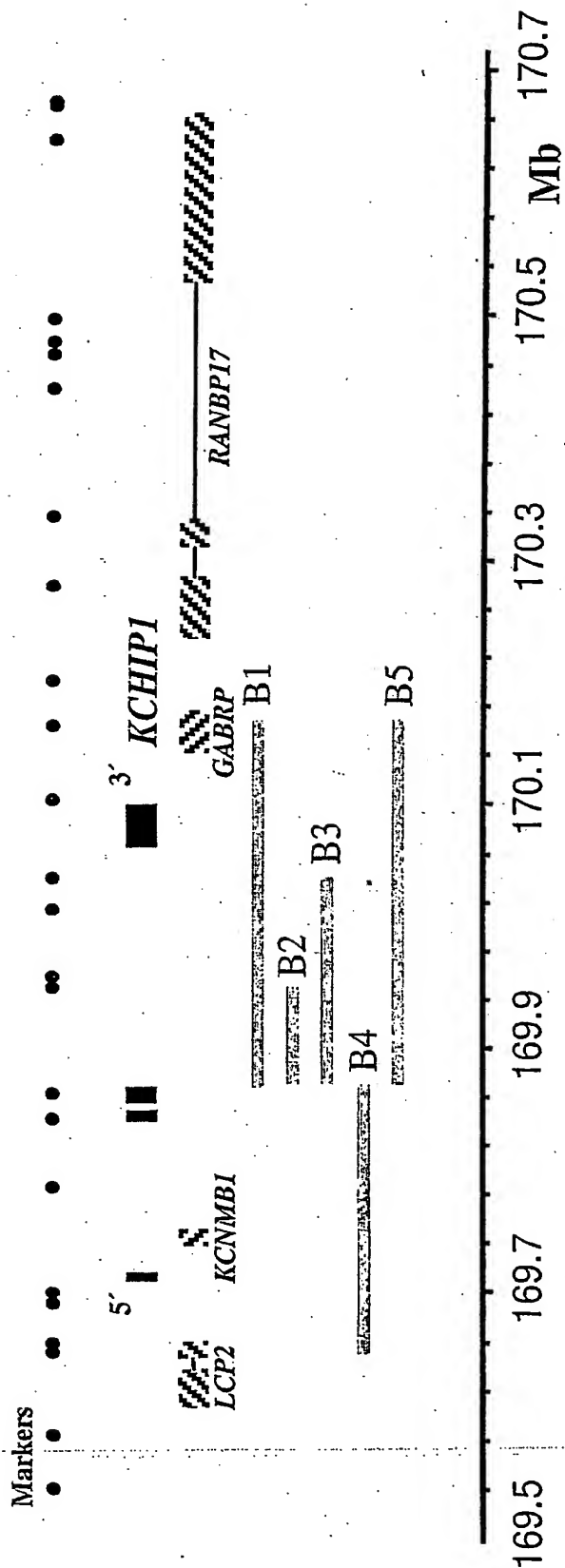


FIG. 7

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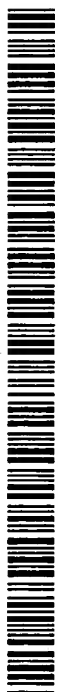
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ance Notes on Codes and Abbreviations" appearing at the begin-  
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(54) Title: HUMAN TYPE II DIABETES GENE-Kv CHANNEL-INTERACTING PROTEIN (KChIP1) LOCATED ON CHRO-  
MOSOME 5

(57) Abstract: Association of Type II diabetes and a locus on chromosome 5 is disclosed. In particular, the gene KChIP 1 within  
this locus is shown by linkage analysis to be a susceptibility gene for Type II diabetes. Pathway targeting for drug delivery and  
diagnosis applications in identifying those who have Type II diabetes or are at risk of developing Type II diabetes, in particular those  
that are non-obese are described.



WO 2004/041193 A3

## INTERNATIONAL SEARCH REPORT

International application

PCT/US03/4681

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07H 21/04; C12Q 1/70; C12P 19/34  
US CL : 435/6, 91.1; 536/23.4, 24.1

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 91.1; 536/23.4, 24.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)  
STN, East

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A, T	KROESE, M. Genetic Tests and Their Evaluation: Can We Answer the Key Questions? Genetics in Medicine. Nov/Dec 2004, vol. 6, pp475-480	
A, T	LUCENTINI, J. Gene Association Studies Typically Wrong. The Scientist; Dec. 2004, Vol. 18, page 20	1-3
A, T	PAGE G. P. Are We There Yet? Deciding When One Has Demonstrated Specific Genetic Causation in Complex Diseases and Quantitative Traits. Am. J. Hum. Genet., 2003, vol. 73, pp. 711-719	1-3
A	US 6,361,971 B1 (RHODES et al.) 26 March 2002 (26.03.2002)	1-3
Y, P	VAN HOORICK, D. Differential Modulation of Kv4 Kinetics by KChI P1 Splice Variants. Molecular and Cellular Neuroscience, 2003, vol. 24, pp. 357-66.	1-3
Y, P	REYNISDOTTIR, I. Localization of a Susceptibility Gene for Type 2 Diabetes to Chromosome 5q34-q35.2 Am. J. Hum. Gen. 2003 vol. 73, pages 323-335	1-3
A, P	MARTIN L.J. A Quantitative Trait Locus Influencing Type 2 Diabetes Susceptibility Maps to a Region on 5q in an Extended French Family. Diabetes, Dec. 2002, vol. 51, pages 3568-	1-3
A	LINDGREN C.M. Contribution of Known and Unknown Susceptibility Genes to Early-Onset Diabetes in Scandinavia. Diabetes, May 2002, vol. 51, pages 1609-1617	1-3



Further documents are listed in the continuation of Box C.



See patent family annex.

## Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

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document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&amp;"

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Form PCT/ISA/210 (second sheet) (July 1998)

# INTERNATIONAL SEARCH REPORT

PCT/US03/34681

## C. (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A, T	PEZZOLESI M.G. Examination of Candidate Chromosomal Regions for Type 2 Diabetes Reveals a Susceptibility Locus on Human Chromosome 8p23.1	1-3
A	TAKIMOTO K. Palmitoylation of KChIP Splicing Variants Is Required for Efficient Cell Surface Expression of Kv4.3 Channels. J. Biol. Chemistry, July 2002, Vol. 277, pp. 26904-26911	1-3
A	AN, W.F. Modulation of A-type Potassium Channels by a Family of Calcuim Sensors. Nautre, 3 February 2000, Vol. 403, pages 553-556	1-3

Form PCT/ISA/210 (second sheet) (July 1998)

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US03/34681

## Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:  
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.: 1-3, species SG05S96, DG00AAJIB, DG00AAJHF
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest ☐ The additional search fees were accompanied by the applicant's protest.  
☐ No protest accompanied the payment of additional search fees.

# INTERNATIONAL SEARCH REPORT

PCT/US03/34681

## BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

Group 1, claims 1-3 a method of diagnosing susceptibility to Type II diabetes by detecting polymorphism in KChIP1.

Group 2, claims 4-5, a nucleic acid molecule comprising KChIP1.

Group 3, claim 6, a method for assaying for presence of nucleic acid molecule in a sample.

Group 4, claims 7-8, a vector and host cell comprising a nucleic acid molecule.

Group 5, claim 9, a method of producing a polypeptide.

Group 6, claim 10, a method of assaying for a polypeptide.

Group 7, claims 11, 13-14, a method of identifying an agent that alters expression of KChIP1 nucleic acid.

Group 8, claims 12, 15-16, an agent that alters expression of KChIP1 nucleic acid.

Group 9, claim 17, a method of altering expression of KChIP1.

Group 10, claim 18, a method of identifying a polypeptide that interacts with KChIP1 polypeptide.

Group 11, claims 19-22, a therapeutic agent.

Group 12, claims 23-25, a method of treating a disease associated with KChIP1.

Group 13, claim 26, a transgenic animal comprising KChIP1.

Group 14, claims 27-30, a method for assaying a sample for the presence of KChIP1.

Group 15, claims 31-35, a reagent for assaying a sample for KChIP1.

Group 16, claims 36-38, the use of a nucleic acid.

Group 17, claims 39-48, a method of diagnosing susceptibility of Type II diabetes by a haplotype of one or more markers.

Group 18, claims 49-51, the use of a therapeutic agent for treatment of Type II diabetes.

Further species election:

For group 1 and 17, the species are each SNP recited in Table 13.

For group 2-6, 14-16, the species are each sequence recited in Table 10.

For group 17, the species are each sequence recited in Table 2, 5, or 13.

The first named invention which will be searched is Group 1, species rs1895301, claims 1-3.

The inventions listed as Groups 1-18 do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: the common technical features that joins all the inventions is gene KChIP1.

## INTERNATIONAL SEARCH REPORT

PCT/US03/34681

An et al (Nature, vol 403, ppp.553-556) teach the KchIP1,2, and 3 cDNA, gene expression and protein localization (see 2<sup>nd</sup> column, 3<sup>rd</sup> paragraph, page 553 and 1<sup>st</sup> column, 1<sup>st</sup> paragraph, page 554). Thus, the technical feature linking the recited groups 1-2 does not constitute a special technical feature as defined by PCT Rule 13.2, as it does not define a contribution over the prior art. Thus, there is no special technical feature that joins the methods.

The species listed above do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, the species lack the same or corresponding special technical features for the following reasons: the species do not share a significant structural element and each element does not belong to a recognized class of chemical compounds (see AI Annex B, part 1(f)). Further, these are known special technical feature in view of the prior art.